

2) INFORMATION FOR SEQ ID NO: 1053

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053

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20 CATACGGCCT ATTATACCGA GCAAGCGTTG CGTGATACCG TTGAAAAAAC      50
   CATTAAAAAC TGTTTGGATT TTGAAAGGAG ACAGGAGCAT GAATAGAATA      100
   AAAGTTGCAA TACTGTTTGG GGGTTGCTCA GAGGAGCATG ACGTATCGGT      150
   AAAATCTGCA ATAGAGATAG CCGCTAACAT TAATAAAGAA AAATACGAGC      200
   CGTTATACAT TGGAATTACG AAATCTGGTG TATGGAAAAT GTGCGAAAAA      250
25 CCTTGCGCGG AATGGGAAAA CGACAATTGC TATTCAGCTG TACTCTCGCC      300
   GGATAAAAAA ATGCACGGAT TACTTGTTAA AAAGAACCAT GAATATGAAA      350
   TCAACCATGT TGATGTAGCA TTTTCAGCTT TGCATGGCAA GTCAGGTGAA      400
   GATGGATCCA TACAAGGTCT GTTTGAATTG TCCGGTATCC CTTTGTAGG      450
   CTGCGATATT CAAAGCTCAG CAATTTGTAT GGACAAATCG TTGACATACA      500
30 TCGTTGCGAA AAATGCTGGG ATAGCTACTC CCGCCTTTTG GGTTATTAAT      550
   AAAGATGATA GGCCGGTGGC AGCTACGTTT ACCTATCCTG TTTTGTAA      600
   GCCGGCGCGT TCAGGCTCAT CCTTCGGTGT GAAAAAGTC AATAGCGCGG      650
   ACGAATTGGA CTACGCAATT GAATCGGCAA GACAATATGA CAGCAAAATC      700
   TTAATTGAGC AGGCTGTTTC GGGCTGTGAG GTCGGTTGTG CCGTATTGGG      750
35 AACAGTGCC GCGTTAGCTG TTGGCGAGGT GGACCAAATC AGGCTGCAGT      800
   ACGGAATCTT TCGTATTCAT CAGGAAGTCG AGCCGAAAAA AGGCTCTGAA      850
   AACGCAGTTA TAACCGTTCC CGCAGACCTT TCAGCAGAGG AGCGAGGACG      900
   GATACAGGAA ACGGCAAAAA AAATATATAA AGCGCTCGGC TGTAGAGGTC      950
   TAGCCCGTGT GGATATGTTT TTACAAGATA ACGGCCGCAT TGTACTGAAC      1000
40 GAAGTCAATA CTCTGCCCGG TTTCACGTCA TACAGTCGTT ATCCCCGTAT      1050
   GATGGCCGCT GCAGGTATTG CACTTCCCGA ACTGATTGAC CGCTTGATCG      1100
   TATTAGCGTT AAAGGGGTGA TAAGCATGGA AATAGGATTT ACTTTTTTAG      1150
   ATGAAATAGT ACACGGTGTT CGTTGGGACG CTAAATATGC CACTTGGGAT      1200
   AATTTCACCG GAAAACCGGT TGACGGGTAT GAAAGTAAAT CGCATTGTAG      1250
45 GGACATTCGA ATT                                     1263

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2) INFORMATION FOR SEQ ID NO: 1054

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

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(B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1054

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5  CGGCCTATTA TNCCGAGCAA GCGTTGCGTG ATACCGTTGA AAAAACCATT      50
   AAAAACTGTT TGGATTTTGA AAGGAGACAG GAGCATGAAT AGAATAAAAAG      100
   TTGCAATACT GTTTGGGGGT TGCTCAGAGG AGCATGACGT ATCGGTAAAA      150
   TCTGCAATAG AGATAGCCGC TAACATTAAT AAAGAAAAAT ACGAGCCGTT      200
   ATACATTGGA ATTACGAAAT CTGGTGTATG GAAAATGTGC GAAAAACCTT      250
10  GCGCGGAATG GGAAAACGAC AATTGCTATT CAGCTGTACT CTCGCCGGAT      300
   AAAAAAATGC ACGGATTACT TGTTAAAAAG AACCATGAAT ATGAAATCAA      350
   CCATGTTGAT GTAGCATTTT CAGCTTTGCA TGGCAAGTCA GGTGAAGATG      400
   GATCCATACA AGGTCTGTTT GAATTGTCCG GTATCCCTTT TGTAGGCTGC      450
   GATATTCAAA GCTCAGCAAT TTGTATGGAC AAATCGTTGA CATACATCGT      500
15  TGCGAAAAAT GCTGGGATAG CTACTCCCGC CTTTGGGTT ATTAATAAAG      550
   ATGATAGGCC GGTGGCAGCT ACGTTTACCT ATCCTGTTTT TGTTAAGCCG      600
   GCGCGTTCAG GCTCATCCTT CGGTGTGAAA AAAGTCAATA GCGCGGACGA      650
   ATTGGACTAC GCAATTGAAT CGGCAAGACA ATATGACAGC AAAATCTTAA      700
   TTGAGCAGGC TGTTTCGGGC TGTGAGGTCG GTTGTGCGGT ATTGGGAAAC      750
20  AGTGCCGCGT TAGTTGTTGG CGAGGTGGAC CAAATCAGGC TGCAGTACGG      800
   AATCTTTCGT ATTCATCAGG AAGTCGAGCC GGAAAAAGGC TCTGAAAACG      850
   CAGTTATAAC CGTTCCCGCA GACCTTTCAG CAGAGGAGCG AGGACGGATA      900
   CAGGAAACGG CAAAAAAAT ATATAAAGCG CTCGGCTGTA GAGGTCTAGC      950
   CCGTGTGGAT ATGTTTTTAC AAGATAACGG CCGCATTGTA CTGAACGAAG      1000
25  TCAATACTCT GCCCGGTTTC ACGTCATACA GTCGTTATCC CCGTATGATG      1050
   GCCGCTGCAG GTATTGCACT TCCCGAACTG ATTGACCGCT TGATCGTATT      1100
   AGCGTTAAAG GGGTGATAAG CATGGAAATA GGATTTACTT TTTTAGATGA      1150
   AATAGTACAC GGTGTTTCGT GGGACGCTAA ATATGCCACT TGGGATAATT      1200
   TCACCGGAAA ACCGGTTGAC GGTATAAAGT AA                          1232
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2) INFORMATION FOR SEQ ID NO: 1055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055

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50  TACCGAGCAA GCGTTGCGTG ATACCGTTGA AAAAACCATT AAAAACTGTT      50
   TGGATTTTGA AAGGAGACAG GAGCATGAAT AGAATAAAAAG TTGCAATACT      100
   GTTTGGGGGT TGCTCAGAGG AGCATGACGT ATCGGTAAAA TCTGCAATAG      150
   AGATAGCCGC TAACATTAAT AAAGAAAAAT ACGAGCCGTT ATACATTGGA      200
   ATTACGAAAT CTGGTGTATG GAAAATGTGC GAAAAACCTT GCGCGGAATG      250
   GGAAAACGAC AATTGCTATT CAGCTGTACT CTCGCCGGAT AAAAAAATGC      300
55  ACGGATTACT TGTTAAAAAG AACCATGAAT ATGAAATCAA CCATGTTGAT      350
   GTAGCATTTT CAGCTTTGCA TGGCAAGTCA GGTGAAGATG GATCCATACA      400
   AGGTCTGTTT GAATTGTCCG GTATCCCTTT TGTAGGCTGC GATATTCAAA      450
   GCTCAGCAAT TTGTATGGAC AAATCGTTGA CATACATCGT TGCGAAAAAT      500
   GCTGGGATAG CTACTCCCGC CTTTGGGTT ATTAATAAAG ATGATAGGCC      550
60  GGTGGCAGCT ACGTTTACCT ATCCTGTTTT TGTTAAGCCG GCGCGTTCAG      600

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	GCTCATCCTT	CGGTGTGAAA	AAAGTCAATA	GCGCGGACGA	ATTGGACTAC	650
	GCAATTGAAT	CGGCAAGACA	ATATGACAGC	AAAATCTTAA	TTGAGCAGGC	700
	TGTTTCGGGC	TGTGAGGTCG	GTTGTGCGGT	ATTGGGAAAC	AGTGCCGCGT	750
	TAGCTGTTGG	CGAGGTGGAC	CAAATCAGGC	TGCAGTACGG	AATCTTTCGT	800
5	ATTCATCAGG	AAGTCGAGCC	GGAAAAAGGC	TCTGAAAACG	CAGTTATAAC	850
	CGTTCCCGCA	GACCTTTCAG	CAGAGGAGCG	AGGACGGATA	CAGGAAACGG	900
	CAAAAAAAT	ATATAAAGCG	CTCGGCTGTA	GAGGTCTAGC	CCGTGTGGAT	950
	ATGTTTTTAC	AAGATAACGG	CCGCATTGTA	CTGAACGAAG	TCAATACTCT	1000
	GCCCGGTTTC	ACGTCATACA	GTCGTTATCC	CCGTATGATG	GCCGCTGCAG	1050
10	GTATTGCACT	TCCCGAACTG	ATTGACCGCT	TGATCGTATT	AGCGTTAAAG	1100
	GGGTGATAAG	CATGGAAATA	GGATTTACTT	TTTTAGATGA	AATAGTACAC	1150
	GGTGTTTCGTT	GGGACGCTAA	ATATGCCACT	TGGGATAATT	TCACCGGAAA	1200
	ACCGGTTGAC	GGTTAGAA				1218

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2) INFORMATION FOR SEQ ID NO: 1056

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1265 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R688

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056

	AATCACACCG	CATACGGCCT	ATTATACCGA	GCAAGCGTTG	CGTGATACCG	50
	TTGAAAAAAC	CATTAAAAAC	TGTTTGGATT	TTGAAAGGAG	ACAGGAGCAT	100
35	GAATAGAATA	AAAGTTGCAA	TACTGTTTGG	GGGTTGCTCA	GAGGAGCATG	150
	ACGTATCGGT	AAAATCTGCA	ATAGAGATAG	CCGCTAACAT	TAATAAAGAA	200
	AAATACGAGC	CGTTATACAT	TGGAATTACG	AAATCTGGTG	TATGGAAAAT	250
	GTGCGAAAAA	CCTTGCGCGG	AATGGGAAAA	CGACAATTGC	TATTCAGCTG	300
	TACTCTCGCC	GGATAAAAAA	ATGCACGGAT	TACTTGTTAA	AAAGAACCAT	350
40	GAATATGAAA	TCAACCATGT	TGATGTAGCA	TTTTCAGCTT	TGCATGGCAA	400
	GTCAGGTGAA	GATGGATCCA	TACAAGGTCT	GTTTGAATTG	TCCGGTATCC	450
	CTTTTGTAGG	CTGCGATATT	CAAAGCTCAG	CAATTTGTAT	GGACAAATCG	500
	TTGACATACA	TCGTTGCGAA	AAATGCTGGG	ATAGCTACTC	CCGCCTTTTG	550
	GGTTATTAAT	AAAGATGATA	GGCCGGTGGC	AGCTACGTTT	ACCTATCCTG	600
45	TTTTTGTAA	GCCGGCGCGT	TCAGGCTCAT	CCTTCGGTGT	GAAAAAAGTC	650
	AATAGCGCGG	ACGAATTGGA	CTACGCAATT	GAATCGGCAA	GACAAATATGA	700
	CAGCAAAATC	TTAATTGAGC	AGGCTGTTTC	GGGCTGTGAG	GTCGGTTGTG	750
	CGGTATTGGG	AAACAGTGCC	GCGTTAGCTG	TTGGCGAGGT	GGACCAAATC	800
	AGGCTGCAGT	ACGGAATCTT	TCGTATTCAT	CAGGAAGTCG	AGCCGAAAAA	850
50	AGGCTCTGAA	AACGCAGTTA	TAACCGTTCC	CGCAGACCTT	TCAGCAGAGG	900
	AGCGAGGACG	GATACAGGAA	ACGGCAAAAA	AAATATATAA	AGCGCTCGGC	950
	TGTAGAGGTC	TAGCCCGTGT	GGATATGTTT	TTACAAGATA	ACGGCCGCAT	1000
	TGTACTGAAC	GAAGTCAATA	CTCTGCCCGG	TTTACGTCA	TACAGTCGTT	1050
	ATCCCCGTAT	GATGGCCGCT	GCAGGTATTG	CACTTCCCGA	ACTGATTGAC	1100
55	CGCTTGATCG	TATTAGCGTT	AAAGGGGTGA	TAAGCATGGA	AATAGGATTT	1150
	ACTTTTTTAG	ATGAAATAGT	ACACGGTGTT	CGTTGGGACG	CTAAATATGC	1200
	CACTTGGGAT	AATTTACCCG	GAAAACCGGT	TGACGGTTAT	GAAGTAAATC	1250
	GCATTGTAGG	GACAT				1265

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2) INFORMATION FOR SEQ ID NO: 1057

- (i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057

	TCACACCGCA	TACGGCCTAT	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	50
	GAAGAAACCA	TTAAAAACTG	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	100
20	ATAGAATAAA	AGTTGCAATA	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	150
	GTATCGGTAA	AATCTGCAAT	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	200
	ATACGAGCCG	TTATACATTG	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	250
	GCGAAAAACC	TTGCGCGGAA	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	300
	CTCTCGCCGG	ATAAAAAAAT	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	350
25	ATATGAAATC	AACCATGTTG	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	400
	CAGGTGAAGA	TGGATCCATA	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	450
	TTTGTAGGCT	GCGATATTCA	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	500
	GACATACATC	GTTGCGAAAA	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	550
	TTATTAATAA	AGATGATAGG	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	600
30	TTTGTTAAGC	CGGCGCGTTC	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	650
	TAGCGCGGAC	GAATTGGACT	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	700
	GCAAAATCTT	AATTGAGCAG	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	750
	GTATTGGGAA	ACAGTGCCGC	GTTAGCTGTT	GGCGAGGTGG	ACCAAATCAG	800
	GCTGCAGTAC	GGAATCTTTC	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	850
35	GCTCTGAAAA	CGCAGTTATA	ACCGTTCCCC	CAGACCTTTC	AGCAGAGGAG	900
	CGAGGACGGA	TACAGGAAAC	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	950
	TAGAGGTCTA	GCCCCGTGTG	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	1000
	TACTGAACGA	AGTCAATACT	CTGCCCGGTT	TCACGTCATA	CAGTCGTTAT	1050
	CCCCGTATGA	TGGCCGCTGC	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	1100
40	CTTGATCGTA	TTAGCGTTAA	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	1150
	TTTTTTAGAT	GAAATAGTAC	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	1200
	CTTGGGATAA	TTTCACCGGA	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	1250
	ATTGTAGGGA	CATACGAAT				1269

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2) INFORMATION FOR SEQ ID NO: 1058

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 1169 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058

	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
5	ATTCTCCAGA	ATACTCAGTG	TCACTAACCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTAACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
10	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
15	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750
	TTGACGATTG	GTGCTTGTGA	TGCGATTTCT	CTTGTCGACG	GTTTTTTTGA	800
	TTTTGAAGAG	AAATACCAAT	TAATCAGCGC	CACGATCACT	GTCCCAGCAC	850
20	CATTGCCTCT	CGCGCTTGAA	TCACAGATCA	AGGAGCAGGC	ACAGCTGCTT	900
	TATCGAAACT	TGGGATTGAC	GGGTCTGGCT	CGAATCGATT	TTTTTCGTCAC	950
	CAATCAAGGA	GCGATTTATT	TAAACGAAAT	CAACACCATG	CCGGGATTTA	1000
	CTGGGCACTC	CCGCTACCCA	GCTATGATGG	CGGAAGTCGG	GTTATCCTAC	1050
	GAAATATTAG	TAGAGCAATT	GATTGCACTG	GCAGAGGAGG	ACAAACGATG	1100
25	AACACATTAC	AATTGATCAA	TAAAAACCAT	CCATTGAAAA	AAAATCAAGA	1150
	GCCCCCGCAC	TTAGTGCTA				1169

30 2) INFORMATION FOR SEQ ID NO: 1059

(i) SEQUENCE CHARACTERISTICS:

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|----|-----|----------------------|
| | (A) | LENGTH: 1166 bases |
| | (B) | TYPE: Nucleic acid |
| 35 | (C) | STRANDEDNESS: Double |
| | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

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| | (A) | ORGANISM: <i>Enterococcus gallinarum</i> |
| | (B) | STRAIN: R631 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059

45	CAAATTTTCT	TTTCTTTTCC	TAGGTACACT	GAATGTAACC	TTAAAAGAAA	50
	AAAGGAAAGG	AAGAAAATGA	TGAAAAAAT	TGCCGTTTTA	TTTGGAGGGA	100
	ATTCTCCAGA	ATACTCAGTG	TCACTAGCCT	CAGCAGCAAG	TGTGATCCAA	150
	GCTATTGACC	CGCTGAAATA	TGAAGTAATG	ACCATTGGCA	TCGCACCAAC	200
50	AATGGATTGG	TATTGGTATC	AAGGAAACCT	CGCGAATGTT	CGCAATGATA	250
	CTTGGCTAGA	AGATCACAAA	AACTGTCACC	AGCTGACTTT	TTCTAGCCAA	300
	GGATTTATAT	TAGGAGAAAA	ACGAATCGTC	CCTGATGTCC	TCTTTCCAGT	350
	CTTGCATGGG	AAGTATGGCG	AGGATGGCTG	TATCCAAGGA	CTGCTTGAAC	400
	TAATGAACCT	GCCTTATGTT	GGTTGCCATG	TCGCTGCCTC	CGCATTATGT	450
55	ATGAACAAAT	GGCTCTTGCA	TCAACTTGCT	GATACCATGG	GAATCGCTAG	500
	TGCTCCCACT	TTGCTTTTAT	CCCCTATGA	AAACGATCCT	GCCACAATCG	550
	ATCGTTTTAT	TCAAGACCAT	GGATTCCCGA	TCTTTATCAA	GCCGAATGAA	600
	GCCGGTTCTT	CAAAAGGGAT	CACAAAAGTA	ACTGACAAAA	CAGCGCTCCA	650
	ATCTGCATTA	ACGACTGCTT	TTGCTTACGG	TTCTACTGTG	TTGATCCAAA	700
60	AGGCGATAGC	GGGTATTGAA	ATTGGCTGCG	GCATCTTAGG	AAATGAGCAA	750

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      TTGACGATTG GTGCTTGTGA TGCGATTTCT CTTGTCGACG GTTTTTTTTGA      800
      TTTTGAAGAG AAATACCAAT TAATCAGCGC CACGATCACT GTCCCAGCAC      850
      CATTGCCTCT CGCGCTTGAA TCACAGATCA AGGAGCAGGC ACAGCTGCTT      900
      TATCGAAACT TGGGATTGAC GGGTCTGGCT CGAATCGATT TTTTCGTCAC      950
5    CAATCAAGGA GCGATTTATT TAAACGAAAT CAACACCATG CCGGGATTTA     1000
      CTGGGCACTC CCGCTACCCA GCTATGATGG CGGAAGTCGG GTTATCCTAC     1050
      GAAATATTAG TAGAGCAATT GATTGCACTG GCAGAGGAGG ACAAACGATG     1100
      AACACATTAC AATTGATCAA TAAAAACCAT CCATTGAAAA AAAATCAAGA     1150
      GCCCCCGCAC TTAGTG                                     1166
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2) INFORMATION FOR SEQ ID NO: 1060

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15    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1028 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Enterococcus casseliflavus
25    (B) STRAIN: ATCC 25788

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060

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      AACATGAAAA AAATCGCCTT ATTTTTGGAG GCAATTCACC GGAATACACC      50
30    GTTTCCTTAG CTTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
      CTATGACTAC GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
      GGTACTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
      TTGGATACGA AACATAAACA GAAAATACAG CCGCTATTCG AAGGAAACGG      250
      CTTTTGGCTA AGTGAAGAGC AGCAAACGTT GGTACCTGAT GTTTTATTTT      300
35    CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
      GAATTGATGA AGCTGCCTTA TGTAGGCTGC GGGGTGGCAG GTTCTGCCTT      400
      ATGTATGAAC AAATGGCTGC TGCATCAAGC TGCAGCAGCC ATTGGCGTAC      450
      AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGAACAA      500
      ATCGAAGCTT TTATCCAGAC CCATGGCTTC CCAGTTTTCT TTAAGCCTAA      550
40    TGAAGCGGGC TCCTCAAAAG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
      TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTCCGC AGTGCTCCTA      650
      CAAAAAATA TTGCCGGTGT TGAGATCGGT TGCGGTATTT TGGGCAACGA      700
      CTCTTTGACT GTCGGTGCTT GTGACGCCAT TTCATTAGTA GACGGCTTTT      750
      TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAAAT CACCGTCCCT      800
45    GCGCCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
      GCTCTATCGT AGTCTTGGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTG      900
      TCACGGAGCG AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
      TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGG TCGGCTTATC     1000
      CTATCAAGAA CTACTACAAA AACTGCTT                                     1028
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2) INFORMATION FOR SEQ ID NO: 1061

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55    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1030 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
60

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061

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10  AATATGAAAA AAATCGCCTT ATTTTGGAG GCAATTCACC GGAGTACGCC      50
    GTTTCCTTAG CCTCAGCAAC TAGCGCAATC GAAGCACTCC AATCATCTCC      100
    CGATGACTAT GACCTCTCTT TGATCGGGAT CGCCCCAGAT GCTATGGATT      150
    GGTATTTGTA TACAGGAGAA CTGGAAAACA TCCGACAAGA CACGTGGTTG      200
    TTGGATACGA AACATAAACA GAAAATCCAG CCGCTTTTGT AAGGAAACGG      250
    CTTTGGGCTA AGTGAAGAGC AACAAACGTT GGTCCTGAT GTTTTATFTC      300
15  CCATTATGCA TGGCAAATAC GGGGAAGATG GCAGTATCCA AGGATTGTTT      350
    GAATTGATGA AACTACCTTA TGTAGGCTGC GGGGTGGCAG CCTCTGCCTT      400
    ATGTATGAAC AAATGGCTGC TGCATCAAGC AGCAGAAGCG ATTGGCGTAC      450
    AAAGTGCTCC TACGATTCTC TTGACAAATC AAGCCAACCA GCAAGATCAA      500
    ATCGAAGCTT TTATCCAGAC CCATGGCTTT CCGGTTTTTT TTAAGCCTAA      550
20  TGAAGCGGGC TCCTCAAAGG GGATCACTAA AGTCACCTGC GTTGAAGAAA      600
    TCGCTTCTGC CTTAAAAGAA GCCTTTACTT ATTGTTTCTG AGTGCTCCTA      650
    CAAAAAATA TTGCCGGTGT TGAGATCGGT TCGCGTATTT TGGGCAACGA      700
    CTCTTTGACT GTCGGTGCTT GTGACGCTAT TTCATTAGTA GACGGCTTTT      750
    TCGATTTTGA AGAAAAGTAC CAGCTGATCA GCGCCAAGAT CACCGTTCCT      800
25  GCACCATTGC CTGAAACGAT TGAAACCAAG GTCAAAGAAC AAGCTCAGCT      850
    GCTCTATCGT AGTCTTTGTC TTAAAGGTCT TGCTCGCATC GACTTTTTTG      900
    TCACGGATCA AGGAGAACTA TACTTGAATG AAATCAATAC TATGCCGGGC      950
    TTTACGAGTC ACTCCCGCTA TCCTGCCATG ATGGCAGCGA TCGGCTTATC     1000
30  CTATCAAGAA CTACTACAAA AACTGCTTGT      1030

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2) INFORMATION FOR SEQ ID NO: 1062

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1031 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Enterococcus casseliflavus*
(B) STRAIN: R754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062

```

50  AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
    CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
    CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
    TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
    TGTTGGATAC GAAACATAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
    GGCTTTTGGC TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTATT      300
55  TCCCATATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
    TTGAATTGAT GAAGCTGCCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
    TTATGTATGA ACAAATGGCT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
    ACAAAGTGCT CCTACGATTC TCTTGACAAA TCAAGCCAAC CAGCAAGAAC      500
    AAATCGAAGC TTTTATCCAG ACCCATGGCT TCCCAGTTT CTTTAAGCCT      550
60  AATGAAGCGG GCTCCTCAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600

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AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC 650
 TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC 700
 GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTTCATTAG TAGACGGCTT 750
 TTTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC 800
 5 CTGCGCCATT GCCTGAAACG ATTGAAACCA AGGTCAAAGA ACAAGCTCAG 850
 CTGCTCTATC GTAGTCTTGG TCTTAAAGGT CTTGCTCGCA TCGACTTTTT 900
 TGTACGGGAG CGAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG 950
 GCTTTACGAG TCACTCCCGC TATCCTGCCA TGATGGCAGC GGTCGGCTTA 1000
 TCCTATCAAG AACTACTACA AAAACTGCTT G 1031
 10

2) INFORMATION FOR SEQ ID NO: 1063

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus casseliflavus*
 25 (B) STRAIN: R775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063

AACATGAAAA AAATCGCCAT TATTTTTGGA GGCAATTCAC CGGAATACAC 50
 30 CGTTTCTTTA GCTTCAGCAA CTAGCGCAAT CGAAGCACTC CAATCATCTC 100
 CCTATGACTA CGACCTCTCT TTGATCGGGA TCGCCCCAGA TGCTATGGAT 150
 TGGTACTTGT ATACAGGAGA ACTGGAAAAC ATCCGACAAG ACACGTGGTT 200
 GTTGGATACG AAACATAAAC AGAAAATACA GCCGCTATTT GAAGGAAACG 250
 GCTTTTGGCT AAGTGAAGAG CAGCAAACGT TAGTACCTGA TATTTTATTT 300
 35 CCCATTATGC ATGGCAAATA CGGGGAAGAT GGCAGTATCC AAGGATTGTT 350
 TGAATTGATG AACTACCTT ATGTAGGTTG CGGGGTGGCA GGTTCTGCCT 400
 TATGTATGAA CAAATGGCTG CTGCATCAAG CTGCAGCAGC CATTGGCGTA 450
 CAAAGTGCTC CTACGATTCT CTTGACAAAT CAAGCCAACC AGCAAGAACA 500
 AATCGAAGCT TTTATCCAGA CCCATGGCTT CCCAGTTTTC TTTAAGCCTA 550
 40 ATGAAGCGGG CTCTTCAAAA GGGATCACTA AAGTCACCTG CGTTGAAGAA 600
 ATCGCTTCTG CCTTAAAAAA AGCCTTTACT TATTGTTCCG CAGTGCTCCT 650
 ACAAAAAAAT ATTGCCGGTG TTGAGATCGG TTGCGGTATT TTGGGCAACG 700
 ACTCTTTGAC TGTCGGTGCT TGTGACGCCA TTTTCATTAGT AGACGGCTTT 750
 TTCGATTTTG AAGAAAAGTA CCAGCTGATC AGCGCCAAAA TCACCGTCCC 800
 45 TGCGCCATTG CCTGAAACGA TTGAAACCAA GGTCAAAGAA CAAGCTCAGC 850
 TGCTCTATCG TAGTCTTGGT CTTAAAGGTC TTGCTCGCAT CGACTTTTTT 900
 GTCACGGATC AAGGAGAACT ATACTTGAAT GAAATCAATA CTATGCCGGG 950
 CTTTACGAGT CACTCCCGTT ATCCTGCCAT GATGGCAGCG GTCGGCTTAT 1000
 CCTATCAAGA ACTACTACAA AACTGCTTG 1030
 50

2) INFORMATION FOR SEQ ID NO: 1064

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1032 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 5 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064

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10 AAACATGAAA AAAATCGCCA TTATTTTGG AGGCAATTCA CCGGAATACA      50
   CCGTTTCTTT AGCTTCAGCA ACTAGCGCAA TCGAAGCACT CCAATCATCT      100
   CCCTATGACT ACGACCTCTC TTTGATCGGG ATCGCCCCAG ATGCTATGGA      150
   TTGGTACTTG TATACAGGAG AACTGGAAAA CATCCGACAA GACACGTGGT      200
   TGTTGGATAC GAAACAGAAA CAGAAAATAC AGCCGCTATT CGAAGGAAAC      250
   GGCTTTTGGT TAAGTGAAGA GCAGCAAACG TTGGTACCTG ATGTTTTATT      300
15 TCCCATTATG CATGGCAAAT ACGGGGAAGA TGGCAGTATC CAAGGATTGT      350
   TTGAATTGAT GAAGCTACCT TATGTAGGCT GCGGGGTGGC AGGTTCTGCC      400
   TTATGTATGA ACAAATGGTT GCTGCATCAA GCTGCAGCAG CCATTGGCGT      450
   ACAAAGTGCT CCTACGATTC TCTTGACAAA TCACGCCAAC CAGCAAGAAC      500
   AAATCGAAGC TTTTATCCAG ACCCATGGCT TTCCAGTTT CTTTAAAGCCT      550
20 AATGAAGCGG GTTCCTCAA AGGGATCACT AAAGTCACCT GCGTTGAAGA      600
   AATCGCTTCT GCCTTAAAAG AAGCCTTTAC TTATTGTTCC GCAGTGCTCC      650
   TACAAAAAAA TATTGCCGGT GTTGAGATCG GTTGCGGTAT TTTGGGCAAC      700
   GACTCTTTGA CTGTCGGTGC TTGTGACGCC ATTTCATTAG TAGACGGCTT      750
   TTTCGATTTT GAAGAAAAGT ACCAGCTGAT CAGCGCCAAA ATCACCGTCC      800
25 CTGCGCCATT GCCTGAAACG ATTGAAACTA AGGTCAAAGA ACAAGCTCAG      850
   CTGCTCTATC GTAGTCTTGG ACTTAAAGGT CTTGCTCGCA TCGACTTTTT      900
   TGTCACGGAT CAAGGAGAAC TATACTTGAA TGAAATCAAT ACTATGCCGG      950
   GCTTTACGAG TCACTCCCGC TATCTGCCA TGATGGCAGC GGTCCGGTTA     1000
30 TCCTATCAAG AACTACTACA AAAACTACTT GT                          1032

```

2) INFORMATION FOR SEQ ID NO: 1065

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 45 (B) STRAIN: R758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065

```

50 AAAAACATGA AAAAAATCGC CATTATTTT GGAGGCAATT CACCGGAATA      50
   CACCGTTTCT TTAGCTTCAG CAACTAGCGC AATCGAAGCA CTCCAATCAT      100
   CTCCCTATGA CTACGACCTC TCTTTGATCG GGATCGCCCC AGATGCTATG      150
   GATTGGTACT TGTATACAGG AGAACTGGAA AACATCCGAC AAGACACGTG      200
   GTTGTGGGAT ACGAAACATA AACAGAAAAT ACAGCCGCTA TTCGAAGGAA      250
   ACGGCTTTTG GCTAAGTGAA GAGCAGCAAA CGTTGGTACC TGATGTTTTA      300
55 TTTCCCATTA TGCATGGCAA ATACGGGGAA GATGGCAGTA TCCAAGGATT      350
   GTTTGAATTG ATGAAGCTGC CTTATGTAGG CTGCGGGGTG GCAAGTTCTG      400
   CCTTATGTAT GAACAAATGG CTGCTGCATC AAGCTGCAGC AGCCATTGGC      450
   GTACAAAGTG CTCCTACGAT TCTCTTGACA AATCAAGCCA ACCAGCAAGA      500
   ACAAATCGAA GCTTTTATCC AGACCCATGG CTTTCCAGTT TTCTTTAAGC      550
60 CTAATGAAGC GGGCTCCTCA AAAGGGATCA CTAAAGTCAC CTGCGTTGAA      600

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5 GAAATCGCTT CTGCCTTAAA AGAAGCCTTT ACTTATTGTT CCGCAGTGCT 650
 CCTACAAAAA AATATTGCCG GTGTTGAGAT CGGTTGCGGT ATTTTGGGCA 700
 ACGACTCTTT GACTGTCCGT GCTTGTGACG CCATTTTCATT AGTAGACGGC 750
 TTTTTCGATT TTGAAGAAAA GTACCAGCTG ATCAGCGCCA AAATCACCGT 800
 5 CCCTGCGCCA TTGCCTGAAA CGATTGAAAC CAAGGTCAAA GAACAAGCTC 850
 AGCTGCTCTA TCGTAGTCTT GGTCTTAAAG GTCTTGCTCG CATCGACTTT 900
 TTTGTACCG ATCAAGGAGA ACTATACTTG AATGAAATCA ATACTATGCC 950
 GGGCTTTACG AGTCACTCCC GCTATCCTGC CATGATGGCA GCGGTCGGCT 1000
 TATCCTATCA AGAACTACTA CAAAACTGCT TTGT 1034
 10

2) INFORMATION FOR SEQ ID NO: 1066

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1012 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus flavescens*
 25 (B) STRAIN: R760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066

30 CATGAAAAAA ATCGCCATTA TTTTGGAGG CAATTCACCG GAATACACCG 50
 TTTCTTTAGC CTCAGCAACT AGCGCAATCG AAGCACTCCA ATCATCTCCC 100
 TATGATTACG ACCTCTCTTT GATCGGGATC GCCCCAGATG CTATGGATTG 150
 GTACTTGTAT ACAGGAGAAC TGGAAAACAT CCGACAAGAC ACGTGCTTGT 200
 TGGATACGAA ACATACACAG AAAATCCAGC CACTTTTGA AGGAAACGGC 250
 TTTTGGATAA GTGAAGCGCA GCAAACGTTG GTACCTGATG TTTTATTTCC 300
 35 CATTATGCAT GGTAATACG GGGAAGATGG CAGTATCCAA GGATTGTTTG 350
 AATTGATGAA GCTGCCTTAT GTAGGCTGTG GGGTGGCAGC CTCTGCCTTA 400
 TGTATGAACA AATGGTTATT GCATCAAGCA GCAGCAGCGA TTGGCGTACA 450
 AAGCGCTCCT ACGATTCTCT TGACAAATCA AGCCAACCAG CAAAGACAAA 500
 TCGAAGCCTT TATCCAGACC CATGGCTTTC CAGTTTTCTT TAAGCCTAAT 550
 40 GAAGCGGGCT CCTCAAAGG GATCACAAAA GTAACCTGTG TTGAAGAAAT 600
 CGCTCCTGCC TTGAAGGAAG CCTTCGCTTA TTGTTCCGCA GTGCTCTTAC 650
 AAAAAAATAT CGCTGGCGTT GAGATTGGTT GCGGTATCTT AGGCAACGAC 700
 TCTTTGACTG TCGGTGCTTG TGACGCTATT TCATTAGTAG ACGGCTTTTT 750
 CGATTTTGAA GAAAAGTACC AGTTGATCAG CGCCAAAATC ACCGTTCCCTG 800
 45 CGCCATTGCC TGAAACGATT GAAACCAAAG TCAAAGAACA AGCTCAGCTG 850
 CTCTATCACA GTCTTGGTCT TAAAGGACTT GCTCGCATCG ACTTTTTTGT 900
 CACGGATCAA GGAGAACTAT ACTTGAATGA AATCAATACT ATGCCGGGCT 950
 TTACGAGTCA CTCCCGCTAT CCTGCCATGA TGGCAGCGGT CGGCTTATCC 1000
 TATCAAGAAT TA 1012
 50

2) INFORMATION FOR SEQ ID NO: 1067

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 721 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067

```

10 CTTACGCTTT ATCGATTAGA CACGGGNAGC TTGTCCAATG GGRAGCCGAT      50
   TTTGATTTTAT GGATGAACGC TCTCATCATG CGGCAAATGG AATATCATGC      100
   AATGAAGCGC AAAATCGCAG ACGTTTGC GC TCCATCATGG AAAACAGTGG      150
   GTTTGAAGCA TATAGCCTCG AATGGTGGCA CTATGTATTA AGAGACGAAC      200
   CATACCCCAA TAGCTATTTT GATTTCCCGG TTAAATAAAC TTTTAACCGT      250
   TGCACGGACA AACTATATAA GCTAACTCTT TCGGCAGGAA ACCCGACGTA      300
15 TGTAAGTGGT TCTTAGGGAA TTTATATATA GTAGATAGTA TTGAAGATGT      350
   AAGGCAGAGC GATATTGCGG TCATTATCTG CGTGCGCTGC GGCAAGATAG      400
   CCTGATAATA AGACTGATCG CATAGAGGGG TGGTATTTCA CACCGCCCAT      450
   TGTCAACAGG CAGTTCAGCC TCGTTAAATT CAGCATGGGT ATCACTTATG      500
   AAAATTCATC TACATTGGTG ATAATAGTAA ATCCAGTAGG GCGAAATAAT      550
20 TGAAGTAAAT TTACGGGGCA AAACGGCACA ATCTCAAACG AGATTGTGCC      600
   GTTTAAGGGG AAGATTCTAG AAATATTTCA TACTTCCAAC TATATAGTTA      650
   AGGAGGAGAC TGAAAATGAA GAAGTTGTTT TTTTATTGTT TATTGTTATT      700
   CTTAATATAC TTAGGTTATT G                                     721

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25

2) INFORMATION FOR SEQ ID NO: 1068

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 668 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: R492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

```

   ATTTTAAAGG ATGAACGCTC TTCATCATGC GGCAAATGGA ATATCATGCA      50
   ATGAAGCGCA AAATCGCAGA CGTTTGCGCT CCATCATGGA AAACAGTGGG      100
45 TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC TATGTATTAA GAGACGAACC      150
   ATACCCCAAT AGCTATTTTG ATTTCCCGGT TAAATAAACT TTTAACCGTT      200
   GCACGGACAA ACTATATAAG CTAACCTCTT CGGCAGGAAA CCCGACGTAT      250
   GTAAGTGGTT CTTAGGGAAT TTATATATAG TAGATAGTAT TGAAGATGTA      300
   AGGCAGAGCG ATATTGCGGT CATTATCTGC GTGCGCTGCG GCAAGATAGC      350
50 CTGATAATAA GACTGATCGC ATAGAGGGGT GGTATTTTAC ACCGCCCATT      400
   GTCAACAGGC AGTTCAGCCT CGTTAAATTC AGCATGGGTA TCACTTATGA      450
   AAATTCATCT ACATTGGTGA TAATAGTAAA TCCAGTAGGG CGAAATAATT      500
   GACTGTAAAT TACGGGGCAA AACGGCACA TCTCAAACGA GATTGTGCCG      550
   TTTAAGGGGA AGATTCTAGA AATATTTTCA ACTTCCAAC ATATAGTTAA      600
55 GGAGGAGACT GAAAATGAAG AAGTTGTTTT TTTTATTGTT ATTGTTATTC      650
   TTAATATACT TAGGTTAT                                     668

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60 2) INFORMATION FOR SEQ ID NO: 1069

606

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069

```

15  CGGCAAGTGC CATTGATCTT ACGCTTTATC GATTAGACAC GGGTRAGCTT      50
    GTACCAATGG GAAGCCGATT TGATTTTATG GATGAACGCT CTCATCATGC      100
    GGCAAATGGA ATATCATGCA ATGAAGCGCA AAATCGCAGA CGTTTGCGCT      150
    CCATCATGGA AAACAGTGGG TTTGAAGCAT ATAGCCTCGA ATGGTGGCAC      200
20  TATGTATTAA GAGACGAACC ATACCCCAAT AGCTATTTTG ATTTCCCCGT      250
    TAAATAAACT TTAAACCGTT GCACGGACAA ACTATATAAG CTAACCTCTT      300
    CGGCAGGAAA CCCGACGTAT GTAAGTGGT CTTAGGGAAT TTATATATAG      350
    TAGATAGTAT TGAAGATGTA AGGCAGAGCG ATATTGCGGT CATTATCTGC      400
    GTGCGCTGCG GCAAGATAGC CTGATAATAA GACTGATCGC ATAGAGGGGT      450
25  GGTATTTTAC ACCGCCCATT GTCAACAGGC AGTTCAGCCT CGTTAAATTC      500
    AGCATGGGTA TCACTTATGA AAATTCATCT ACATTGGTGA TAATAGTAAA      550
    TCCAGTAGGG CGAAATAATT GACTGTAATT TACGGGGCAA AACGGCACAA      600
    TCTCAAACGA GATTGTGCCG TTTAAGGGGA AGATTCTAGA AATATTTTCAT      650
    ACTTCCAAC TATAGTTTAA GGAGGAGACT GAAAATGAAG AAGTTGTTTT      700
30  TTTTATTGTT ATTGTTATTC TTAATATACT TAGGTTATGA CTACGTAAAT      750
    GAAANCCTGA                                     760
  
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2) INFORMATION FOR SEQ ID NO: 1070

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070

```

50  AAAAGGAATA CGGGGCTTTC AAAAATCCAA GCCATAACCC GCGGGCAAGT      50
    GCCATTTGAT TCTTACGCTT TAATCGATTA GACACGGGTA AGCTTGTTACC      100
    AATGGGGAAC CGATTTGATT TTAATGNATG AACGCTCTTC ATCATGCGGC      150
    AAATGGAATA TCATGCAATG AAGCGCAAAA TCGCAGACGT TTGCGCTCCA      200
55  TCATGGAAAA CAGTGGGTTT GAAGCATATA GCCTCGAATG GTGGCACTAT      250
    GTATTAAGAG ACGAACCATA CCCCAATAGC TATTTTGATT TCCCCGTAA      300
    ATAACTTTT AACCGTTGCA CGGACAAACT ATATAAGCTA ACTCTTTCGG      350
    CAGGAAACCC GACGTATGTA ACTGGTTCTT AGGGAATTGA TATATAGTAG      400
    ATAGTATTGA AGATGTAAGG CAGAGCGATA TTGCGGTCAT TATCTGCGTG      450
60  CGCTGCGGCA AGATAGCCTG ATAATAAGAC TGATCGCATA GAGGGGTGGT      500
  
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	ATTTACACACC	GCCCATTTGTC	AACAGGCAGT	TCAGCCTCGT	TAAATTCAGC	550
	ATGGGTATCA	CTTATGAAAA	TTCATCTACA	TTGGTGATAA	TAGTAAATCC	600
	AGTAGGGCGA	AATAATTGAC	TGTAATTTAC	GGGGCAAAAC	GGCACAATCT	650
	CAAACGAGAT	TGTGCCGTTT	AAGGGGAAGA	TTCTAGAAAT	ATTTCATACT	700
5	TCCAACATA	TAGTTAAGGA	GGAGACTGAA	AATGAAGAAG	TTGTTTTTTT	750
	TTATTGTTAT	TGTTATTCTT	AATATACTTA	GGTTATGACT	ACGTTAATGA	800
	A					801

10

2) INFORMATION FOR SEQ ID NO: 1071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071

	TTGTACCAAT	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	50
	GCGGCAAATG	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	100
	CTCCATCATG	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	150
30	ACTATGTATT	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	200
	GTAAATAAAA	CTTTTAACCG	TTGCACGGAC	AACTATATA	AGCTAACTCT	250
	TTCGGCAGGA	AACCCGACGT	ATGTAAGTGG	TTCTTAGGGA	ATTTATATAT	300
	AGTAGATAGT	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	350
	GCGTGCGCTG	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	400
35	GTGGTATTTT	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	450
	TCAGCATGGG	TATCACTTAT	GAAAATTCAT	CTACATTGGT	GATAATAGTA	500
	AATCCAGTAG	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	550
	AATCTCAAAC	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	600
	ATACTTCCAA	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	650
40	TTTTTTATTG	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	700
	ATGAAGCACT	G				711

45 2) INFORMATION FOR SEQ ID NO: 1072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072

60

	GCCATTGATC	TTACGCTTTA	TCGATTAGAC	ACGGGTNAGC	TTGTACCAAT	50
	GGGGAGCCGA	TTTGATTTTA	TGGATGAACG	CTCTCATCAT	GCGGCAAATG	100
	GAATATCATG	CAATGAAGCG	CAAAATCGCA	GACGTTTGCG	CTCCATCATG	150
	GAAAACAGTG	GGTTTGAAGC	ATATAGCCTC	GAATGGTGGC	ACTATGTATT	200
5	AAGAGACGAA	CCATACCCCA	ATAGCTATTT	TGATTTCCCC	GTAAATAAAA	250
	CTTTTAACCG	TTGCACGGAC	AAACTATATA	AGCTAACTCT	TTCGGCAGGA	300
	AACCCGACGT	ATGTAAGTGG	TTCTTAGGGA	ATTTATATAT	AGTAGATAGT	350
	ATTGAAGATG	TAAGGCAGAG	CGATATTGCG	GTCATTATCT	GCGTGCGCTG	400
	CGGCAAGATA	GCCTGATAAT	AAGACTGATC	GCATAGAGGG	GTGGTATTTT	450
10	ACACCGCCCA	TTGTCAACAG	GCAGTTCAGC	CTCGTTAAAT	TCAGCATGGG	500
	TATCACTTAT	GAAAATTCAT	CTACATTGGT	GATAATAGTA	AATCCAGTAG	550
	GGCGAAATAA	TTGACTGTAA	TTTACGGGGC	AAAACGGCAC	AATCTCAAAC	600
	GAGATTGTGC	CGTTTAAGGG	GAAGATTCTA	GAAATATTTT	ATACTTCCAA	650
	CTATATAGTT	AAGGAGGAGA	CTGAAAATGA	AGAAGTTGTT	TTTTTTTATT	700
15	TTATTGTTAT	TCTTAATATA	CTTAGGTTAT	GACTACGTTA	ATGAAGCACT	750
	G					751

20 2) INFORMATION FOR SEQ ID NO: 1073

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: R689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073

35	ATTTGATTTT	ATGGATGAAC	GCTCTCATCA	TGCGGCAAAT	GGAATATCAT	50
	GCAATGAAGC	GCAAAATCGC	AGACGTTTGC	GCTCCATCAT	GGAAAACAGT	100
	GGGTTTGAAG	CATATAGCCT	CGAATGGTGG	CACTATGTAT	TAAGAGACGA	150
	ACCATACCCC	AATAGCTATT	TTGATTTCCC	CGTTAAATAA	ACTTTTAACC	200
40	GTTGCACGGA	CAAACATATAT	AAGCTAACTC	TTTCGGCAGG	AAACCCGACG	250
	TATGTAAGT	GTTCTTAGGG	AATTTATATA	TAGTAGATAG	TATTGAAGAT	300
	GTAAGGCAGA	GCGATATTGC	GGTCATTATC	TGCGTGCGCT	GCGGCAAGAT	350
	AGCCTGATAA	TAAGACTGAT	CGCATAGAGG	GGTGGTATTT	CACACCGCCC	400
	ATTGTCAACA	GGCAGTTCAG	CCTCGTTAAA	TTCAGCATGG	GTATCACTTA	450
45	TGAAAATTCA	TCTACATTGG	TGATAATAGT	AAATCCAGTA	GGGCGAAATA	500
	ATTGACTGTA	ATTTACGGGG	CAAAACGGCA	CAATCTCAA	CGAGATTGTG	550
	CCGTTTAAGG	GGAAGATTCT	AGAAATATTT	CATACTTCCA	ACTATATAGT	600
	TAAGGAGGAG	ACTGAAAATG	AAGAAGTTGT	TTTTTTTATT	GTTATTGTTA	650
	TTCTTAATAT	ACTTAGGTTA	TGACTACGTT	AATGA		685
50						

2) INFORMATION FOR SEQ ID NO: 1074

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: R690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074

```

10 ATCGATTAGA CACGGGTGAG CTTGTACCAA TGGGGAGCCG ATTTGATTTT      50
   ATGGATGAAC GCTCTCATCA TGCGGCAAAT GGAATATCAT GCAATGAAGC      100
   GCAAAATCGC AGACGTTTGC GCTCCATCAT GGAAACAGT GGGTTTGAAG      150
   CATATAGCCT CGAATGGTGG CACTATGTAT TAAGAGACGA ACCATACCCC      200
   AATAGCTATT TTGATTTCCC CGTTAAATAA ACTTTTAACC GTTGCACGGA      250
   CAAACTATAT AAGCTAACTC TTTCGGCAGG AAACCCGACG TATGTAACTG      300
15 GTTCTTAGGG AATTTATATA TAGTAGATAG TATTGAAGAT GTAAGGCAGA      350
   GCGATATTGC GGTCATTATC TGCGTGCGCT GCGGCAAGAT AGCCTGATAA      400
   TAAGACTGAT CGCATAGAGG GGTGGTATTT CACACCGCCC ATTGTCAACA      450
   GGCAGTTCAG CCTCGTTAAA TTCAGCATGG GTATCACTTA TGAAAATTCA      500
   TCTACATTGG TGATAATAGT AAATCCAGTA GGGCGAAATA ATTGACTGTA      550
20 ATTTACGGGG CAAAACGGCA CAATCTCAAA CGAGATTGTG CCGTTTAAGG      600
   GGAAGATTCT AGAAATATTT CATACTTCCA ACTATATAGT TAAGGAGGAG      650
   ACTGAAAATG AAGAAGTTGT TTTTTTTATT GTTATTGTTA TTCTTAATAT      700
   ACTTAGGTTA TGACTACGTT AATGAAGCAC TG                          732

```

25

2) INFORMATION FOR SEQ ID NO: 1075

(i) SEQUENCE CHARACTERISTICS:

```

30 (A) LENGTH: 670 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(B) STRAIN: R691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075

```

   TCTCATCATG CGGCAAATGG AATATCATGC AATGAAGCGC AAAATCGCAG      50
   ACGTTTGCGC TCCATCATGG AAAACAGTGG GTTTGAAGCA TATAGCCTCG      100
45 AATGGTGGCA CTATGTATTA AGAGACGAAC CATACCCCAA TAGCTATTTT      150
   GATTTCCCGG TTAAATAAAC TTTTAACCGT TGCACGGACA AACTATATAA      200
   GCTAACTCTT TCGGCAGGAA ACCCGACGTA TGTAAGTGGT TCTTAGGGAA      250
   TTTATATATA GTAGATAGTA TTGAAGATGT AAGGCAGAGC GATATTGCGG      300
   TCATTATCTG CGTGCGCTGC GGCAAGATAG CCTGATAATA AGACTGATCG      350
50 CATAGAGGGG TGGTATTTC AACC GCCCAT TGTCAACAGG CAGTTCAGCC      400
   TCGTTAAATT CAGCATGGGT ATCACTTATG AAAATTCATC TACATTGGTG      450
   ATAATAGTAA ATCCAGTAGG GCGAAATAAT TGACTGTAAT TTACGGGGCA      500
   AAACGGCACA ATCTCAAACG AGATTGTGCC GTTTAAGGGG AAGATTCTAG      550
   AAATATTTCA TACTTCCAAC TATATAGTTA AGGAGGAGAC TGAAAATGAA      600
55 GAAGTTGTTT TTTTATTGT TATTGTTATT CTTAATATAC TTAGGTTATG      650
   ACTACGTTAA TGAAGCACTG                          670

```

60 2) INFORMATION FOR SEQ ID NO: 1076

610

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 948 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: DG131/3 serotype OX3:H8
 (C) ACCESSION NUMBER: Z36901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076

ATGAAATAA	TAATTTT	AGTGCTAACT	TTTTTCTTTG	TTATCTTTTC	50
TGTTAATGTG	GTTGCGAAGG	AATTTACCTT	AGATTTCTCG	ACAGCAAAGA	100
CGTATGTAGA	TTCGCTGAAT	GTCATTCGCT	CTGCAATAGG	TACTCCATTA	150
CAGACTATTT	CATCAGGAGG	TACGTCTTTA	CTGATGATTG	ATAGTGGCAC	200
AGGGGATAAT	TTGTTTGCAG	TTGATGTCAG	AGGGATAGAT	CCAGAGGAAG	250
GGCGGTTTAA	TAATCTACGG	CTTATTGTTG	AACGAAATAA	TTTATATGTG	300
ACAGGATTTG	TTAACAGGAC	AAATAATGTT	TTTTATCGCT	TTGCTGATTT	350
TTCACATGTT	ACCTTTCCTG	GTACAACTGC	GGTTACATTG	TCTGGTGACA	400
GTAGCTATAC	CACGTTACAG	CGTGTTGCGG	GGATCAGTCG	TACGGGGATG	450
CAGATAAATC	GCCATTTCGT	GACTACTTCT	TATCTGGATT	TAATGTCGCA	500
TAGCGGAACC	TCACTGACGC	AGTCTGTGGC	AAGAGCGATG	TTACGGTTTG	550
TTACTGTGAC	AGCTGAAGCT	TTACGTTTTC	GGCAAATTCA	GAGGGGATTT	600
CGTACAACAC	TTGATGATCT	CAGTGGGCGT	TCTTATGTAA	TGACTGCTGA	650
AGATGTTGAT	CTTACGTTGA	ACTGGGGAAG	GTTGAGTAGT	GTCCTGCCTG	700
ACTATCATGG	ACAAGACTCT	GTTCTGTGTTG	GAAGAATTC	TTTTGGAAGT	750
GTTAATGCAA	TTCTGGGTAG	CGTGGCATT	ATACTGAATT	GTCATCATCA	800
TGCATCGCGA	GTTGCCAGAA	TTGTACCTAA	TGAGTTTCCT	TCTATGTGCC	850
CGGTAGATGG	AAGAGTGCGT	GGGATTACGC	ACAATAAAAT	ATTGTGGGAC	900
TCATCCACTC	TGGGGGCAAT	TTTGATACGC	AGGGCTATTA	GCAGTTGA	948

2) INFORMATION FOR SEQ ID NO: 1077

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1259 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: 94C serotype O48:H21
 (C) ACCESSION NUMBER: extracted from Z37725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077

CACCTGTATA	TGAAGTGTAT	ATTATTTAAA	TGGGTACTGT	GCCTGTTACT	50
GGGTTTTTCT	TCGGTATCCT	ATTCCTGGGA	GTTTACGATA	GACTTTTCGA	100
CCCAACAAAG	TTATGTCTCT	TCGTAAATA	GTATACGGAC	AGAGATATCG	150
ACCCCTCTTG	AACATATATC	TCAGGGGACC	ACATCGGTGT	CTGTTATTAA	200
CCACACCCCA	CCGGGCAGTT	ATTTTGCTGT	GCATATACGA	GGGCTTGATG	250

	TCTATCAGGC	GCGTTTTGAC	CATCTTCGGC	TGATTATTGA	GCAAAATAAT	300
	TTATATGTGG	CCGGGTTCGT	TAATACGGCA	ACAAATACTT	TCTACCGTTT	350
	TTCAGATTTT	ACACATATAT	CAGTGCCCGA	TGTGACAACG	GTTTCCATGA	400
	CAACGGACAG	CAGTTATAAC	ACTCTGCAAC	GTGTGCGCAGC	GCTGGAACGT	450
5	TCCGGAATGC	AAATCAGTCG	TCCTCACTG	GTTTCATCAT	ATCTGGCGTT	500
	AATGGAGTTC	AGTGGTAATA	CAATGACCAG	AGATGCATCC	AGAGCAGTTC	550
	TGCGTTTTGT	CACTGTCACA	GCAGAAGCCT	TACGCTTCAG	GCAGATACAG	600
	AGAGAATTTT	GTCAGGCACT	GTCTGAAACT	GCTCCTGTGT	ATACCATGAC	650
	GCCGGGAGAC	GTGGACCTCA	CTCTGAACTG	GGGGCGAATC	AGCAATGTGC	700
10	TTCCGGAGTA	TCCGGGAGAG	GATGGTGTCA	GAGTGGGGAG	AATATCCTTT	750
	AATAATATAT	CAGCGATACT	GGGTACTGTG	GCCGTTATAC	TGAATTGCCA	800
	TCATCAGGGG	GCGCGTTCTG	TTCGCGCCGT	GAATGAAGAG	AGTCAACCAG	850
	AATGTCAGAT	AACTGGCGAC	AGGCCCGTTA	TAAAAATAAA	CAATACATTA	900
	TGGGAAAGTA	ATACAGCTGC	AGCGTTTCTG	AACAGAAAGT	CACAGTTTTT	950
15	ATATACAACG	GGTAAATAAA	GGAGTTAAGT	ATGAAGAAGA	TGTTTATGGC	1000
	GGTTTTATTT	GCATTAGTTT	CTGTTAATGC	AATGGCGGCG	GATTGTGCTA	1050
	AAGGTAAAAT	TGAGTTTTTC	AAGTATAATG	AGGATGACAC	ATTTACAGTG	1100
	AAGGTTGACG	GGAAAGAATA	CTGGACCAGT	CGCTGGAATC	TGCAACCGTT	1150
	ACTGCAAAGT	GCTCAGCTGA	CAGGAATGAC	TGTCACAATC	AAATCCAGTA	1200
20	CCTGTGAATC	AGGCTCCGGA	TTTGCTGAAG	TGCAGTTTAA	TAATGACTGA	1250
	GGCATAACC					1259

25 2) INFORMATION FOR SEQ ID NO: 1078

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078

AGTTCTGCGT TTTGTCACTG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1079

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079

CGGAAGCACA TTGCTGATT

19

55

2) INFORMATION FOR SEQ ID NO: 1080

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 25 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080

10 TATAGCTACT GTCACCAGAC AATGT 25

2) INFORMATION FOR SEQ ID NO: 1081

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081

25 ATGTCAGAGG GATAGATCCA 20

2) INFORMATION FOR SEQ ID NO: 1082

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082

40 TTGARCRAAA TAATTTATAT GTG 23

45 2) INFORMATION FOR SEQ ID NO: 1083

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- 50 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083

TGATGATGRC AATTCAGTAT 20

60

2) INFORMATION FOR SEQ ID NO: 1084

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084

CCACGCCGCT TTGCTGATTT TTCACATGTT ACCGCGTGG

39

15

2) INFORMATION FOR SEQ ID NO: 1085

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085

CCACGCCACT GTCTGAAACT GCTCCTGTGC GTGG

34

30

2) INFORMATION FOR SEQ ID NO: 1086

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086

45 CTACTCCCGC CTTTGGGTT

20

50

2) INFORMATION FOR SEQ ID NO: 1087

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087

60

5 2) INFORMATION FOR SEQ ID NO: 1088

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088

TGCCGTTTCC TGTATCCGTC

20

20

2) INFORMATION FOR SEQ ID NO: 1089

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089

ATCCACACGG GCTAGACCTC

20

35

2) INFORMATION FOR SEQ ID NO: 1090

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090

AATAGCGCGG ACGAATTGGA C

21

50

2) INFORMATION FOR SEQ ID NO: 1091

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091

5 AACGCGGCAC TGTTTCCCAA

20

2) INFORMATION FOR SEQ ID NO: 1092

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092

20

TCGGCAAGAC AATATGACAG C

21

25 2) INFORMATION FOR SEQ ID NO: 1093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSsa-165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093

40

TAACGGGCGT	CTCGATAGAA	AAACACGTGA	AAATCCCAAT	GATTATAAAC	50
AATCAATATA	CGATTTTGCT	GAAGCTGTAA	CAAAAGGTAT	TAAGGAACAA	100
ACAAATAAAA	ATTAATAGGC	AACTTAACCA	GAATCGTTAA	AACTATATGA	150
CGATTCTGGT	TTTTTAAATT	CAAAAAGTTT	TCTAAAAAAT	TTACCTGCTT	200
45 TTTTAAAGTA	TAGGTATAAA	ATACAATTGA	TTAAAATAGT	AAAGGAAATG	250
AATCATGAAA	CAATTAACTA	AGCCTTTATA	CTTTTACCTA	TTACTTTTTA	300
TTACAACAAC	ACTGATTGGC	GCGTTACTAT	TATATTTGCC	AATCACAGGT	350
AAACATCCTA	TTGATTTTGT	GGACGCCCGT	T		381

50

2) INFORMATION FOR SEQ ID NO: 1094

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094

GGTAAAACAG GTACTTCTAA CTA

23

5

2) INFORMATION FOR SEQ ID NO: 1095

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095

20 CGATAGAAGC AGCAGGACAA

20

2) INFORMATION FOR SEQ ID NO: 1096

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096

CTGATGGATG CGGAAGATAC

20

40

2) INFORMATION FOR SEQ ID NO: 1097

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097

TCYTCAAAAG GGATCACWAA AGTMAC

26

55

2) INFORMATION FOR SEQ ID NO: 1098

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 23 bases

617

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098

10 TCTTCAAAAT CGAAAAAGCC GTC 23

2) INFORMATION FOR SEQ ID NO: 1099

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099

25 TCAAAAGGGA TCACWAAAGT MAC 23

2) INFORMATION FOR SEQ ID NO: 1100

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100

40 GTAAAKCCCG GCATRGTRTT GATTTC 26

2) INFORMATION FOR SEQ ID NO: 1101

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101

55 GACGGYTTTT TYGATTTTGA AGA 23

60 2) INFORMATION FOR SEQ ID NO: 1102

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102

AAAAARTCGA TKCGAGCMAG ACC

23

15

2) INFORMATION FOR SEQ ID NO: 1103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103

ATCCCGCTAT GAAAACGATC

20

30

2) INFORMATION FOR SEQ ID NO: 1104

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104

GGATCAACAC AGTAGAACCG

20

45

2) INFORMATION FOR SEQ ID NO: 1105

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105

CTCCTACGAT TCTCTTGAYA AATCA

25

2) INFORMATION FOR SEQ ID NO: 1106

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106

15

CAACCGATCT CAACACCGGC AAT

23

20 2) INFORMATION FOR SEQ ID NO: 1107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107

30

CTCATTTGAC TTCCTCCTTT GCT

23

35

2) INFORMATION FOR SEQ ID NO: 1108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108

45

GTAAGAATCG GAAAAGCGGA AGG

23

50

2) INFORMATION FOR SEQ ID NO: 1109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109

ACATCGTGAT CGCTAAAAGG AGC

23

5

2) INFORMATION FOR SEQ ID NO: 1110

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110

20 ACGAGAAAGA CAACAGGAAG ACC

23

2) INFORMATION FOR SEQ ID NO: 1111

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111

35

CTTTTCCGG CTCGWYTTCC TGATG

25

10 2) INFORMATION FOR SEQ ID NO: 1112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112

50

GGCTGYGATA TTCAAAGCTC

20

55

2) INFORMATION FOR SEQ ID NO: 1113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

50

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113

ACCGACCTCA CAGCCCGAAA

20

10

2) INFORMATION FOR SEQ ID NO: 1114

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114

TCWGAGCCTT TTTCCGGCTC G

21

25

2) INFORMATION FOR SEQ ID NO: 1115

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115

40

TTTCGGGCTG TGAGGTCGGB TGHGCG

26

2) INFORMATION FOR SEQ ID NO: 1116

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116

55

TTTCGGGCTG TGAGGTCGGB TGHGCGG

27

60

2) INFORMATION FOR SEQ ID NO: 1117

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: 94
 (C) ACCESSION NUMBER: U94526
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117

```

AAATTCGATC CGCACTACAT CGGAATTACA AAAAACGGTG TATGGAAGCT    50
ATGCAAGAAG CCATGTACGG AATGGGAAGC CGACAGTCTC CCCGCCATAC    100
TCTCCCCGGA TAGGAAAACG CATGGGCTGC TTGTCATGAA AGAAAGCGAA    150
20 TACGAAACAC GCGGTATTGA TGTGGCTTTC CCGGTTTTGC ATGGCAAATG    200
CGGGGAGGAT GGTGCGATAC AGGGGCTGTT TGTATTGTCT GGTATCCCCT    250
ATGTGGGCTG TGATATTCAA AGCTCCGCAG CTTGCATGGA CAAATCACTG    300
GCCTACATTC TTACAAAAAA TCGGGGCATC GCCGTTCCCG AATTTCAAAT    350
GATTGATAAA GGTGACAAGC CGGAGGCGGG TCGCCTTACC TACCCTGTCT    400
25 TTGTGAAGCC GGCACGGTCA GGTTCTGCTT TTGGCGTAAC CAAAGTAAAC    450
GGTACGGAAG AACTTAACGC TGCGATAGAA GCGGCAGGAC AATATGATGG    500
AAAAATCTTA ATTGAGCAAG CGATTTCCGG CTGTGAGGTC GGGTGTGCGG    550
TCATGGGGAA CGAGGATGAT TTGATTGTCT GCGAAGTGGA TCAAATCCGG    600
CTGAGCCACG GTATCTTCCG CATCCATCAG GAAAACGAGC CGGAAAAAAG    650
30 CTCAGAAAAT GCGATGATTA CAGTTCCCGC AGACATTCCG GTCGAGGAAC    700
GAAATCGGGT GCAGGAAACG GCAAAGAAAG TATATCGGGT GCTTGATGTC    750
AGAGGGCTTG CCCGTGTTGA TCTTTTTTTG CAGGAGGATG GCGGCATCGT    800
T                                                                801

```

35

2) INFORMATION FOR SEQ ID NO: 1118

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118

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TTTTCWGAGC CTTTTTCCGG CTCG    24
50

```

2) INFORMATION FOR SEQ ID NO: 1119

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119

5 TTTCGGGCTG TGAGGTCGGB TGHGC 25

2) INFORMATION FOR SEQ ID NO: 1120

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120

20

TTTCGGGCTG TGAGGTCGGB TGHG 24

25 2) INFORMATION FOR SEQ ID NO: 1121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121

TGTTTGWATT GTCYGGYATC CC 22

40

2) INFORMATION FOR SEQ ID NO: 1122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122

TGGTGCAATTG CTACGTGG 18

55

2) INFORMATION FOR SEQ ID NO: 1123

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 22 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123

10 TTTCGGGCTG TGAGGTCGGB TG 22

2) INFORMATION FOR SEQ ID NO: 1124

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124

25 GATTTGRTCC ACYTCGCCRA CA 22

2) INFORMATION FOR SEQ ID NO: 1125

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125

40 ACTCACAAC TGGATGGATG 20

2) INFORMATION FOR SEQ ID NO: 1126

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
50 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126

60 TTATGGTTGT GCTGGTTGAG G 21

2) INFORMATION FOR SEQ ID NO: 1127

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127

KCAAAYGCCA TTTCAAGTAA

20

15

2) INFORMATION FOR SEQ ID NO: 1128

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128

GACGACYTTA TKGATATACA

20

30

2) INFORMATION FOR SEQ ID NO: 1129

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129

45 ATGATGACHG AMATGATGAA AAC

23

50

2) INFORMATION FOR SEQ ID NO: 1130

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130

60

5 2) INFORMATION FOR SEQ ID NO: 1131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131

CATCTGGAGC TACRTARCCA GT

22

20

2) INFORMATION FOR SEQ ID NO: 1132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132

AGTGAAAARA TGGCTGCTGC

20

35

2) INFORMATION FOR SEQ ID NO: 1133

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133

CATCAAGAAC ACTGGCTAYG TAG

23

50

2) INFORMATION FOR SEQ ID NO: 1134

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134

5 CTAGATAGAG CTAAACCTT CCT 23

2) INFORMATION FOR SEQ ID NO: 1135

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135

20

CATTATGCAA ACGCCATTTC AAG 23

25 2) INFORMATION FOR SEQ ID NO: 1136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136

ACTTGTCCAC GTTSGATRTC T 21

40

2) INFORMATION FOR SEQ ID NO: 1137

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137

AATTAATGGC TGCWGTGAY GAA 23

55

2) INFORMATION FOR SEQ ID NO: 1138

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 1032 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*
 (C) ACCESSION NUMBER: M75132

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138

	ATGAAAAAAA	TTGCCGTTTT	ATTTGGAGGG	AATTCTCCAG	AATACTCAGT	50
	GTCACATAACC	TCAGCAGCAA	GTGTGATCCA	AGCTATTGAC	CCGCTGAAAT	100
15	ATGAAGTAAT	GACCATTGGC	ATCGCACCAA	CAATGGATTG	GTATTGGTAT	150
	CAAGGAAACC	TCGCGAATGT	TCGCAATGAT	ACTTGGCTAG	AAGATCACAA	200
	AAACTGTCAC	CAGCTGACTT	TTTCTAGCCA	AGGATTTATA	TTAGGAGAAA	250
	AACGAATCGT	CCCTGATGTC	CTCTTTCCAG	TCTTGCATGG	GAAGTATGGC	300
	GAGGATGGCT	GTATCCAAGG	ACTGCTTGAA	CTAATGAACC	TGCCTTATGT	350
20	TGGTTGCCAT	GTCGCTGCCT	CCGCATTATG	TATGAACAAA	TGGCTCTTGC	400
	ATCAACTTGC	TGATACCATG	GGAATCGCTA	GTGCTCCAC	TTTGCTTTTA	450
	TCCCGCTATG	AAAACGATCC	TGCCACAATC	GATCGTTTTA	TTCAAGACCA	500
	TGGATTCCCG	ATCTTTATCA	AGCCGAATGA	AGCCGGTTCT	TCAAAAGGGA	550
	TCACAAAAGT	AACTGACAAA	ACAGCGCTCC	AATCTGCATT	AACGACTGCT	600
25	TTTGCTTACG	GTTCTACTGT	GTTGATCCAA	AAGGCGATAG	CGGGTATTGA	650
	AATTGGCTGC	GGCATCTTAG	GAAATGAGCA	ATTGACGATT	GGTGCTTG TG	700
	ATGCGATTTT	TCTTGTCGAC	GGTTTTTTTG	ATTTTGAAGA	GAAATACCAA	750
	TTAATCAGCG	CCACGATCAC	TGTCCCAGCA	CCATTGCCTC	TCGCGCTTGA	800
	ATCACAGATC	AAGGAGCAGG	CACAGCTGCT	TTATCGAAAC	TTGGGATTGA	850
30	CGGGTCTGGC	TCGAATCGAT	TTTTTCGTCA	CCAATCAAGG	AGCGATTTAT	900
	TTAAACGAAA	TCAACACCAT	GCCGGGATTT	ACTGGGCACT	CCCCTACCC	950
	AGCTATGATG	GCGGAAGTCG	GGTTATCCTA	CGAAATATTA	G TAGAGCAAT	1000
	TGATTGCACT	GGCAGAGGAG	GACAAACGAT	GA		1032

35

2) INFORMATION FOR SEQ ID NO: 1139

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1768 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: BM4147
 50 (C) ACCESSION NUMBER: X56895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139

	GATATCGTTA	CGCTTCATGT	GCCGCTCAAT	ACGGATACGC	ACTATATTAT	50
55	CAGCCACGAA	CAAATACAGA	GAATGAAGCA	AGGAGCATTT	CTTATCAATA	100
	CTGGGCGCGG	TCCACTTGTA	GATACCTATG	AGTTGGTTAA	AGCATTAGAA	150
	AACGGGAAAC	TGGGCGGTGC	CGCATTGGAT	GTATTGGAAG	GAGAGGAAGA	200
	GTTTTTCTAC	TCTGATTGCA	CCCAAAAACC	AATTGATAAT	CAATTTTAC	250
	TTAAACTTCA	AAGAATGCCT	AACGTGATAA	TCACACCGCA	TACGGCCTAT	300
60	TATACCGAGC	AAGCGTTGCG	TGATACCGTT	GAAAAACCA	TTAAAACTG	350

	TTTGGATTTT	GAAAGGAGAC	AGGAGCATGA	ATAGAATAAA	AGTTGCAATA	400
	CTGTTTGGGG	GTTGCTCAGA	GGAGCATGAC	GTATCGGTAA	AATCTGCAAT	450
	AGAGATAGCC	GCTAACATTA	ATAAAGAAAA	ATACGAGCCG	TTATACATTG	500
	GAATTACGAA	ATCTGGTGTA	TGGAAAATGT	GCGAAAAACC	TTGCGCGGAA	550
5	TGGGAAAACG	ACAATTGCTA	TTCAGCTGTA	CTCTCGCCGG	ATAAAAAAAT	600
	GCACGGATTA	CTTGTTAAAA	AGAACCATGA	ATATGAAATC	AACCATGTTG	650
	ATGTAGCATT	TTCAGCTTTG	CATGGCAAGT	CAGGTGAAGA	TGGATCCATA	700
	CAAGGTCTGT	TTGAATTGTC	CGGTATCCCT	TTTGTAGGCT	GCGATATTCA	750
	AAGCTCAGCA	ATTTGTATGG	ACAAATCGTT	GACATACATC	GTTGCGAAAA	800
10	ATGCTGGGAT	AGCTACTCCC	GCCTTTTGGG	TTATTAATAA	AGATGATAGG	850
	CCGGTGGCAG	CTACGTTTAC	CTATCCTGTT	TTTGTTAAGC	CGGCGCGTTC	900
	AGGCTCATCC	TTCGGTGTGA	AAAAAGTCAA	TAGCGCGGAC	GAATTGGACT	950
	ACGCAATTGA	ATCGGCAAGA	CAATATGACA	GCAAAATCTT	AATTGAGCAG	1000
	GCTGTTTCGG	GCTGTGAGGT	CGGTTGTGCG	GTATTGGGAA	ACAGTGCCGC	1050
15	GTTAGTTGTT	GGCGAGGTGG	ACCAAATCAG	GCTGCAGTAC	GGAATCTTTC	1100
	GTATTCATCA	GGAAGTCGAG	CCGGAAAAAG	GCTCTGAAAA	CGCAGTTATA	1150
	ACCGTTCCCG	CAGACCTTTC	AGCAGAGGAG	CGAGGACGGA	TACAGGAAAC	1200
	GGCAAAAAAA	ATATATAAAG	CGCTCGGCTG	TAGAGGTCTA	GCCCGTGTGG	1250
	ATATGTTTTT	ACAAGATAAC	GGCCGCATTG	TACTGAACGA	AGTCAATACT	1300
20	CTGCCCCGGT	TCACGTCATA	CAGTCGTTAT	CCCCGTATGA	TGGCCGCTGC	1350
	AGGTATTGCA	CTTCCCGAAC	TGATTGACCG	CTTGATCGTA	TTAGCGTTAA	1400
	AGGGGTGATA	AGCATGGAAA	TAGGATTTAC	TTTTTTAGAT	GAAATAGTAC	1450
	ACGGTGTTTC	TTGGGACGCT	AAATATGCCA	CTTGGGATAA	TTTCACCGGA	1500
	AAACCGGTTG	ACGGTTATGA	AGTAAATCGC	ATTGTAGGGA	CATACGAGTT	1550
25	GGCTGAATCG	CTTTTGAAGG	CAAAAGAACT	GGCTGCTACC	CAAGGGTACG	1600
	GATTGCTTCT	ATGGGACGGT	TACCGTCCTA	AGCGTGCTGT	AAACTGTTTT	1650
	ATGCAATGGG	CTGCACAGCC	GGAAAATAAC	CTGACAAAGG	AAAGTTATTA	1700
	TCCCAATATT	GACCGAACTG	AGATGATTTT	AAAAGGATAC	GTGGCTTCAA	1750
	AATCAAGCCA	TAGCCGCG				1768
30						

2) INFORMATION FOR SEQ ID NO: 1140

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1086 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus casseliflavus*
- 45 (C) ACCESSION NUMBER: L29638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140

	GTAAGAATCG	GAAAAGCGGA	AGGAAGAAAA	ACATGAAAAA	AATCGCCATT	50
50	ATTTTGGAG	GCAATTCACC	GGAATACACC	GTTTCTTTAG	CTTCAGCAAC	100
	TAGCGCAATC	GAAGCACTCC	AATCATCTCC	CTATGACTAC	GACCTCTCTT	150
	TGATCGGGAT	CGCCCCAGAT	GCTATGGATT	GGTACTTGTA	TACAGGAGAA	200
	CTGGAAAACA	TCCGACAAGA	CACGTGGTTG	TTGGATACGA	AACATAAACA	250
	GAAAATACAG	CCGCTATTCC	AAGGAAACGG	CTTTTGGCTA	AGTGAAGAGC	300
55	AGCAAACGTT	GGTACCTGAT	GTTTTATTTT	CCATTATGCA	TGGCAAATAC	350
	GGGGAAGATG	GCAGTATCCA	AGGATTGTTT	GAATTGATGA	AGCTGCCTTA	400
	TGTAGGCTGC	GGGGTGGCAG	GTTCTGCCTT	ATGTATGAAC	AAATGGCTGC	450
	TGCATCAAGC	TGCAGCAGCC	ATTGGCGTAC	AAAGTGCTCC	TACGATTCTC	500
	TTGACAAATC	AAGCCAACCA	GCAAGAACAA	ATCGAAGCTT	TTATCCAGAC	550
60	CCATGGCTTC	CCAGTTTTCT	TTAAGCCTAA	TGAAGCGGGC	TCCTCAAAAG	600

	GGATCACTAA	AGTCACCTGC	GTTGAAGAAA	TCGCTTCTGC	CTTAAAAGAA	650
	GCCTTTACTT	ATTGTTCCGC	AGTGCTCCTA	CAAAAAAATA	TTGCCGGTGT	700
	TGAGATCGGT	TGCGGTATTT	TGGGCAACGA	CTCTTTGACT	GTCGGTGCTT	750
	GTGACGCCAT	TTCATTAGTA	GACGGCTTTT	TCGATTTTGA	AGAAAAGTAC	800
5	CAGCTGATCA	GCGCCAAAAT	CACCGTCCCT	GCGCCATTGC	CTGAAACGAT	850
	TGAAACCAAG	GTCAAAGAAC	AAGCTCAGCT	GCTCTATCGT	AGTCTTGGTC	900
	TTAAAGGTCT	TGCTCGCATC	GACTTTTTTG	TCACGGAGCG	AGGAGAACTA	950
	TACTTGAATG	AAATCAATAC	TATGCCGGGC	TTTACGAGTC	ACTCCCGCTA	1000
	TCCTGCCATG	ATGGCAGCGG	TCGGCTTATC	CTATCAAGAA	CTACTACAAA	1050
10	AACTGCTTGT	CTTAGCAAAG	GAGGAAGTCA	AATGAG		1086

2) INFORMATION FOR SEQ ID NO: 1141

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3946 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4147
- (C) ACCESSION NUMBER: extracted from M97297

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141

30	ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
	TGCATTCCAT	GCTCTTTCGC	CTCGCTTTGG	CGTTATGGCA	ACGATAATTA	100
	ACGCCAACGT	GTCGGAATCC	AACGCCAAAT	CCGCGCCTTT	CAATCAATGT	150
	ATCAGTGTGG	GACATAAATC	AGAGATTTCC	GCCTCTATTC	TTCTTGCGCT	200
	GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
35	ATATAGATAC	AACTGCTGCT	AAGAGAATGG	GCATCACTGT	CGACAATGTG	300
	GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTCTTAT	350
	GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
	TCAGGTTGGA	CAGCGACCGT	GGCAAGGTAC	TCAGCGACAT	GACAGTTGGT	450
	GTGGTGGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
40	ATTTGGATGT	AAAGTGTTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
	ACTATGTACC	GTTTGATGAG	TTGCTGCAAA	ATAGCGATAT	CGTTACGCTT	600
	CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
	ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
	TTGTAGATAC	CTATGAGTTG	GTAAAGCAT	TAGAAAACGG	GAAACTGGGC	750
45	GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
	TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
	TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
	TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAAG	950
	GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
50	TCAGAGGAGC	ATGACGTATC	GGTAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
	CATTAATAAA	GAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
	GTGTATGGAA	AATGTGCGAA	AAACCTTGCG	CGGAATGGGA	AAACGACAAT	1150
	TGCTATTTCAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
	TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
55	CTTTGCATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTTGAA	1300
	TTGTCCGGTA	TCCCTTTTGT	AGGCTGCGAT	ATTCAAAGCT	CAGCAATTTG	1350
	TATGGACAAA	TCGTTGACAT	ACATCGTTGC	GAAAAATGCT	GGGATAGCTA	1400
	CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
	TTTACCTATC	CTGTTTTTGT	TAAGCCGGCG	CGTTCAGGCT	CATCCTTCGG	1500
60	TGTGAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550

	CAAGACAATA	TGACAGCAAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
	GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCGCGTTAG	TTGTTGGCGA	1650
	GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCGTATT	CATCAGGAAG	1700
	TCGAGCCGGA	AAAAGGCTCT	GAAAACGCAG	TTATAACCGT	TCCCGCAGAC	1750
5	CTTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
	TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCC	TGTGGATATG	TTTTTACAAG	1850
	ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
	TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
	CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTTAAAGGGG	TGATAAGCAT	2000
10	GGAAATAGGA	TTTACTTTTT	TAGATGAAAT	AGTACACGGT	GTTTCGTTGGG	2050
	ACGCTAAATA	TGCCACTTGG	GATAATTTCA	CCGAAAACC	GGTTGACGGT	2100
	TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
	GAAGGCAAAA	GAAGTGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
	ACGGTTACCG	TCCTAAGCGT	GCTGTAAACT	GTTTTATGCA	ATGGGCTGCA	2250
15	CAGCCGGAAA	ATAACCTGAC	AAAGGAAAGT	TATTATCCCA	ATATTGACCG	2300
	AACTGAGATG	ATTTCAAAAG	GATACGTGGC	TTCAAAATCA	AGCCATAGCC	2350
	GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
	GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
	GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
20	CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
	TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTTG	ATTTCCCCCGT	2600
	TAAATAAACT	TTTAACCGTT	GCACGGACAA	ACTATATAAG	CTAACTCTTT	2650
	CGGCAGGAAA	CCCACGTAT	GTAAGTGGT	CTTAGGGAAT	TTATATATAG	2700
	TAGATAGTAT	TGAAGATGTA	AGGCAGAGCG	ATATTGCGGT	CATTATCTGC	2750
25	GTGCGCTGCG	GCAAGATAGC	CTGATAATAA	GACTGATCGC	ATAGAGGGGT	2800
	GGTATTTTAC	ACCGCCCAT	GTCAACAGGC	AGTTCAGCCT	CGTTAAATTC	2850
	AGCATGGGTA	TCACCTTATG	AAATTCATCT	ACATTGGTGA	TAATAGTAAA	2900
	TCCAGTAGGG	CGAAATAATT	GACTGTAATT	TACGGGGCAA	AACGGCACAA	2950
	TCTCAAACGA	GATTGTGCCG	TTTAAGGGGA	AGATTCTAGA	AATATTTTCT	3000
30	ACTTCCAAC	ATATAGTTAA	GGAGGAGACT	GAAAATGAAG	AAGTTGTTTT	3050
	TTTTATTGTT	ATTGTTATTC	TTAATATACT	TAGGTTATGA	CTACGTTAAT	3100
	GAAGCACTGT	TTTCTCAGGA	AAAAGTCGAA	TTTCAAAATT	ATGATCAAAA	3150
	TCCCAAAGAA	CATTTAGAAA	ATAGTGGGAC	TTCTGAAAAT	ACCCAAGAGA	3200
	AAACAATTAC	AGAAGAACAG	GTTTATCAAG	GAAATCTGCT	ATTAATCAAT	3250
35	AGTAAATATC	CTGTTTCGCCA	AGAAAGTGTG	AAGTCAGATA	TCGTGAATTT	3300
	ATCTAAACAT	GACGAATTAA	TAAATGGATA	CGGGTTGCTT	GATAGTAATA	3350
	TTTATATGTC	AAAAGAAATA	GCACAAAAAT	TTTCAGAGAT	GGTCAATGAT	3400
	GCTGTAAAGG	GTGGCGTTAG	TCATTTTATT	ATTAATAGTG	GCTATCGAGA	3450
	CTTTGATGAG	CAAAGTGTGC	TTTACCAAGA	AATGGGGGCT	GAGTATGCCT	3500
40	TACCAGCAGG	TTATAGTGAG	CATAATTCAG	GTTTATCACT	AGATGTAGGA	3550
	TCAAGCTTGA	CGAAAATGGA	ACGAGCCCCCT	GAAGGAAAGT	GGATAGAAGA	3600
	AAATGCTTGG	AAATACGGGT	TCATTTTACG	TTATCCAGAG	GACAAAACAG	3650
	AGTTAACAGG	AATTCAATAT	GAACCATGGC	ATATTCGCTA	TGTTGGTTTA	3700
	CCACATAGTG	CGATTATGAA	AGAAAAGAAT	TTCGTTCTCG	AGGAATATAT	3750
45	GGATTACCTA	AAAGAAGAAA	AAACCATTTC	TGTTAGTGTA	AATGGGGAAA	3800
	AATATGAGAT	CTTTTATTAT	CCTGTTACTA	AAAATACCAC	CATTATCATG	3850
	CCGACTAATC	TTCGTTATGA	GATATCAGGA	AACAATATAG	ACGGTGTAAT	3900
	TGTGACAGTG	TTTCCCGGAT	CAACACATAC	TAATTCAGG	AGGTAA	3946

50

2) INFORMATION FOR SEQ ID NO: 1142

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- 60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142

GATCCTCTAA ATGATTCTCA GGTGG

25

5

2) INFORMATION FOR SEQ ID NO: 1143

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143

20 CAATTAGCTT AGCAATAGGT GTTGG

25

2) INFORMATION FOR SEQ ID NO: 1144

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144

35

TGTYTTCCAA GGTTCACTC

20

40 2) INFORMATION FOR SEQ ID NO: 1145

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145

AACATATTKG GTTGATAGGT

20

55

2) INFORMATION FOR SEQ ID NO: 1146

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146

GGGATTACCT ATGCCAATAT GAT

23

10

2) INFORMATION FOR SEQ ID NO: 1147

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147

AGCTGTGTTA GCVCGAACAT CTTG

24

25

2) INFORMATION FOR SEQ ID NO: 1148

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148

40

GACTTTGTTT GCGTGATAT

20

2) INFORMATION FOR SEQ ID NO: 1149

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149

55

TCCYACWATT TCTTTTGWG

20

60 2) INFORMATION FOR SEQ ID NO: 1150

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150

TGATAATCAC ACCGCATACG

20

15

2) INFORMATION FOR SEQ ID NO: 1151

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151

TGCTGTCATA TTGTCTTGCC

20

30

2) INFORMATION FOR SEQ ID NO: 1152

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152

ATAAAGATGA TAGGCCGGTG

20

45

2) INFORMATION FOR SEQ ID NO: 1153

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153

CTCGTATGTC CCTACAATGC

20

60

2) INFORMATION FOR SEQ ID NO: 1154

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154

15

GTTTGAAGCA TATAGCCTCG

20

20 2) INFORMATION FOR SEQ ID NO: 1155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155

30

CAGTGCTTCA TTAACGTAGT C

21

35

2) INFORMATION FOR SEQ ID NO: 1156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156

GTTGAAATGC ATCACGAACA ATT

23

50

2) INFORMATION FOR SEQ ID NO: 1157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157

AAGAACGTTT CAGTTAAGGA AAT

23

5

2) INFORMATION FOR SEQ ID NO: 1158

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158

20 AAGAGGTAAT GTCTGTGGT

19

2) INFORMATION FOR SEQ ID NO: 1159

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159

35

TGAAGGTTTG CCAGGTGA

18

40 2) INFORMATION FOR SEQ ID NO: 1160

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1160

CGTTTCTGTT AAAGAAATTA GAAG

24

55

2) INFORMATION FOR SEQ ID NO: 1161

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

60

(B) TYPE: Nucleic acid

637

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161

TCCAGGTGAT AACGTTGG

18

10

2) INFORMATION FOR SEQ ID NO: 1162

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162

CAAGTCCGTG GAAATGCA

18

25

2) INFORMATION FOR SEQ ID NO: 1163

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1163

40

GTTGGTTTCA ACGTTAAGAA C

21

2) INFORMATION FOR SEQ ID NO: 1164

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164

55

GGTTTCAACG TCAAGAAC

18

60 2) INFORMATION FOR SEQ ID NO: 1165

638

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165

GGTTTCAACG TGAAGAAC

18

15

2) INFORMATION FOR SEQ ID NO: 1166

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166

ACGTTAAGAA TGTTTCTGTC AA

22

30

2) INFORMATION FOR SEQ ID NO: 1167

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167

GTTGGTTTCA ACGT

14

45

2) INFORMATION FOR SEQ ID NO: 1168

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168

60 GAACAATTGG TTGAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1169

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2160 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 10 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: SP-665
 (C) ACCESSION NUMBER: AF139883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169

20 ATGAACAAAC CAACGATTCT GCGCCTAATC AAGTATCTGA GCATTAGCTT 50
 CTTAAGCTTG GTTATCGCAG CCATTGTCTT AGGCGGAGGA GTTTTTTTCT 100
 ACTACGTTAG CAAGGCTCCT AGCCTATCCG AGAGTAAACT AGTTGCAACA 150
 ACTTCTAGTA AAATCTACGA CAATAAAAT CAACTCATTG CTGACTTGGG 200
 25 TTCTGAACGC CGCGTCAATG CCCAAGCTAA TGATATTCCC ACAGATTGG 250
 TTAAGGCAAT CGTTTCTATC GAAGACCATC GCTTCTTCGA CCACAGGGGG 300
 ATTGATTCCA TCCGTATCCT GGGAGCTTTC TTGCGCAATC TGCAAAGTAA 350
 TTCCCTCCAA GGTGGATCAA CTCTCACCCA ACAGTTGATT AAGTTGACTT 400
 ACTTTTCAAC CTCGACTTCC GACCAGACTA TTTCTCGTAA GGCTCAGGAA 450
 30 GCTTG GTTAG CGATT CAGTT AGAACAAAA GCAACCAAAC AGGAAATCTT 500
 GACCTACTAT ATAAATAAGG TCTACATGTC TAATGGCAAC TATGGAATGC 550
 AGACAGCAGC TCAAACTAC TATGGTAAAG ACCTCAATAA TTTAAGTTTA 600
 CCTCAGTTAG CTTGCTGGC TGGAATGCCT CAGGCACCAA ACCAATATGA 650
 CCCCTATTCA CATCCAGAAG CAGCCCAAGA CCGCCGAAAC TTGGTCTTAT 700
 35 CTGAAATGAA AAATCAAGGT TACATCTCTG CTGAACAGTA TGAGAAAGCA 750
 GTCAATACAC CAATTACTGA TGGACTACAA AGTCTCAAAT CAGCAAGTAA 800
 TTACCCTGCT TACATGGATA ATTACCTCAA GGAGGTCATC AATCAAGTAG 850
 AACAGAAGAC TGGCTATAAC CTTCTAACTA CTGGGATGGA TGTTTACACA 900
 AATGTAGACC AAGAAGCTCA AAAACATCTG TGGGATATCT ACAACTCCGA 950
 40 TCAATACGTC TCTTACCCTG ACGATGATTT GCAAGTCGCA TCTACGGTCG 1000
 TAGATGTTTC AAATGGTAAA GTCATCGCCC AACTTGGAGC TCGTCACCAA 1050
 GCAAGTAACG TTTCAATTTG TACCAACCAA GCTGTGGAAA CCAATCGTGA 1100
 CTGGGGTTCT GCTATGAAAC CAATCACCGA TTATGCACCT GCCATAGAAT 1150
 ACGGTGTTTA TGATTCCACT GCAACTATGG TTAATGATAT TCCTTATAAC 1200
 45 TATCCGGGAA CAAGCACACC TGTCTACAAC TGGGATAGAG CATATTTCCG 1250
 TAATATTACT CTGCAATATG CTCTTCAACA ATCACGAAAT GTCACAGCCG 1300
 TTGAGACTTT GAATAAGGTC GGTCTAGATA GAGCTAAAC CTTCTTAAT 1350
 GGTCTTGGTA TCGACTATCC AAGCATGCAT TATGCAAACG CCATTTCAAG 1400
 TAATACAACA GAATCTAATA AACAAACCG AGCAAGTAGT GAAAAAATGG 1450
 50 CTGCTGCTTA TGCTGCCTTT GCAAATGGTG GCACTTACTA TAAACCAATG 1500
 TATATCCATA AAGTCGTCTT CAGTGATGGA AGTAAAAAAG AGTTCTCTAA 1550
 TGTCGGAACG CGTGCCATGA AGGAAACGAC AGCCTATATG ATGACCGACA 1600
 TGATGAAAAC AGTCTTGACT TATGGAACG GCGTGGAGC CTATCTTCCT 1650
 TGGCTTCCTC AAGCTGGTAA AACAGGAACC TCTAACTATA CAGATGAGGA 1700
 55 AGTTGAAAAC CACATCAAGA AACTGGCTA TGTAAGCTCCA GATGAAATGT 1750
 TTGTTGGTTA TACTCGTAAG TATTCTATGG CTGTATGGAC AGGTTATTCG 1800
 AATCGTTTAA CTCCTATCGT TGGAGATGGT TTCCTAGTTG CAGCTAAAGT 1850
 TTATCGCTCA ATGATAACGT ATCTATCAGA AGATACTCAT CCAGAAGACT 1900
 GGACGATGCC AGACGGACTT TTCAGAAACG GGAATTTGT ATTCAAAAAT 1950
 60 GGAGCTCGCC CAATATGGAC TGAACCCTCT ACTCAACAAT CCTCAACAGC 2000

TGAAAGTTCA AGCTCATCAT CAGATAGTTC AACTTCACAG TCTAGCTCAA 2050
CCACTCCAAG CACAAATAAT AGTACGACTA CCAATCCTAA CAATAATACG 2100
CAACAATCAA ATACAACCCC TGATCAACAA AATCAGAATC CTCAACCAGC 2150
ACAACCATAA 2160

5

2) INFORMATION FOR SEQ ID NO: 1170

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170

20 ACGAATTGGA CTACGCAATT

20

2) INFORMATION FOR SEQ ID NO: 1171

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171

35

ACGAGGATGA TTTGATTGTC

20

40 2) INFORMATION FOR SEQ ID NO: 1172

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1560 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: 64147
(C) ACCESSION NUMBER: X13136

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172

GATCCTCTAA ATGATTCTCA GGTGGCTGTT ATTGCCTCTA TTTCAAAGGA 50
GATGCCTGGC ATTAGTATTT CTACTTCTTG GGATAGAAAG GTTTTGGAAA 100
CTTCCCTTTC TTCTATAGTT GGGAGTGTAT CCAGTGAAAA AGCTGGTCTC 150
60 CCAGCGGAAG AAGCAGAAGC CTATCTTAAA AAAGGCTATT CTCTAAATGA 200

	CCGTGTAGGA	ACCTCCTATT	TGGAAAAGCA	ATATGAAGAG	ACCTTACAAG	250
	GAAAACGCTC	GGTAAAAGAA	ATCCATCTGG	ACAAATATGG	CAACATGGAA	300
	AGCGTGGATA	CAATTGAGGA	AGGTAGTAAG	GGAAACAATA	TCAAGCTGAC	350
	CATTGATTTG	GCCTTCCAAG	ATAGCGTGGA	TGCTTTGCTG	AAAAGTTATT	400
5	TCAATTCAGA	GTTGGGAAAT	GGTGGAGCCA	AGTATTCTGA	AGGTGTCTAT	450
	GCAGTCGCCC	TTAACCCAAA	AACAGGTGCT	GTTTTGTCTA	TGTCAGGAAT	500
	TAAACATGAC	TTGAAAACAG	GAGAGTTGAC	GCCGGATTCC	TTGGGAACGG	550
	TAACCAATGT	CTTTGTCCCA	GGTTCGGTTG	TCAAAGCAGC	GACCATCAGC	600
	TCTGGTTGGG	AAAATGGAGT	CTTGTCAGGA	AATCAGACCT	TGACAGACCA	650
10	GTCCATTGTC	TTTCAAGGTT	CAGCTCCAAT	TAATTCTTGG	TATCCTGCCT	700
	TTTCTAGACC	AATGCCGATT	ACGGCGGTTC	AGGCTCTAGA	GTATTCATCC	750
	AATGCTTATA	TGGTCCAAAC	AGCCCTAGGT	CTTATGGGGC	AGACCTATCA	800
	ACCCAATATG	TTTGTGCGCA	CCAGCAATCT	AGAGTCTGCT	ATGGGGAAAT	850
	TGCGTTCAAC	CTTTGGTGAA	TATGGTTTGG	GTTCTGCGAC	CGGAATTGAC	900
15	CTACCAGATG	AATCTACTGG	ATTTGTTCCC	AAAGAGTATA	GCTTTGCTAA	950
	TTTCATTACC	AATGCCTTTG	GGCAGTTTGA	TAACTATACG	CCGATGCAGT	1000
	TGGCTCAGTA	TGTAGCAACT	ATTGCAAATG	ATGGTGTTTCG	TGTGGCTCCT	1050
	CGTATTGTTG	AAGGCATTTA	TGTAATAAT	GATAAGGGAG	GACTGGGTGA	1100
	CTTGATTTCAG	CAACTGCAAC	CGACAGAGAT	GAATAAGGTC	AATATATCCG	1150
20	ACTCCGATAT	GAGCATCTTG	CACCAAGGTT	TTTATCAGGT	TGCCCATGGT	1200
	ACTAGTGAAT	TGACAACCTG	ACGTGCCTTT	TCAAATGGCG	CCTTGGTATC	1250
	CATTAGCGGA	AAAACAGGTA	CAGCCGAAAG	CTATGTGGCA	GATGGTCAGC	1300
	AAGCAACCAA	TACCAATGCG	GTGGCCTATG	CCCCATCTGA	TAATCCCCAA	1350
	ATCGCTGTAG	CTGTTGTCTT	CCCTCATAAC	ACCAACCTTA	CAAATGGTGT	1400
25	CGGACCTTCC	ATTGCGCGCG	ATATTATCAA	CCTCTATAAC	CAACATCATC	1450
	CAATGAATTA	GAAAGGAACA	TATGCTTTAT	CCAACACCTA	TTGCTAAGCT	1500
	AATTGACAGT	TATTCGAAGT	TACCGGGTAT	CGGGATTAAG	ACGGCTACCC	1550
	GTTTGGCCTT					1560

30

2) INFORMATION FOR SEQ ID NO: 1173

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- 45 (C) ACCESSION NUMBER: Z49096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173

	GAGTCCCGAT	TGCTGAGGAT	GCAACCTCCT	ATAATGTCTA	TGCGGTCATT	50
50	GATGAGAACT	ATAAGTCAGC	AACGGGTAAG	ATTCTTTACG	TAGAAAAAAC	100
	ACAATTTAAC	AAGGTTGCAG	AGGTCTTTCA	TAAGTATCTG	GACATGGAAG	150
	AATCCTATGT	AAGAGAGCAA	CTCTCGCAAC	CTAATCTCAA	GCAAGTTTCC	200
	TTTGGAGCAA	AGGGAAATGG	GATTACCTAT	GCCAATATGA	TGACTATCAA	250
	AAAAGAGTTG	GAAACTGCAG	AGGTCAAGGG	GATTGATTTT	ACAACCAGTC	300
55	CCAATCGTAG	TTATCCAAAC	GGACAATTTG	CTTCTAGTTT	TATCGGTCTA	350
	GCTCAGCTCC	ATGAAAATGA	AGATGGCAGC	AAGAGCTTGC	TGGGAAC TTC	400
	TGGAATGGAG	AGTTCCTTGA	ACAGTATTCT	TGCAGGGACA	GACGGCATT A	450
	TTACCTATGA	AAAGGATCGT	CTGGGCAATA	TTGTACCCGG	AACAGA ACTG	500
	GTATCGCAAC	AAACTGTGGA	TGGCAAGGAT	GTTTATACAA	CATTGTCTAG	550
60	TCCGCTACAA	TCTTTCATGG	AAACTCAGAT	GGATGCCTTT	CTAGAAAAAG	600

	TAAAAGGTAA	GTATATGACC	GCGACCTTGG	TCAGTGCAAA	GACCGGTGAA	650
	ATTCTCGCTA	CCACCCAACG	ACCTACCTTT	AATGCAGATA	CTAAAGAAGG	700
	AATCACTGAG	GACCTTTGTTT	GGCGTGATAT	TCTTTATCAA	AGTAACTATG	750
	AACCAGGATC	AGCCTTTAAG	GTCATGATGT	TAGCTTCTTC	TATTGATAAT	800
5	AATACCTTCC	CAAGTGGAGA	ATACTTCAAT	AGCAGTGAAT	TCAAAATAGC	850
	GGATGCGACG	ACTCGAGATT	GGGATGTTAA	TGAGGGTTTG	ACTACTGGTG	900
	GGATGATGAC	TTTCTCACAA	GGTTTCGCTC	ACTCCAGTAA	TGTTGGAACG	950
	AGTCTACTTG	AACAAAAAAT	GGGAGATGCT	ACTTG GTTG	ATTATCTAAA	1000
	ACGCTTTAAA	TTTGGGGTTC	CAACTCGCTT	TGGCTTGACA	GATGAATACG	1050
10	CTGGTCAACT	TCCAGCTGAT	AATATTGTTA	GTATTGCTCA	AAGCTCATTT	1100
	GGGCAAGGAA	TTTCAGTGAC	ACAAACACAA	ATGCTTCGTG	CCTTTACAGC	1150
	TATTGCTAAT	GATGGAGTTA	TGCTGGAGCC	AAAATTTATA	AGTGCTATTT	1200
	ATGATACTAA	CAATCAGTCT	GTACGTAAGT	CACAAAAAGA	AATAGTAGGA	1250
	AATCCTGTTT	CCAAAGAGGC	AGCAAGCACA	ACTCGAAATC	ACATGATCTT	1300
15	AGTTGGGACG	GACCCTCTAT	ATGGAACAT	GTATAATCAC	TACACAGGAA	1350
	AGCCAATTAT	AACAGTTCCT	GGACAAAATG	TAGCAGTTAA	ATCCGGTACG	1400
	GCTCAAATCG	CTGATGAGAA	AAATGGAGGA	TACTTG GTTG	GTTCTACCAA	1450
	TTATATTTTC	TCAGTTGTGA	CTATGAATCC	TGCTGAAAAT	CCTGATTTTA	1500
	TCTTGATATG	AACGGTTCAA	CAGCCTGAGC	ATTATTCAGG	TATCCAGTTG	1550
20	GGAGAATTTG	CCACCCCAAT	CTTGGAGCGG	GCTTCAGCTA	TGAAAGAATC	1600
	TCTCAATCTT	CAATCTCCAG	CCAAAAATTT	AGATAAAGTT	ACGACAGAAT	1650
	CTTCTTATGC	AATGCCTAGC	ATCAAGGATA	TTTCACCTGG	TGAGTTGGCG	1700
	GAAGCCTTAC	GCCGAAATAT	TGTGCAACCA	ATCGTTGTAG	GTA CTGGAAC	1750
	AAAGATTAAA	GAGACTTCTG	TAGAAGAAGG	GACCAATCTT	GCACCAAACC	1800
25	AACAAGTTCT	CCTTTTATCG	GATAAGGTAG	AAGAAATTC	AGACATGTAT	1850
	AGCTGGAAAA	AAGAGACTGC	CGAGACCTTT	GCTAAATGGT	TGGATATTGA	1900
	ACTGGAATTT	GAAGGTTTCA	GTTCCGTTGT	TCAGAAGCAA	GATGTTTCGA	1950
	CTAATACAGC	TATCAAAAAC	ATTAAAAAAA	TTAAATTAAC	TTTAGGAGAC	2000
	TAATATG					2007
30						

2) INFORMATION FOR SEQ ID NO: 1174

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- 40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174

45 GAACGTGGTG AAGTTCGC

18

2) INFORMATION FOR SEQ ID NO: 1175

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175

60

5 2) INFORMATION FOR SEQ ID NO: 1176

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176

TACTGGTGTA GAAATGTTC

19

20

2) INFORMATION FOR SEQ ID NO: 1177

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177

GCTCAACAAG TTCCAGATTA

20

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2) INFORMATION FOR SEQ ID NO: 1178

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 2456 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: NCTC8325
(C) ACCESSION NUMBER: X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178

ATGAACTGAT	TATACTTAAC	ATTAAAAAAG	ATGATAACAC	CTTCTACACC	50
55 TCCATATCAC	AAAAAATTAT	AACATTATTT	TGACATAAAT	ACTACATTTG	100
TAATATACTA	CAAATGTAGT	CTTATATAAG	GAGGATATTG	ATGAAAAAGA	150
TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	GTTTGGGTATA	200
TATTTTATG	CTTCAAAGA	TAAAGAAATT	AATAATACTA	TTGATGCAAT	250
TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	TATATTTCTA	300
60 AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	AAAAATATAT	350

	AATAGTTT	AG	GC	GT	TAA	AG	TATA	AA	CATT	CAG	GAT	CG	TA	AA	AAAA	400
	AGTATCT	AAA	AA	AAAA	AA	C	GAG	TAG	AT	GC	TCA	AT	ATA	AAA	CAA	450
	ACTACGG	TAA	CATT	GAT	CG	C	AAC	GTT	CA	AT	TTA	ATTT	TGT	TAA	AGA	500
	GGTATGT	GGA	AG	TTAG	ATT	G	GG	ATC	AT	AG	C	GTC	ATT	AT	TCA	550
5	GAAAGAC	CAA	AG	CATA	CATA	T	TTG	AAA	ATTT	AAA	ATC	AG	AA	CG	TGG	600
	TTTTAG	ACCG	AA	CA	AT	GT	G	AAT	TGG	CCA	AT	AC	AG	GA	AC	650
	TTAGGC	ATCG	TT	CC	AA	AG	A	TGT	AT	CT	AAA	AA	AG	AT	TATA	700
	TAAAGA	ACTA	AG	TATTT	CTG	A	AAG	ACT	TAT	AT	CA	AC	AA	CA	AAA	750
	TTGGGT	ACAA	GAT	GAT	ACCT	T	TCG	TT	CC	ACT	TT	AAA	ACC	CGT	TAAAA	800
10	GATGAAT	ATT	TA	AGT	GATT	T	CG	AAAA	AAAA	TT	T	CAT	CT	TA	CA	850
	AACAGAA	AGT	CG	TA	ACT	ATC	CT	CT	AG	AAAA	AG	CG	ACT	TCA	CAT	900
	GTTATGT	TGG	TCCC	ATT	AAC	T	CT	G	A	GA	AT	T	AAA	AC	AAAA	950
	GGCTATA	AAAG	AT	GAT	GC	AGT	TAT	TGG	TAA	A	AAG	GG	ACT	CG	AAAA	1000
	CGATAAAA	AG	CT	CC	AA	CAT	G	AAG	AT	GG	CTA	T	CG	TG	CACA	1050
15	ATAATAG	CAA	TACA	AT	CG	CA	CATA	CAT	TAA	TAG	AG	AAAA	AAAA	AG	AT	1100
	GGCAAAG	ATA	TT	CA	ACT	AA	C	TAT	TG	AT	GC	T	AA	GT	TCAA	1150
	TAACAAC	ATG	AAAA	AT	GATT	A	AT	GG	CT	CAG	T	ACT	G	CT	ATC	1200
	CAGGTGA	ATT	ATT	AG	CACT	T	GTA	AG	CAC	AC	CT	T	CAT	AT	G	1250
	TTTATGT	ATG	GC	AT	GAG	TAA	C	G	A	GA	AT	AT	AT	TAA	CC	1300
20	AAAAAGA	ACCT	CT	G	CT	CA	ACA	AG	TT	CC	AG	AT	T	CA	CC	1350
	CTCAAAAA	AT	TTA	AC	AG	CA	A	AT	G	AT	TGG	G	T	AAA	TA	1400
	GATAAA	ACAA	G	T	T	AAAA	AT	CG	AT	GG	TAA	AA	GG	T	GG	1450
	TTGGGG	TGGT	TACA	AC	G	T	T	CA	AT	AT	G	A	AT	T	AA	1500
	ACTTAAA	ACA	AG	CA	AT	AG	AA	TC	AT	CAG	ATA	AC	AT	TTT	CTT	1550
25	GCACTCG	AAT	TAG	G	CAG	TAA	G	AA	AT	TT	G	AA	AA	AG	G	1600
	TGTTGGT	GAA	GAT	ATA	CCAA	A	G	T	G	AT	TAT	CC	AT	TTT	TATA	1650
	CAAACAAA	AAAA	TT	TAG	ATA	AT	G	AA	AT	TAT	T	AG	CT	G	AT	1700
	CAAGGTG	AAA	TAC	T	GATT	AA	CC	CAG	TAC	AG	AT	C	TTT	TCAA	TCT	1750
	ATTAGAAA	AT	AAT	GG	CAATA	T	TTA	AC	G	CACC	TCA	CT	T	TATTA	AA	1800
30	AAAACAA	AGT	TT	GGA	AG	AAA	A	AT	AT	TATTT	CC	AA	AG	AAAA	TAT	1850
	TTAAATG	ATG	GT	AT	GCA	ACA	AG	TC	G	TAA	AT	AAA	AC	ACATA	AAG	1900
	TTATAG	ATCT	TAT	G	CAAA	CT	TA	AT	TGG	CAA	AT	CC	G	G	TACT	1950
	AAATGAA	ACA	AG	G	AG	AA	AGT	G	C	AG	ACAA	TT	G	G	TGGT	2000
	GATAAAG	ATA	AT	CC	AA	CAT	G	AT	G	AT	GG	CT	AT	T	AT	2050
35	AGATAA	AGGA	AT	GG	CTAG	CT	ACA	AT	G	CCAA	AA	AT	CT	CAG	GT	2100
	ATGAGCT	TATA	TG	AG	AA	CGGT	AA	T	AAAA	AA	AT	AC	G	AT	ATAG	2150
	AACAGT	GAA	CA	AT	CC	G	TAA	CG	AT	GG	TTG	CT	T	CA	CTG	2200
	TATTAAT	AAG	TG	CT	G	T	TACT	TCT	CC	CTTAA	AT	ACA	AT	TTT	C	2250
	TTGTATG	TTG	AA	AG	TG	AC	CAC	TG	TAA	CG	AGT	CC	AT	TTT	CTT	2300
40	TTTCTT	ATTT	GTA	AT	TTT	CAG	CG	ATA	AC	G	T	CA	AT	G	TATTA	2350
	AGTTTA	ATAA	AT	TTA	AC	G	T	AT	T	TG	T	G	T	C	TGCTA	2400
	TCCGTAT	TTA	CCT	T	CTT	CTA	CC	CATA	AT	TTT	AA	AT	G	AT	ATT	2450
	GCATGC															2456

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2) INFORMATION FOR SEQ ID NO: 1179

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179

ATTGTTGAC GGGTGACTTT

60

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2) INFORMATION FOR SEQ ID NO: 1180

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180

15 TCCACCGTTG CCAATCGCA

19

2) INFORMATION FOR SEQ ID NO: 1181

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181

30 AGCAGCTTAC TAGATGCCGT

20

35 2) INFORMATION FOR SEQ ID NO: 1182

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182

AACTGCAAGA GATCCTTTGG

20

50 2) INFORMATION FOR SEQ ID NO: 1183

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2535 bases
55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 175

(C) ACCESSION NUMBER: M18729

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(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1183

	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	CAACAGTATG	TGGATATTAA	50
10	AAAGCAATAT	CCAGATGCTT	TTTTGCTCTT	TCGGATGGGT	GATTTTTTATG	100
	AATTATTTTA	TGAGGATGCG	GTCAATGCTG	CGCAGATTCT	GGAAATTTCC	150
	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	CCGATCCCTA	TGGCGGGTGT	200
	TCCCTATCAT	TCTGCCCAAC	AGTATATCGA	TGTCTTGATT	GAGCAGGGTT	250
	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	ATCCTAAACA	AGCAGTTGGG	300
15	GTTGTTAAC	GAGAGGTTGT	TCAGGTCATT	ACGCCAGGGA	CAGTGGTCGA	350
	TAGCAGTAAG	CCGGACAGTC	AGAATAATTT	TTTGGTTTCC	ATAGACCGCG	400
	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	ATTTGGTGAC	GGGTGACTTT	450
	TATGTGACAG	GTCTTTTGGA	TTTCACGCTG	GTTTGTGGGG	AAATCCGTAA	500
	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	TGACTTGTCT	GAGGAAGAAG	550
20	AACAAATCCT	CAGCCGCCAG	ATGAATCTGG	TACTCTCTTA	TGAAAAAGAA	600
	AGCTTTGAAG	ACCTTCATTT	ATTGGATTTG	CGATTGGCAA	CGGTGGAGCA	650
	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	TCATCGGACT	CAGATGAGGG	700
	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	ACGAAATTAA	GGATTTCTTG	750
	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	AGAATGCTCG	800
25	CTCAGGTAAG	AAACAAGGCA	GTCTTTTCTG	GCTTTTGGAT	GAAACCAAAA	850
	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	GGATTCATCG	CCCCTTGATT	900
	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	GTAGTGCAGG	TCTTTCTCGA	950
	CCATTTCTTT	GAGCGTAGTG	ACTTGACAGA	CAGTCTCAAG	GGTGTTTATG	1000
	ACATTGAGCG	CTTGGCTAGT	CGTGTTTCTT	TTGGCAAAAC	CAATCCAAAG	1050
30	GATCTCTTGC	AGTTGGCGAC	TACCTTGCTC	AGTGTGCCAC	GGATTCGTGC	1100
	GATTTTAGAA	GGGATGGAGC	AACCTACTCT	AGCCTATCTC	ATCGCACAAAC	1150
	TGGATGCAAT	CCCTGAGTTG	GAGAGTTTGA	TTAGCGCAGC	GATTGCTCCT	1200
	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	ATTATCCGGA	CTGGATTTGA	1250
	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	CAGAGAAGGG	ACTAGCTGGA	1300
35	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	ACTCTGGTAT	CAGCACGCTC	1350
	AAGATTGACT	ACAATAAAAA	GGATGGCTAC	TATTTTCATG	TGACCAATTC	1400
	GCAACTGGGA	AATGTGCCAG	CCCACTTTTT	CCGCAAGGCG	ACGCTGAAAA	1450
	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	CCCGTATCGA	GGGAGATATG	1500
	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	GAATACGAAA	TATTTATGCG	1550
40	CATTCGTGAA	GAGGTCGGCA	AGTACATCCA	GCGTTTACAA	GCTCTAGCCC	1600
	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	GTCTGGCGGT	TGTGGCTGAA	1650
	ACCCAGCATT	TGATTGACAC	TGAGTTTGGT	GACGATTAC	AAATTGATAT	1700
	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAAA	GGTTATGGGG	GCTCAGACCT	1750
	ATATTCCAAA	TACGATTCAG	ATGGCAGAAG	ATACCAGTAT	TCAATTGGTT	1800
45	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	TATATGCGTC	AGTTAGCCAT	1850
	GACGGCGGTT	ATGGCCCAGC	TGGGTTTCTA	TGTTCTTGCT	GAAAGCGCCC	1900
	ATTTACCGAT	TTTTGATGCG	ATTTTTACCC	GTATCGGAGC	AGCAGATGAC	1950
	TTGGTTTCGG	GTCAGTCAAC	CTTTATGGTG	GAGATGATGG	AGGCCAATAA	2000
	TGCCATTTTCG	CATGCGACCA	AGAACTCTCT	CATTCTCTTT	GATGAATTGG	2050
50	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	CTCTTGCTCA	GTCCATCATC	2100
	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	ACCTCTTTTG	CGACCCACTA	2150
	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	ACAACACTTG	GTCAATGTCC	2200
	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	TCACCTTCCT	TCACAAGATT	2250
	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	ATCCATGTTG	CCAAGATTGC	2300
55	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	GGATAAGATT	TTGACTCAGC	2350
	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	CCATGAGACA	AACTAGTGCT	2400
	GTCAGTGAAC	AGATTTCACT	CTTTGATAGG	GCAGAAGAGC	ATCCTATCCT	2450
	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	TATGACACCT	ATGCAGGTTA	2500
60	TGAATGTCTT	AGTAGAGTTA	AAACAGAAAC	TATAA		2535

2) INFORMATION FOR SEQ ID NO: 1184

- (i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-05

15 (xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1184

	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTTAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
20	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
25	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
30	AAACCAATCC	AAAGGATCTC	TTG			623

2) INFORMATION FOR SEQ ID NO: 1185

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 621 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 45 (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-06

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1185

50	TGACGGGTGA	CTTTTATGTG	ACAGGTCTTT	TGGATTTTAC	GCTGGTTTGT	50
	GGGGAAATCC	GTAACCTCAA	GGCTCGAGAA	GTGGTGTTGG	GTTATGACTT	100
	GTCTGAGGAA	GAAGAACAAA	TCCTCAGCCG	CCAGATGAAT	CTGGTACTCT	150
	CTTATGAAAA	AGAAAGCTTT	GAAGACCTTC	ATTTATTGGA	TTTGCGATTG	200
	GCAACGGTGG	AGCAAACGGC	ATCTAGTAAG	CTGCTCCAGT	ATGTTTCATCG	250
55	GACTCAGATG	AGGGAATTGA	ACCACCTCAA	ACCTGTTATC	CGATACGAAA	300
	TTAAGGATTT	CTTGCAGATG	GATTATGCGA	CCAAGGCTAG	TCTGGATTTG	350
	GTTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTC	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
60	CAGGTCTTTC	TCGACCATTT	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550

CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC T 621

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2) INFORMATION FOR SEQ ID NO: 1186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-11

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1186

TGACGGGTGA CTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCAGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350
 GTTGAGAATG CTCGCTCAGG TAAGAAACAA GGCAGTCTTT TCTGGCTTTT 400
 GGATGAAACC AAAACGGCTA TGGGGATGCG TCTCTGCGT TCTTGATTG 450
 ATCGCCCCTT GATTGATAAG GAACGAATCG TCCAACGTCA AGAAGTAGTG 500
 CAGGTCTTTC TCGACCATTT CTTTGAGCGT AGTGACTTGA CAGACAGTCT 550
 CAAGGGTGTT TATGACATTG AGCGCTTGGC TAGTCGTGTT TCTTTTGGCA 600
 AAACCAATCC AAAGGATCTC TT 622

35

2) INFORMATION FOR SEQ ID NO: 1187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-55

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1187

TGACGGGTGA CTTTATGTG ACAGGTCTTT TGGATTTCAC GCTGGTTTGT 50
 GGGGAAATCC GTAACCTCAA GGCTCGAGAA GTGGTGTTGG GTTATGACTT 100
 GTCTGAGGAA GAAGAACAAA TCCTCAGCCG CCAGATGAAT CTGGTACTCT 150
 CTTATGAAAA AGAAAGCTTT GAAGACCTTC ATTTATTGGA TTGCGATTG 200
 GCAACGGTGG AGCAAACGGC ATCTAGTAAG CTGCTCCGGT ATGTTTCATCG 250
 GACTCAGATG AGGGAATTGA ACCACCTCAA ACCTGTTATC CGCTACGAAA 300
 TTAAGGATTT CTTGCAGATG GATTATGCGA CCAAGGCTAG TCTGGATTG 350

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	GTGAGAATG	CTCGCTCAGG	TAAGAAACAA	GGCAGTCTTT	TCTGGCTTTT	400
	GGATGAAACC	AAAACGGCTA	TGGGGATGCG	TCTCTTGCGT	TCTTGGATTG	450
	ATCGCCCCTT	GATTGATAAG	GAACGAATCG	TCCAACGTCA	AGAAGTAGTG	500
	CAGGTCTTTC	TCGACCATTG	CTTTGAGCGT	AGTGACTTGA	CAGACAGTCT	550
5	CAAGGGTGTT	TATGACATTG	AGCGCTTGGC	TAGTCGTGTT	TCTTTTGGCA	600
	AAACCAATCC	AAAGGATCTC	TT			622

10 2) INFORMATION FOR SEQ ID NO: 1188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1188

25	GGGTGACTTT	TATGTAACGG	GGCTATTGGA	TTTCACGTTG	GTTTGTGGGG	50
	AAATTCGCAA	TCTCAAGGCT	AGAGAAGTGG	TGCTGGGTTA	TGACTTGTCT	100
	GAGGAAGAAG	AACAAATCCT	CAGTCGTCAG	ATGAATCTGG	TGCTTTCTTA	150
	TGAGAAGGAA	GGCTTTGAGG	ACCTTCATTT	ACTGGATCCA	CGACTGGCAG	200
30	CTGTGGAGCA	AGCGGCAGCT	AGTAAGCTCC	TCCAGTATGT	TCACCGGACC	250
	CAGATGCGGG	AATTGAACCA	CCTCAAACCA	GTTATCCGCT	ATGAAATCAA	300
	AGATTTCTTA	CAGATGGACT	ATGCGACCAA	GGCTAGTCTG	GATTTGGTTG	350
	AGAATGCCCC	TTCAGGCAAG	AAGCAAGGCA	GTCTTTTCTG	GCTTTTAGAT	400
	GAAACCAAGA	CGGCTATGGG	AATGCGTCTC	TTGCGTTCTT	GGATTCATCG	450
35	TCCTTTGATT	GATAAGGAGC	GAATCGTCCA	GCGTCAAGAG	GTGGTGCAGG	500
	TCTTTCTTGA	CCACTTCTTT	GAGCGTAGTG	ATTTAACGGA	CAGTCTTAAG	550
	GGTGTTTATG	ATATCGAACG	CTTGGCTAGT	CGGGTTTCTT	TTGGCAAGA	599

40

2) INFORMATION FOR SEQ ID NO: 1189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 49456

55 (x) SEQUENCE DESCRIPTION: SEQ ID NO: 1189

	GGTGACGGGT	GACTTTTATG	TGACAGGTCT	TTTGGATTTT	ACGCTGGTTT	50
	GTGGGGAAAT	CCGCAATCTC	AAGGCTCGAG	AAGTGGTGCT	GGGTTATGAC	100
	TTGTCTGAGG	AAGAAGAACA	GATCCTTAGT	CGTCAGATGA	ATCTGGTACT	150
60	TTCCTATGAA	AAAGAAGGCT	TTGAAGACCT	TCATTTACTG	GATTCACGAT	200

TGGCAGCTGT GGAGCAAGCG GCATCTAGTA AACTGCTTCA GTATGTTTCAT 250
 CGGACTCAGA TGAGGGAATT GAACCACCTC AAGCCTGTTA TCCGCTATGA 300
 AATCAAAGAT TTTTTCGAGA TGGATTATGC GACCAAGGCT AGTCTGGATT 350
 TGGTTGAGAA TGCCCGTTCA GGCAAGAAGC AAGGTAGTCT TTTTGGCTT 400
 5 TTGGATGAAA CCAAAACAGC TATGGGAATG CGTCTCTTGC GGTCTTGGAT 450
 TCATCGCCCC CTGATTGATA AGGAACGAAT TGTCCAACGC CAAGAAGTTG 500
 TGCAGGTCTT TCTCGACCAT TTCTTTGAGC GTAGTGATTT GACAGACAGT 550
 CTCAAGGGTG TTTATGACAT TGAGCGCTTG GCTAGTCGTG TTTCTTTTGG 600
 CAAAACCAAT CCAAAGGATC TCTT 624
 10

2) INFORMATION FOR SEQ ID NO: 1190

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 599 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus mitis*
 25 (B) STRAIN: LSPQ 2583
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190

TGACGGGTGA CTTTCAGGTG ACTAGTTTAG AGGACTTTGT CTTGGTCTGC 50
 30 GGGGAAATCC GCAATTTGAA AGCTAGGGAA GTGGTGCTGG GCTATGCCTT 100
 GCCAGAAGCT GAGGAGCAGG TTTTGGCTGG ACAGATGAAC CTTTTACTGT 150
 CCTATGTGGA GAAGGTTTTG GAGGATGTTT AGCTGCTGGG CGAGGAGCTG 200
 TCTCCTATGG AGCGTCAGGC AGCAGGGAAA CTGCTGGAGT ATGTGCACCG 250
 GACCCAGATG AGGGAGCTCA GCCATTTGAA GAAGGCTCAG CATTATGAAA 300
 35 TCAAGGACTT CCTGCAAATG GACTATGCCA CCAAGGCGAG TCTGGATTTG 350
 ACAGAAAATG CTCGCTCGGG CAAGAAGCAC GGCAGTCTTT ATTGGCTGAT 400
 GGACGAGACT AAGACGGCCA TGGGCGGCCG CATGCTGCGC TCTTGGATCC 450
 AGCGTCCGCT GATTGATGAA GCGCGAATTA GCCAGCGACA GAATGTCGTT 500
 GAGGTTTTTC TGGATCATTT CTTTGAGCGG AGTGATTTGA CGGAGAGCCT 550
 40 CAAGGGGGTC TATGATATCG AGCGGCTGGC TAGTCGGGTG TCTTTTGGC 599

2) INFORMATION FOR SEQ ID NO: 1191

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Streptococcus mitis*
 (B) STRAIN: ATCC 903
 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 1191

60 TGACGGGTGA CTTTCAGGTG ACTAGTTTAG AGGACTTTGC CCTGGTCTGC 50

	GGGGAAATCC	GTAATTTGAA	GGCTAGGGAA	GTGGTGCTGG	GCTATGCTTT	100
	GCCAGAAGCT	GAGGAGCAGG	TCTTGGCTGG	ACAGATGAAT	CTTTTGCTGT	150
	CCTATGTACA	GACGGCCTTG	GACGATGTCC	AGCTGCTGGG	CGAGGAACTG	200
	TCTCCTATGG	AGCGTCAGGC	AGCGGGGAAA	TTGCTAGAGT	ATGTGCACCG	250
5	GACCCAGATG	AGGGAGCTCA	GCCATTTGAA	GAAGGCCAG	CATTATGAAA	300
	TCAAGGACTT	TCTGCAAATG	GATTATGCTA	CCAAGGCGAG	TCTGGATTG	350
	ACAGAAAATG	CTCGCTCGGG	TAAGAAACAC	GGCAGTCTTT	ATTGGCTGAT	400
	GGACGAGACC	AAGACGGCCA	TGGGCGGCCG	TATGCTGCGC	TCTTGGATCC	450
	AGCGTCCGTT	GATTGATGAA	GTGCGAATTA	GCCAGCGGCA	GAATGTCGTC	500
10	GAGGTTTTTC	TGGAACATTT	CTTTGAGCGG	AGTGATTGTA	CGGAGAGCCT	550
	CAAGGGAGTC	TATGATATCG	AGCGGCTGGC	TAGTCGGGTG	TCTTTTGGCA	600
	AGACCAATCC	AAAGGATCTC	TT			622

15

2) INFORMATION FOR SEQ ID NO: 1192

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192

GGTAAAACAG GAACCTCTAA CT

22

30

2) INFORMATION FOR SEQ ID NO: 1193

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193

GGTAAGACAG GTACTTCTAA CT

22

45

2) INFORMATION FOR SEQ ID NO: 1194

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

55

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194

60

5 2) INFORMATION FOR SEQ ID NO: 1195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195

CATTCAAGT AACACAACAG AATC

24

20

2) INFORMATION FOR SEQ ID NO: 1196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196

GCCATTCAAGT GTAATACAAC AGAA

24

35

2) INFORMATION FOR SEQ ID NO: 1197

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197

CAAACGCCAT TTCAAGTAAT ACAAC

25

50

2) INFORMATION FOR SEQ ID NO: 1198

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 381 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 43867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198

```
10 AACGGGCGTC TCGATAGAAA AACACGTGAA AATCCCAATG ATTATAAACA      50
   ATCAATATAC GATTTTGCTG AAGCTGTAAC AAAAGGTATT AAGGAACAAA      100
   CAAATAAAAA TTAATAGGCA ACTTAACCAG AATCGTTAAA ACTATATGAC      150
   GATTCTGGTT TTTTAAATTC AAAAAGTTTT CTAAAAAATT TACTTGCTTC      200
   TTAAAGTAT  AGGTATGAAA TACAATTGAT TAAATAGTA  AAGGAAATGA      250
   ATCATGAAAC AATTAATAA  GCCTTTATAC TTTTACCTAT TACTTTTAT      300
15  TACAACAACG CTGATTGGCG CGTTACTATT ATATTGCCA ATCACAKGTA      350
   AACATCCTAT TGATTTTGTG GACGCCCGTT A                      381
```

20 2) INFORMATION FOR SEQ ID NO: 1199

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199

GTATTAAAGA AGATATCCAA AAAGC 25

35 2) INFORMATION FOR SEQ ID NO: 1200

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200

TCAAAGAAGA AACTAAAAAA GCTGT 25

50 2) INFORMATION FOR SEQ ID NO: 1201

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201

AACGTAGGTG TCCTTCTTC

19

5

2) INFORMATION FOR SEQ ID NO: 1202

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202

20 GTGTTGAAAT GTTCCGTAAA CA

22

2) INFORMATION FOR SEQ ID NO: 1203

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203

35

GGIGARMGIG GIAAYGARAT G

21

40 2) INFORMATION FOR SEQ ID NO: 1204

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

45

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1204

GCIAAYAACI TCIWMYATGC C

21

55

2) INFORMATION FOR SEQ ID NO: 1205

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

50

(B) TYPE: Nucleic acid

655

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205

AAYACITCIA WYATGCCIGT

20

10

2) INFORMATION FOR SEQ ID NO: 1206

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206

CKISRIGTIG ARTCIGCCA

19

25

2) INFORMATION FOR SEQ ID NO: 1207

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207

40

CCITCITCWC CIGGCATYTC

20

2) INFORMATION FOR SEQ ID NO: 1208

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208

55

TCAAAAAGTT TTCTAAAAAA TTTAC

25

60 2) INFORMATION FOR SEQ ID NO: 1209

656

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209

ACGGGCGTCC ACAAATCAA TAGGA

25

15

2) INFORMATION FOR SEQ ID NO: 1210

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210

ACCAGCTTGC CCAATACAAA GG

22

30

2) INFORMATION FOR SEQ ID NO: 1211

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211

ATTCTTGTA CAGGCTTTGA TCCC

24

45

2) INFORMATION FOR SEQ ID NO: 1212

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212

60 CCICCCIRGIG GIGAIACIGC WCC

23

2) INFORMATION FOR SEQ ID NO: 1213

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213

15

AARGGIGGIA CIGCIGCIAT HCCIGG

26

20 2) INFORMATION FOR SEQ ID NO: 1214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214

GGTAAAACAG GTACCTCTAA CTA

23

35

2) INFORMATION FOR SEQ ID NO: 1215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
 (B) STRAIN: D471
 (C) ACCESSION NUMBER: X65717

50

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 1215

	AACAAAATAA	AAGAACTTAC	CTATTTTCCA	TCCAAAATGT	TTAGCAATCA	50
	TCATCTGCAA	GGCAACGTAT	TGCATGGCAT	TGATGTGATG	AGCAACTAAT	100
55	ATGTCATTAG	AACGTTGCGT	CAAAC TAGCA	TCTAAATAAA	GATCGAAAATG	150
	CAGTTATCAA	AAATGCAAGC	TCCTATCGGC	CCTTGTTTTA	ATTATTACTC	200
	ACATTGCCTT	AATGTATTTA	CTTGCTTATT	ATTAACTTTT	TTGCTAAGTT	250
	AGTAGCGTCA	GTTATTTCATT	GAAAGGACAT	TATTATGAAA	ATTCTTGTA	300
	CAGGCTTTGA	TCCCTTTGGC	GGCGAAGCTA	TTAATCCTGC	CCTTGAAGCT	350
60	ATCAAGAAAT	TGCCAGCAAC	CATTTCATGA	GCAGAAATCA	AATGTATTGA	400

	AGTTCCAACG	GTTTTTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
	AAAGCTTTCA	ACCTGATGCA	GTCCTTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
	ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
	TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
5	GTAAAGCAGC	TTATTTTTC	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
	ATTCATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAATACAG	CTGGTACCTT	700
	TGTTTGCAAT	CATTTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
	GTCCAAATGC	CAAAGCTGGG	TTATGCATA	TTCCCTTTAT	GATGGAACAG	800
	GTTGTTGATA	AACCTAATAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
10	AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTTCAAA	GATCGTTCCG	900
	ATTTAAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
	TATTTTAAAA	AAACAGAGAT	ATGAATAAC	TCTGTTTTTT	TTGTGCTAAA	1000
	AATGAAAGAC	CTAGGGAAAC	TTTTTCATCG	TCTTTCTCAA	TTGTCATCTT	1050
	AATCTAATAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
15	AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAAACAT	TAAGGTCAGG	1150
	GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TAACAAAGGA	CTAATATCAT	1200
	AGGTGGCTAC	CACCTTTCCA	GAATCAGGTT	GGAGTTTGAC	AATAGTATTG	1250
	GTTTGCCAAA	TATTGGCATA	GAGATAACCA	TCTACATACT	CTAATTCGTT	1300
	AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

2) INFORMATION FOR SEQ ID NO: 1216

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216

35 GGTAAGACTG GTACATCAAA CTA 23

2) INFORMATION FOR SEQ ID NO: 1217

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217

50 CAAATGCCAT TTCAAGTAAC ACAAC 25

55 2) INFORMATION FOR SEQ ID NO: 1218

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218

CAAACGCCAT TTCAAGTAAC ACAAC

25

10

2) INFORMATION FOR SEQ ID NO: 1219

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219

CAAATGCTAT TTCAAGTAAT ACAAC

25

25

2) INFORMATION FOR SEQ ID NO: 1220

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220

CAAACGCCAT TTCAAGTAAT ACGAC

25

40

2) INFORMATION FOR SEQ ID NO: 1221

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221

55 GAYACICCG GICAYGTIGA YTT

23

60

2) INFORMATION FOR SEQ ID NO: 1222

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222
10 ATYGAYACIC CIGGICAYGT IGAYTT 26

15 2) INFORMATION FOR SEQ ID NO: 1223

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223
AYITCIARRT GIARYTCRCC CATICC 26

30 2) INFORMATION FOR SEQ ID NO: 1224

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224
CCIGYIHTIY TIGARCCAT IATG 24

45

2) INFORMATION FOR SEQ ID NO: 1225

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225
TAICCRAACA TYTCISMIAR IGGIAC 26

60

2) INFORMATION FOR SEQ ID NO: 1226

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226

15 GTIRMRTAIC CRAACATYTC

20

2) INFORMATION FOR SEQ ID NO: 1227

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227

30 GTICCIYTIK CIGARATGTT YGGITA

26

35 2) INFORMATION FOR SEQ ID NO: 1228

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228

GTICCIYTIK CIGARATGTT YGGITAYGC

29

50 2) INFORMATION FOR SEQ ID NO: 1229

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
55 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229

TCCATYTGIG CIGCICCICT IATCAT

26

5 2) INFORMATION FOR SEQ ID NO: 1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2145 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (D) ACCESSION NUMBER: X00415

(xiii) SEQUENCE DESCRIPTION: SEQ ID NO: 1230

20 TGAACGCCTA AAAGATAAAC GAGGAAACAA ATGGCTCGTA CAACACCCAT 50
 CGCACGCTAC CGTAACATCG GTATCAGTGC GCACATCGAC GCCGGTAAAA 100
 CCACTACTAC CGAACGTATT CTGTTCTACA CCGGTGTAAA CCATAAAATC 150
 GGTGAAGTTC ATGACGGCGC TGCAACCATG GACTGGATGG AGCAGGAGCA 200
 25 GGAACGTGGT ATTACCATCA CTTCCGCTGC GACTACTGCA TTCTGGTCTG 250
 GTATGGCTAA GCAGTATGAG CCGCATCGCA TCAACATCAT CGACACCCCG 300
 GGGCACGTTG ACTTCACAAT CGAAGTAGAA CGTTCCATGC GTGTTCTCGA 350
 TGGTGGCGTA ATGGTTTACT GCGCAGTTGG TGGTGTTTCA CCGCAGTCTG 400
 AAACCGTATG GCGTCAGGCA AACAAATATA AAGTTCCGCG CATTGCGTTC 450
 30 GTTAACAAAA TGGACCGCAT GGGTGCGAAC TTCCTGAAAG TTGTAAACCA 500
 GATCAAAACC CGTCTGGGCG CGAACCCGGT TCCGCTGCAG CTGGCGATTG 550
 GTGCTGAAGA ACATTTACC GGTGTTGTTG ACCTGGTGAA AATGAAAGCT 600
 ATCAACTGGA ACGACGCTGA CCAGGGCGTA ACCTTCGAAT ACGAAGATAT 650
 CCCGGCAGAC ATGGTTGAAC TGGCTAACGA ATGGCACCAG AACCTGATCG 700
 35 AATCCGCAGC TGAAGCTTCT GAAGAGCTGA TGGAAAAATA CCTGGGTGGT 750
 GAAGAACTGA CTGAAGCAGA AATCAAAGGT GCTCTGCGTC AGCGCGTTCT 800
 GAACAACGAA ATCATCCTGG TAACCTGTGG TTCTGCGTTC AAGAACAAAG 850
 GTGTTTCAGG CATGCTGGAT GCGCTAATTG ATTACCTGCC ATCCCCGGTT 900
 GACGTACCTG CGATCAACGG TATCCTGGAG GACGGTAAAG ACACTCCGGC 950
 40 TGAACGTCAC GCAAGTGATG ACGAGCCGTT CTCTGCACTG GCGTTCAAAA 1000
 TCGCTACCGA CCCGTTTGTT GGTAACCTGA CTTCTTCCG TGTTTACTCC 1050
 GGTGTGGTTA ACTCTGGTGA TACCGTACTG AACTCCGTGA AAGCTGCACG 1100
 TGAGCGTTTC GGTCTGATCG TTCAGATGCA CGCTAACAAA CGTGAAGAGA 1150
 TCAAAGAAGT TCGCGCGGGC GACATCGCTG CTGCTATCGG TCTGAAAGAC 1200
 45 GTAACCACTG GTGACACCTT GTGTGACCCG GATGCGCCGA TCATTCTGGA 1250
 ACGTATGGAA TTCCCTGAGC CGGTAATCTC CATCGCAGTT GAACCGAAAA 1300
 CCAAAGCTGA CCAGGAAAAA ATGGGTCTGG CTCTGGGCCG TCTGGCTAAA 1350
 GAAGACCCGT CTTTCCGTGT ATGGACTGAC GAAGAATCTA ACCAGACCAT 1400
 CATCGCGGGT ATGGGCGAAC TGCACCTCGA CATCATCGTT GACCGTATGA 1450
 50 AGCGTGAATT CAACGTTGAA GCGAACGTAG GTAAACCGCA GGTTGCTTAC 1500
 CGTGAAACTA TCCGCCAGAA AGTTACCGAT GTTGAAGGTA AACACGCGAA 1550
 ACAGTCTGGT GGTCGTGGTC AGTATGGTCA TGTTGTTATC GACATGTACC 1600
 CGCTGGAGCC GGGTTCAAAC CCGAAAGGCT ACGAGTTCAT CAACGACATT 1650
 AAAGGTGGTG TAATCCCTGG CGAATACATC CCGGCCGTTG ATAAAGGTAT 1700
 55 CCAGGAACAG CTGAAAGCAG GTCCGCTGGC AGGCTACCCG GTAGTAGACA 1750
 TGGGTATTCTG TCTGCACTTC GGTTCTTACC ATGACGTTGA CTCCTCTGAA 1800
 CTGGCGTTTA AACTGGCTGC TTCTATCGCC TTAAAGAAG GCTTTAAGAA 1850
 AGCGAAACCA GTTCTGCTTG AGCCGATCAT GAAGGTTGAA GTAGAAACTC 1900
 CGGAAGAGAA CACCGGTGAC GTTATCGGTG ACTTGAGCCG TCGTCGTGGT 1950
 60 ATGCTCAAAG GTCAGGAATC TGAAGTTACT GCGTTAAGA TCCACGCTGA 2000

AGTACCGCTG	TCTGAAATGT	TCGGATACGC	AACTCAGCTG	CGTTCTCTGA	2050
CCAAAGGTCG	TGCATCATAC	ACTATGGAAT	TCCTGAAGTA	TGATGAAGCG	2100
CCGAGTAACG	TTGCTCAGGC	CGTAATTGAA	GCCCGTGGTA	AATAA	2145

5

2) INFORMATION FOR SEQ ID NO: 1231

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231

20 GCGAGCCCGA AGATAAAAAA GAACCTCTGC TGCTCGC 37

2) INFORMATION FOR SEQ ID NO: 1232

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232

35 GGAGCCGCGC GATTTTATAA ATGAATGTTG ATAACCGGCT CC 42

2) INFORMATION FOR SEQ ID NO: 1233

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233

50 GCGAGCGTTA CTGGTGTAGA AATGTTCCGG CTCGC 35

55 2) INFORMATION FOR SEQ ID NO: 1234

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Single

664

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234

ACTAAATAAA CGCTCATTCG

20

10

2) INFORMATION FOR SEQ ID NO: 1235

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235

GCGAGCCGAA GTTGAAGTTG TTGGTATTGC TGGCTCGC

38

25

2) INFORMATION FOR SEQ ID NO: 1236

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236

GCGAGCCGTG GTGAAGTTGC CGTTGGTGGC TCGC

34

40

2) INFORMATION FOR SEQ ID NO: 1237

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237

55 GCGAGCCGCG AAATCGAAGT TGCTGTATTA GGGCTCGC

38

60 2) INFORMATION FOR SEQ ID NO: 1238

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238

10 GCGAGCGGCG TTAATTTTGG CACCGAAGAA GAGCTCGC 38

15 2) INFORMATION FOR SEQ ID NO: 1239

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239

GCGAGCGCAG ACCTTTCAGC AGAGGAGGCT CGC 33

30 2) INFORMATION FOR SEQ ID NO: 1240

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240

GCGAGCCGGC AAGACAATAT GACAGCAAAA TCGCTCGC 38

45

2) INFORMATION FOR SEQ ID NO: 1241

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241

60 GCGAGCGGGG AACGAGGATG ATTTGATTGG CTCGC 35

2) INFORMATION FOR SEQ ID NO: 1242

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (E) STRAIN: BM4147-1
 (F) ACCESSION NUMBER: U39790

15

(xiv) SEQUENCE DESCRIPTION: SEQ ID NO: 1242

20 TTCTTAGAGA CATTGAATAT GCCTTATGTC GGCGCAGGCG TATTGACCAG 50
 TGCATGTGCC ATGGATAAAA TCATGACCAA GTATATTTTA CAAGCTGCTG 100
 GTGTGCCGCA AGTTCCTTAT GTACCAGTAC TTAAGAATCA ATGGAAAGAA 150
 AATCCTAAAA AAGTATTTGA TCAATGTGAA GGTTCTTTGC TTTATCCGAT 200
 GTTTGTCAAA CCTGCGAATA TGGGTTCTAG TGTCGGCATT ACAAAGGCAG 250
 25 AAAACCGAGA AGAGCTGCAA AATGCTTTAG CAACAGCCTA TCAGTATGAT 300
 TCTCGAGCAA TCGTTGAACA AGGAATTGAA GCGCGCGAAA TCGAAGTTGC 350
 TGTATTAGGA AATGAAGATG TTCGGACGAC TTTGCCTGGC GAAGTCGTAA 400
 AAGACGTAGC ATTCTATGAT TATGAAGCCA AATATATCAA TAATAAAATC 450
 GAAATGCAGA TTCCAGCCGA AGTGCCGGAA GAAGTTTATC AAAAAGCGCA 500
 30 AGAGTACGCG AAGTTAGCTT ACACGATGTT AGGTGGAAGC GGATTGAGCC 550
 GGTGCGATTT CTTTTTGACA AATAAAAATG AATTATTCCT GAATGAATTA 600

35 2) INFORMATION FOR SEQ ID NO: 1243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (C) ACCESSION NUMBER: M38386

45

(xv) SEQUENCE DESCRIPTION: SEQ ID NO: 1243

50 GGTACCAAAG AAAAAACGA ACGCCACAAC CAACAGCCTC TAAAGCAACA 50
 CCTGCTTCTG AAATTGAGGG AGATTTAGCA AATGTCAATG AGATTCTTTT 100
 GGTTACGAT GATCGTGTCG GGTCAGCAAC GATGGGAATG AAAGTCTTAG 150
 AAGAAATTTT AGATAAAGAG AAAATTTCAA TGCCGATTCG AAAAATTAAT 200
 55 ATTAATGAAT TAACTCAACA AACACAGGCT TTAATTGTCA CAAAAGCTGA 250
 ACTAACGGAA CAAGCACGTA AAAAAGCACC GAAAGCGACA CACTTATCAG 300
 TAAAAAGTTA TGGTTAATCC CAAAAATAT GAAACAGTGG GTTTCGCTCT 350
 TAAAAGAAAG TGCCTAGAGA GGAAGAAAAC AATGGAAAAT CTTACGAATA 400
 TTTCAATTGA ATTAAATCAA CAGTTTAATA CAAAAGAAGA AGCTATTCGC 450
 60 TTTTCCGGCC AGAACTAGT CGAGGCAGGC TGTGTTGAGC CCGCTTATAT 500

	CGAAGCAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCCAT	ATGGGGAATT	550
	TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTGAAAAAA	600
	TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCAG	650
	AGAAGATGAA	AAAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
5	AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
	GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800
	AAATTTAGCC	ATTGCTTAAA	GGAGAGAATA	AGAATGAACG	CAGTACATTT	850
	TGGAGCAGGA	AATATTGGAC	GCGGCTTTAT	TGGCGAAATT	TTAGCTAAAA	900
	CGGGTTTCAT	ATTACCGTTT	GTGGATGTTA	ATGGAAACCA	TCATCAAGCG	950
10	TTAAAAGAAC	GTAAAAGTTA	TACAATTGAA	TTGGCCGATG	CCTCACATCA	1000
	ACAAATTAAC	GTTGAAAATG	TGACCGGGTT	AAATAACATG	ACAGAACCAG	1050
	AAAAAGTAGT	AGAAGCAATT	GCGGAAGCCG	ATTTAGTCAC	GACGGCAATT	1100
	GGTCCTAATA	TTTTACCAAG	AATTGCTGAA	TTAATTGCTC	AAGGAATTGA	1150
	TGCACGTGCC	GAAGCAAATT	GTCAAAACGG	CCCGCTGGAT	ATTATCGCTT	1200
15	GTGAAAATAT	GATTGGTGGT	TCAACCTTTT	TAGCAGAAGA	AGTGGCCATA	1250
	ATATTTGAAA	AACCCAGCTT	ATCTGAACAA	TGGATTGGTT	TTCCTGATGC	1300
	GGCAGTTGAT	CGGATTGTTC	CATTACAAAA	ACATAAAGAT	CCACTTTTGT	1350
	TTCAAGTTGA	GCCTTTTTGT	GAATGGGTCA	TTGATGATAC	CAACCGAAAA	1400
	GCCAAAGAGA	TTCAGTTAGA	AGGCGTCATT	ACTTGTCGAT	TAGAGCCGTA	1450
20	TATTGAACGA	AAATTATTTA	GTGTAACCAG	TGGCCATGCT	ACAGTTGCCT	1500
	ATACAGGGGC	GTTGTTAGGC	TATCAAACCA	TTGACGAAGC	GATGCAGGAC	1550
	GCCTTAGTGG	TAGCGCAACT	CAAATCAGTT	TTGCAGGAAA	CCGGTAAACT	1600
	TTTAGTGGCC	AAATGGAATT	TTGATGAACA	AGAACATGCA	GCCTATATTG	1650
	AAAAAATTAT	CAACCGTTTC	CAAAATAAAT	ATATTTTACA	TGCTATTACA	1700
25	CGTGTAGCAC	GGACACCAAT	CAGAAAATTA	GGTGCGCAAG	AACGGTTTAT	1750
	TCGACCAATC	CGTGAATTAC	AGGAACGCAA	TCTAGTGTCT	GCCGCATTTA	1800
	TAGCAATGAT	TGGTATTGTC	TTTAATTATC	ATGATCCAGA	AGATGAACAA	1850
	AGCCGTCAAT	TACAGGAAAT	GCTTGACCAA	GAAAGTGTTG	ATACAGTGGA	1900
	TCGCTGAAGT	AACGGGCATT	GAAATCCAG	AAACGGTTAA	AAATATTAAA	1950
30	CAAAACGTAG	AACTGCTATG	CGCGACCACA	AGTAGCATAA	TTAACAAAAT	2000
	CCTTCTACCA	AGATACTTCA	CATTTCTTAA	TTAAAGAAAA	AACAACCGCG	2050
	CCTCACCTGA	GCCGACCCCC	AAAAGTTAGA	CCTAGAAATC	TAACTTTTGG	2100
	AGGTTTTTTTT	GTATGGCAAA	ATACAGTTTT	GAAATTTAAA	CTTAAACTTG	2150
	TTCATGACTA	CTTATATGGT	CAAGGAGGTC	TAAGGTTTCT	CGCAAAGAAG	2200
35	TATGGGTTTA	AAGATAGTCT	CAAATAAGCA	AATGGATAAA	TGCCTATAAA	2250
	GAACCTGGTG	AAGAAGGGGG	GATCC			2275

40 2) INFORMATION FOR SEQ ID NO: 1244

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 442 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
 (B) STRAIN: ATCC 25923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244

55	GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
	TTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
	AATCTCATT	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
	CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
60	CCAGCCAAAA	CGATATTTTT	ATAATCATT	CGTGAAAAAG	GTTTCCCTTC	250

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PCT/CA00/01150

ATTATCACAC	AAATATTTTA	GCTTTTCAGT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTTGC	350
ACACCTTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

2) INFORMATION FOR SEQ ID NO: 1245

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245

GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAACAGAG 50
 CAACGAAAC GGAACAAGCA TTAAGTTAAC ATTTGAAGTT GCACTTCATT 100
 TAGGTGATGA CACAGTTCGT ACAGTTGCAA TGTCTCCAC AGATGGACTT 150
 20 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
 TGGTGATGCA ACACTTGGTC GTGTATTTAA CGTATTAGGT GATGCAATTG 250
 ACTTAGATGG TGAGGTTCCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
 CAAGCACCTG CATTCAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350
 TGGTATTAAA GTAGTAGACT TACTTGCTCC TTACATTAAG GGTGGTAAGA 400
 25 TCGGTCTATT CCGTGGTGCC GGTGTAGGTA AAACGGTATT AATTCAGGAA 450
 TTAATCAATA ACATCGCACA AGAACACGGT GGTATCTCTG TATTCGCTGG 500
 TGTAGGTGAG CGTACTCGTG AGGGTAATGA CTTATACCAC GAAATGAGCG 550
 ATTCTGGCGT AATTAAGAAA ACTGCGATGG TATTCGGACA AATGAACGAG 600
 CCACCTGGAG CACGTCAACG TGTTGCGTTA ACAGGTTTAA CAATGGCTGA 650
 30 GCATTTCCGT GATGAGCAAG GACAAGATGT ACTTCTGTTC ATCGATAATA 700
 TCTTCCGTTT CACGCAAGCA GGTTCTGAAG TATCTGCCCT TCTTGGCCGT 750
 ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA 800
 ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTC 845

35

2) INFORMATION FOR SEQ ID NO: 1246

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 11986

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246

TGCACTTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA ATGTCTTCCA 50

	CAGATGGACT	TGTTTCGTGGC	ACAGAAGTAG	AAGATACTGG	TAAAGCAATC	100
	TCTGTACCAG	TTGGTGATGT	AACACTTGGT	CGTGTATTTA	ACGTATTAGG	150
	TGATGCAATT	GACTTAGATG	GTGATGTTCC	TGCGGATGTA	CGTCGTGATC	200
	CAATTCACCG	TCAAGCGCCT	GCATTCGAAG	AGTTATCTAC	TAAAGTAGAA	250
5	ATTCTTGAAA	CTGGTATTAA	AGTAGTAGAC	TTACTTGCTC	CTTACATTAA	300
	GGGTGGTAAG	ATTGGTCTAT	TCGGTGGTGC	CGGCGTAGGT	AAAACAGTAT	350
	TAATTCAGGA	ATTAATTAAT	AACATCGCAC	AAGAGCACGG	TGGTATCTCT	400
	GTATTCGCTG	GTGTAGGTGA	GCGTACTCGT	GAAGGTAACG	ACTTATACCA	450
	CGAAATGAGC	GATTCTGGCG	TAATTAAGAA	AACTGCGATG	GTATTCGGAC	500
10	AAATGAACGA	GCCACCTGGA	GCACGTCAAC	GTGTTGCATT	AACAGGTTTA	550
	ACAATGGCTG	AACATTTCCG	TGATGAGCAA	GGACAAGACG	TACTATTGTT	600
	CATCGATAAC	ATCTTCCGTT	TCACGCAAGC	GGGTTCTGAA	GTATCTGCC	650
	TTCTTG					656

15

2) INFORMATION FOR SEQ ID NO: 1247

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247

	CGAAAACGGA	AGTATTAACT	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTCTG	100
35	GGCACAGAAG	TAGAAGATAC	TGGTAAACCA	ATCTCTGTAC	CAGTTGGTGA	150
	TGTAACACTT	GGTCGCGTAT	TTAACGTATT	AGGTGATGCA	ATTGACTTAG	200
	ATGGTGAGGT	TCCTGCAGAT	GTACATCGTG	ATCCAATTCA	CCGTCAAGCA	250
	CCTGCATTCTG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AACTGGTAT	300
	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350
40	TATTCGGTGG	TGCCGGCGTA	GGTAAACAG	TATTAATTCA	GGAATTAATT	400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTCTG	CTGGTGTAGG	450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500
	GCGTAATCAA	GAAAACCTGCG	ATGGTATTCTG	GACAAATGAA	CGAGCCACCT	550
	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT	600
45	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750
	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT	A	791

50

2) INFORMATION FOR SEQ ID NO: 1248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: BGSC 4AC1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248

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15 ATCTACAATG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGCATGAA      50
   CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
   TTGCGATGTC TTCCACAGAT GGACTTGTTT GTGGCACAGA AGTAGAAGAT      150
   ACTGGTAAAG CAATCTCTGT ACCAGTTGGT GATGCAACAC TTGGACGTGT      200
   ATTC AACGTA TTAGGTGATG CAATTGACTT AGATGGTGAA CTCCTGCGG      250
20 ATGTACACCG TGATCCAATT CACCGTCAAG CACCTGCATT CGAAGAATTA      300
   TCTACTAAAG TAGAAATTCT TGAACTGGT ATTAAAGTAG TAGACTTACT      350
   TGCTCCTTAC ATTAAGGGTG GTAAGATCGG CCTATTCCGGT GGTGCCGGCG      400
   TAGGTAAAC AGTATTAATT CAGGAGTTAA TCAATAACAT CGCACAAGAG      450
   CACGGTGGTA TCTCTGTATT CGCTGGTGTA GGTGAGCGTA CTCGTGAGGG      500
25 TAATGACTTA TACCACGAAA TGAGCGATTC TGGCGTAATC AAGAAACTG      550
   CGATGGTATT CGGACAAATG AACGAGCCAC CTGGAGCACG TCAACGTGTT      600
   GCATTAACAG GTTTAACAAT GGCTGAGCAT TTCCGTGATG AGCAAGGACA      650
   AGACGTA CTT CTGTTTCATCG ATAACATCTT CCGTTTCACG CAAGCGGGTT      700
   CTGAAGTATC TGCCCTTCTT GGTCGTATGC CATCTGCGGT AGGTTACCAA      750
30 CCAACACTTG CAACAGAAAT GGGTCAATTA CAAGAGCGTA TTACATCTAC      800
   AAATAAAGGG TCTATCACGT CTATC                                825

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35 2) INFORMATION FOR SEQ ID NO: 1249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249

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50 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAAGTATTAA      50
   CTTAACATTT GAAGTTGCAC TTCATTTAGG TGATGATACA GTTCGTACAG      100
   TTGCGATGTC TTCCACAGAT GGACTTGTTT GTGGCACAGA AGTAGAAGAT      150

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	ACTGGTAAAC	CAATCTCTGT	ACCA GTTGGT	GATGTAACAC	TTGGTCGCGT	200
	ATTTAACGTA	TTAGGTGATG	CAATTGACTT	AGATGGTGAG	GTTCTGTCAG	250
	ATGTACATCG	TGATCCAATT	CACCGTCAAG	CACCTGCATT	CGAAGAATTA	300
	TCTACTAAAG	TAGAAATTCT	TGAAACTGGT	ATTAAAGTAG	TAGACTTACT	350
5	TGCTCCTTAC	ATTAAGGGTG	GTAAGATCGG	CCTATTCGGT	GGTGCCGGCG	400
	TAGGTAAAAC	AGTATTAATT	CAGGAATTAA	TTAACAACAT	CGCACAAGAG	450
	CACGGTGGTA	TCTCTGTATT	CGCTGGTGTA	GGTGAGCGTA	CTCGTGAGGG	500
	TAATGACTTA	TACCACGAAA	TGAGCGATTG	TGGCGTAATC	AAGAAAAC TG	550
	CGATGGTATT	CGGACAAATG	AACGAGCCAC	CTGGAGCACG	TCAACGTGTT	600
10	GCATTAAACAG	GTTTAACAAT	GGCTGAGCAT	TTCCGTGATG	AGCAAGGACA	650
	AGACGTACTT	CTGTTTCATCG	ATAACATCTT	CCGTTTCACG	CAAGCGGGTT	700
	CTGAAGTATC	TGCCCTTCTT	GGTCGTATGC	CATCTGCGGT	AGGTTACCAA	750
	CCAACACTTG	CAACAGAAAT	GGGTC			775

15

2) INFORMATION FOR SEQ ID NO: 1250

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus weihenstephanensis*

(B) STRAIN: WSBC 10204

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250

	CCAGCAATCT	ACAACGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAGC	50
	GAGCATCAAC	TTAACATTTG	AAGTTGCACT	TCATTTAGGT	GATGACACAG	100
35	TTCGTACAGT	TGCGATGTCT	TCCACAGATG	GACTTGTTTCG	TGGCACAGAA	150
	GTAGAAGATA	CTGGTAAAGC	AATCTCTGTA	CCAGTTGGTG	ATGTAACACT	200
	TGGTCGCGTA	TTCAACGTAT	TAGGTGATGC	AATTGACTTA	GATGGTGATG	250
	TTCCTGCGGA	TGTACGTCGT	GATCCAATTC	ACCGTCAAGC	ACCTGCATTC	300
	GAAGAACTAT	CTACAAGAAT	AGAAATTCTT	GAAACTGGTA	TTAAAGTAGT	350
40	AGATTTACTT	GCTCCTTACA	TTAAGGGTGG	TAAGATCGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACG	GTATTAATTC	AGGAATTAAT	TAACAACATC	450
	GCACAAGAGC	ACGGTGGTAT	CTCTGTATTC	GCTGGTGTAG	GTGAGCGTAC	500
	TCGTGAGGGT	AATGACTTAT	ACCACGAAAT	GAGCGATTCT	GGCGTAATTA	550
	AGAAAAC TGC	GATGGTATTT	GGACAAATGA	ACGAGCCACC	TGGAGCACGT	600
45	CAACGTGTTG	CATTAAACAGG	TTTAACAATG	GCTGAACATT	TCCGTGATGA	650
	GCAAGGACAA	GACGTACTAT	TGTTTCATCGA	TAACATCTTC	CGTTTCACGC	700
	AAGCAGGTTC	TGAAGTATCT	GCCCTTCTTG	GTCGTATGCC	ATCTGCGGTA	750
	GGTTACCAAC	CAACACTTGC	AACAGAAATG	GGTCAATTAC	AAGAGCGTAT	800
	TACATCTACA	AATAAAGGGT	CTATCACGTC	TA		832

50

2) INFORMATION FOR SEQ ID NO: 1251

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251

15 AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100
 AGTTGCGATG TCTTCCACAG ATGGACTTGT TCGTGGCACA GAAGTAGAAG 150
 ATACTGGTAA ACCAATCTCT GTACCAGTTG GTGATGTAAC ACTTGGTCGC 200
 20 GTATTTAACG TATTAGGTGA TGCAATTGAC TTAGATGGTG AGGTTCTGC 250
 AGATGTACAT CGTGATCCAA TTCACCGTCA AGCACCTGCA TTCGAAGAAT 300
 TATCTACTAA AGTAGAAATT CTTGAAACTG GTATTAAAGT AGTAGACTTA 350
 CTTGCTCCTT ACATTAAGGG TGGTAAGATC GGCCTATTCG GTGGTGCCGG 400
 CGTAGGTAAA ACAGTATTAA TTCAGGAATT AATTAACAAC ATCGCACAAAG 450
 25 AGCACGGTGG TATCTCTGTA TTCGCTGGTG TAGGTGAGCG TACTCGTGAG 500
 GGTAATGACT TATACCACGA AATGAGCGAT TCTGGCGTAA TCAAGAAAAC 550
 TGCGATGGTA TTCGGACAAA TGAACGAGCC ACCTGGAGCA CGTCAACGTG 600
 TTGCATTAAC AGGTTTAAACA ATGGCTGAGC ATTTCCGTGA TGAGCAAGGA 650
 CAAGACGTAC TTCTGTTTCA CGATAACATC TTCCGTTTCA CGCAAGCGGG 700
 30 TTCTGAAGTA TCTGCCCTTC TTGGTCGTAT GCCATCTGCG GTAGGTTACC 750
 AACCAACACT TGCAACAGAA ATGGGTCAAT TACAAGAGCG TATTACATCT 800
 AC 802

35

2) INFORMATION FOR SEQ ID NO: 1252

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: HER 1410

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252

AAATCTACAA CGCCCTTACG GTAAAACAAA GCAACGAAAA CGGAAGTATT 50
 AACTTAACAT TTGAAGTTGC ACTTCATTTA GGTGATGATA CAGTTCGTAC 100

	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	GAAGTAGAAG	150
	ATACTGGTAA	ACCAATCTCT	GTACCAGTTG	GTGATGTAAC	ACTTGGTCGC	200
	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	AGGTTCCCTGC	250
	AGATGTACAT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	TTCGAAGAAT	300
5	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	AGTAGACTTA	350
	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCG	GTGGTGCCGG	400
	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATTAAACAAC	ATCGCACAAAG	450
	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	TACTCGTGAG	500
	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	TCAAGAAAAC	550
10	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	CGTCAACGTG	600
	TTGCATTAAAC	AGGCTTAACA	ATGGCTGAGC	ATTTCCGTGA	TGAGCAAGGA	650
	CAAGACGTAC	TTCTGTTTCA	CGATAACATC	TTCCGTTTCA	CGCAAGCGGG	700
	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	GTAGGTTACC	750
	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	TATTACATCT	800
15	ACAAATAAAG	GGTCTATCAC	GTC			823

2) INFORMATION FOR SEQ ID NO: 1253

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253

35	CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
	CATGAACCTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
	GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCGTGG	CACAGAAGTA	150
	GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTTGGTGATG	CAACACTTGG	200
	ACGTGTATTG	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAACCTC	250
40	CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTTCGAA	300
	GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
	CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCCGGTGGTG	400
	CCGGCGTAGG	TAAACAGTA	TTAATTCAGG	AATTAATCAA	TAACATCGCA	450
	CAAGAGCATG	GTGGTATCTC	TGTATTCGCT	GGTGTAGGTG	AGCGTACTCG	500
45	TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
	AAACTGCGAT	GGTATTCGGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
	CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
	AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
	CGGGTTCTGA	AGTATCTGCC	CTTCTTGCTC	GTATGCCATC	TGCGGTAGGT	750
50	TACCAACCGA	CACTTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATT	798

2) INFORMATION FOR SEQ ID NO: 1254

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 767 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 7064
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254

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CATTGAAGT TGCATTTCAT TTAGGTGATG ACACAGTTCG TACAGTTGCA      50
ATGTCTTCCA CAGATGGACT TGTTTCGTGGC ACAGAAGTAG AAGATACTGG     100
TAAAGCAATC TCTGTACCAG TTGGTGATGC AACACTTGGT CGTGTATTTA     150
ACGTATTAGG TGATGCAATT GACTTAGATG GTGAGGTTCC TGCGGATGTA     200
CGTCGTGATC CAATTCACCG TCAAGCACCT GCATTGGAAG AATTATCTAC     250
TAAAGTAGAA ATTCCTGAAA CTGGTATTAA AGTAGTAGAC TTACTTGCTC     300
CTTACATTAA GGGTGGTAAG ATCGGTCTAT TCGGTGGTGC CGGTGTAGGT     350
AAAACGGTAT TAATTCAGGA ATTAATCAAT AACATCGCAC AAGAACACGG     400
TGGTATCTCT GTATTCGCTG GTGTAGGTGA GCGTACTCGT GAGGGTAATG     450
ACTTATACCA CGAAATGAGC GATTCTGGCG TAATTAAGAA AACTGCGATG     500
GTATTCGGAC AAATGAACGA GCCACCTGGA GCACGTCAAC GTGTTGCGTT     550
AACAGGTTTA ACAATGGCTG AGCATTTCCTG TGATGAGCAA GGACAAGACG     600
TACTTCTGTT CATCGATAAT ATCTTCCGTT TCACGCAAGC AGGTTCTGAA     650
GTATCTGCCC TTCTTGGCCG TATGCCATCT GCGGTAGGTT ACCAACCAAC     700
ACTTGCAACA GAAATGGGTC AATTACAAGA GCGTATTACA TCTACAAATA     750
AAGGGTCTAT CACGTCT

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2) INFORMATION FOR SEQ ID NO: 1255

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1174 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: C-14
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255

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GAAATGCGTG AATCATTTTT AGATTATGCG ATGAGTGTTA TCGTTGCTCG      50
TGCATTGCCA GATGTTTCGTG ACGGTTTAAA ACCAGTACAT CGTCGTATAC     100

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	TATATGGATT	AAATGAACAA	GGTATGACAC	CGGATAAATC	ATATAAAAAA	150
	TCAGCACGTA	TCGTTGGTGA	CGTAATGGGT	AAATATCACC	CTCATGGTGA	200
	CTTATCTATT	TATGAAGCAA	TGGTACGTAT	GGCTCAAGAT	TTCAGTTATC	250
	GTTATCCGCT	TGTTGATGGC	CAAGGTAAC	TTGGTTCAAT	GGATGGAGAT	300
5	GGCGCAGCAG	CAATGCGTTA	TACTGAAGCG	CGTATGACTA	AAATCACACT	350
	TGAACTGTTA	CGTGATATTA	ATAAAGATAC	AATAGATTTT	ATCGATAACT	400
	ATGATGGTAA	TGAAAGAGAG	CCGTCAGTCT	TACCTGCTCG	ATTCCCTAAC	450
	TTATTAGCCA	ATGGTGCATC	AGGTATCGCG	GTAGGTATGG	CAACGAATAT	500
	TCCACCACAT	AACTTAACAG	AATTAATCAA	TGGTGTACTT	AGCTTAAGTA	550
10	AGAACCCTGA	TATTTCAATT	GCTGAGTTAA	TGGAGGATAT	TGAAGGTCCT	600
	GATTTCCCAA	CTGCTGGACT	TATTTTAGGT	AAGAGTGGTA	TTAGACGTGC	650
	ATATGAAACA	GGTCGTGGTT	CAATTCAAAT	GCGTTCTCGT	GCAGTTATTG	700
	AAGAACGTGG	AGNCGGACGT	CAACGTATTG	TTGTCACTGA	AATTCCTTTC	750
	CAAGTGAATA	AGGCTCGTAT	GATTGAAAAA	ATTGCAGAGC	TCGTTCTGTA	800
15	CAAGAAAATT	GACGGTATCA	CTGATTTACG	TGATGAAACA	AGTTTACGTA	850
	CTGGTGTGCG	TGTCGTTATT	GATGTGCGTA	AGGATGCAAA	TGCTAGTGTC	900
	ATTTTAAATA	ACTTATACAA	ACAAACACCT	CTTCAAACAT	CATTGTTGT	950
	GAATATGATT	GCACTTGTA	ATGGTAGACC	GAAGCTTATT	AATTTAAAAG	1000
	AAGCGTTGGT	ACATTATTTA	GAGCATCAAA	AGACAGTTGT	TAGAAGACGT	1050
20	ACGCAATACA	ACTTACGTAA	AGCTAAAGAT	CGTGCCCA	TTTTAGAAGG	1100
	ATTACGTATC	GCACTTGACC	ATATCGATGA	AATTATTTCA	ACGATTCGTG	1150
	AGTCAGATAC	AGATAAAGTT	GCAA			1174

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2) INFORMATION FOR SEQ ID NO: 1256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
 (B) STRAIN: WSBC 10209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256

	ATCTACAACG	CCCTTACGGT	AAAACAAAGC	AACGAAAACG	GAGCAAGCAT	50
	TAACTTAACA	TTTGAAGTTG	CACTTCATTT	AGGTGATGAC	ACAGTTCGTA	100
	CAGTTGCAAT	GTCTTCCACA	GATGGACTTG	TTCGTGGCAC	AGAAGTAGAA	150
45	GATACTGGTA	AAGCAATCTC	TGTACCAGTT	GGTGATGTAA	CACTTGGTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGA	GATGTTCTCTG	250
	CGGATGTACG	TCGTGATCCA	ATTCACCGTC	AAGCGCCTGC	ATTCGAAGAG	300
	TTATCTACTA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
	ACTTGCTCCT	TACATTAAGG	GTGGTAAGAT	CGGTCTATTC	GGTGGTGCCG	400
50	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTA CTCTGTA	500
	AGGTAACGAC	TTATACCACG	AAATGAGCGA	TTCTGGCGTA	ATTAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGAGC	ACGTCAACGT	600

GTTGCATTAA	CAGGTTTAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
GCAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
GTTCTGAAGT	ATCTGCCCTT	CTTGGTCGTA	TGCCATCTGC	GGTAGGTTAC	750
CAGCCAACAC	TTGCAACAGA	AATGGGTCAA			780

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2) INFORMATION FOR SEQ ID NO: 1257

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 7700

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257

CTACCAGAAA	TCTACAACGC	CCTTACGGTA	AAACAGAGCA	ACGAAAACGG	50
25 AACAAGCATT	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGACA	100
CAGTTCGTAC	AGTTGCAATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
ACTTGGTCGT	GTATTTAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
AGGTTCTCTG	GGATGTACGT	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
30 TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGTCTATTCG	400
GTGGTGCCGG	TGTAGGTAAA	ACGGTATTAA	TTCAGGAATT	AATCAATAAC	450
ATCGCACAAAG	AACACGGTGG	TATCTCTGTA	TTGCTGGTGG	TAGGTGAGCG	500
TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
35 TTAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
CGTCAACGTG	TTGCGTTAAC	AGGTTTAACA	ATGGCTGAGC	ATTTCCGTGA	650
TGAGCAAGGA	CAAGATGTAC	TTCTGTTCAT	CGATAATATC	TTCCGTTTCA	700
CGCAAGCAGG	TTCTGAAGTA	TCTGCCCTTC	TTGGCCGTAT	GCCATCTGCG	750
GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
40 TATTACATCT	ACAAATA				817

2) INFORMATION FOR SEQ ID NO: 1258

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1404

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258

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CCAGAAATCT ACAACGCCCT TACGGTAAAA CAAAGCAACG AAAACGGAAG      50
TATTAACCTA ACATTTGAAG TTGCACTTCA TTTAGGTGAT GATACAGTTC      100
GTACAGTTGC GATGTCTTCC ACAGATGGAC TTGTTCTGGT CACAGAAGTA      150
10 GAAGATACTG GTAAACCAAT CTCTGTACCA GTTGGTGATG TAACACTTGG      200
TCGCGTATTT AACGTATTAG GTGATGCAAT TGACTTAGAT GGTGAGGTTC      250
CTGCAGATGT ACATCGTGAT CCAATTCACC GTCAAGCACC TGCATTGAA      300
GAATTATCTA CTAAAGTAGA AATTCTTGAA ACTGGTATTA AAGTAGTAGA      350
CTTACTTGCT CCTTACATTA AGGGTGGTAA GATCGGCCTA TTCGGTGGTG      400
15 CCGGCGTAGG TAAAACAGTA TTAATTCAGG AATTAATTAA CAACATCGCA      450
CAAGAGCACG GTGGTATCTC TGTATTGCTG GGTGTAGGTG AGCGTACTCG      500
TGAGGGTAAT GACTTATACC ACGAAATGAG CGATTCTGGC GTAATCAAGA      550
AAACTGCGAT GGTATTGCGA CAAATGAACG AGCCACCTGG AGCAGGTCAA      600
CGTGTTGCAT TAACAGGTTT AACAATGGCT GAGCATTTCG GTGATGAGCA      650
20 AGGACAAGAC GTACTTCTGT TCATCGATAA CATCTTCCGT TTCACGCAAG      700
CGGGTTCTGA AGTATCTGCC CTTCTTGGTC GTATGCCATC TCGGGTAGGT      750
TACCAACCAA CACTTGCAAC AGAAATGGGT CAATTACAAG AGCGTATTAC      800
ATCTACAAAT AAAGGGTCTA TCACGTCTA      829

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2) INFORMATION FOR SEQ ID NO: 1259

(i) SEQUENCE CHARACTERISTICS:

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30 (A) LENGTH: 844 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus cereus*

(B) STRAIN: ATCC 15816

40 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259

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TGGCGGAAAG CTACCAGAAA TCTACAACGC CCTTACGGTA AAACAGAGCA      50
45 ACGAAAACGG TGAACCTAAC TTAACATTTG AAGTTGCACT TCATTTAGGT      100
GATGATACAG TTCGTACAGT TGCGATGTCT TCCACAGATG GACTTGTTCTG      150
TGGCACAGAA GTAGAAGATA CTGGTAAAGC AATCTCTGTA CCAGTTGGTG      200
ATGCAACACT TGGTCGCGTA TTTAACGTAT TAGGTGATGC TATTGACTTA      250
GATGGTGAGG TTCCTGCGGA TGTACGTCGT GATCCAATTC ACCGTCAAGC      300
50 ACCTGCATTC GAAGAATTAT CTAATAAAGT AGAAATTCTT GAAACTGGTA      350
TTAAAGTAGT AGACTTACTT GCTCCTTACA TTAAGGGTGG TAAGATCGGC      400
CTATTCGGTG GTGCCGGTGT AGGTAAAACA GTATTAATTC AGGAGTTAAT      450
CAACAACATC GCACAAGAGC ACGGTGGTAT CTCTGTATTG GCTGGTGTAG      500

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GTGAGCGTAC TCGTGAGGGT AATGACTTAT ACCACGAAAT GAGCGATTCT 550
 GGC GTAATTA AGAAACTGC GATGGTATTC GGACAAATGA ACGAGCCACC 600
 TGGAGCACGT CAACGTGTTG CATTAAACAGG CTTAACAATG GCTGAATATT 650
 TCCGTGATGA GCAAGGACAA GACGTACTTC TGTTTCATCGA TAATATCTTC 700
 5 CGTTTCACGC AAGCAGGTTT TGAAGTATCT GCCCTTCTTG GCCGTATGCC 750
 ATCTGCGGTA GGTTACCAAC CAACACTTGC AACAGAAATG GGTCAATTAC 800
 AAGAGCGTAT TACATCTACA AATAAAGGGT CTATCACGTC TATC 844

10

2) INFORMATION FOR SEQ ID NO: 1260

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
 20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260

AAGCTACCAG AAATCTACAA CGCCCTTACG GTAAAACAGA GCAACGAAAA 50
 CGGAACAAGC ATTAACCTAA CATTGGAAGT TGCACTTCAT TTAGGTGATG 100
 ACACAGTTCG TACAGTTGCA ATGTCTTCCA CAGATGGACT TGTTTCGTGGC 150
 30 ACAGAAGTAG AAGATACTGG TAAAGCAATC TCTGTACCAG TTGGTGATGC 200
 AACACTTGGT CGTGTATTTA ACGTATTAGG TGATGCAATT GACTTAGATG 250
 GTGAGGTTCC TGCGGATGTA CGCCGTGATC CAATTCACCG TCAAGCACCT 300
 GCATTCGAAG AATTATCTAC TAAAGTAGAA ATTCTTGAAA CTGGTATTAA 350
 AGTAGTAGAC TTACTTGCTC CTTACATTAA GGGTGGTAAG ATCGGTCTAT 400
 35 TCGGTGGTGC CGGTGTAGGT AAAACAGTAT TAATTCAGGA ATTAATCAAC 450
 AACATCGCAC AAGAACACGG TGGTATCTCT GTATTCGCTG GTGTAGGTGA 500
 GCGTACTCGT GAGGGTAATG ACTTATACCA CGAAATGAGC GATTACAGGCG 550
 TAATTAAGAA AACTGCGATG GTATTCGGAC AAATGAACGA GCCACCTGGA 600
 GCGCGTCAAC GTGTTGCGTT AACAGGTTTA ACAATGGCTG AGCATTTCGG 650
 40 TGATGAGCAA GGACAAGACG TTCTTCTGTT CATCGATAAT ATCTTCCGTT 700
 TCACGCAAGC AGGTTCTGAA GTATCTGCCC TTCTTGGTCG TATGCCATCT 750
 GCGGTAGGTT ACCAACCAAC ACTTGCAACA GAAATGGGTC AATTACAAGA 800
 GCGTATTACA TCTACAAATA AAGGGTCTAT CACGTCTATC 840

45

2) INFORMATION FOR SEQ ID NO: 1261

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4AZ1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261

10	GCGGAAAGCT	ACCAGAAATC	TACAAATGCC	TTACGGTAAA	ACAAAGCAAC	50
	GAAAACGGAA	GCATGAACTT	AACATTTGAA	GTTGCACTTC	ATTTAGGTGA	100
	TGATACAGTT	CGTACAGTTG	CGATGCTTTC	CACAGATGGA	CTTGTTCTGTG	150
	GCACAGAAGT	AGAAGATACT	GGTAAAGCAA	TCTCTGTACC	AGTTGGTGAT	200
	GCAACACTTG	GACGTGTATT	CAACGTATTA	GGTGATGCAA	TTGACTTAGA	250
15	TGGTGAACCT	CCTGCGGATG	TACACCGTGA	TCCAATTCAC	CGTCAAGCAC	300
	CTGCATTCTGA	AGAATTATCT	ACTAAAGTAG	AAATTCTTGA	AACTGGTATT	350
	AAAGTAGTAG	ACTTACTTGC	TCCTTACATT	AAGGGTGGTA	AGATCGGCCT	400
	ATTCGGTGGT	GCCGGCGTAG	GTAAAACAGT	ATTAATTCAG	GAGTTAATCA	450
	ATAACATCGC	ACAAGAGCAC	GGTGGTATCT	CTGTATTTCGC	TGGTGTAGGT	500
20	GAGCGTACTC	GTGAGGGTAA	TGACTTATAC	CACGAAATGA	GCGATTCTGG	550
	CGTAATCAAG	AAAACGCGA	TGGTATTTCG	ACAAATGAAC	GAGCCACCTG	600
	GAGCACGTCA	ACGTGTTGCA	TTAACAGGTT	TAACAATGGC	TGAGCATTTC	650
	CGTGATGAGC	AAGGACAAGA	CGTACTTCTG	TTCATCGATA	ACATCTTCCG	700
	TTTCACGCAA	GCGGGTTCTG	AAGTATCTGC	CCTTCTTGGT	CGTATGCCAT	750
25	CTGCGGTAGG	TTACCAACCA	ACACTTGCAA	CAGAAATGGG	TCAATTACAA	800
	GAGCGTATTA	CATCTACAAA	TAAAGGGTCT	ATCACGTCT		839

30 2) INFORMATION FOR SEQ ID NO: 1262

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: BGSC 4H2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262

45	AAGCTACCAG	AAATCTACAA	TGCCCTTACG	GTAAAACAAA	GCAACGAAAA	50
	CGGAAGCATG	AACTTAACAT	TTGAAGTTGC	ACTTCATTTA	GGTGATGATA	100
	CAGTTCGTAC	AGTTGCGATG	TCTTCCACAG	ATGGACTTGT	TCGTGGCACA	150
	GAAGTAGAAG	ATACTGGTAA	AGCAATCTCT	GTACCAGTTG	GTGATGCAAC	200
50	ACTTGGAAGT	GTATTCAACG	TATTAGGTGA	TGCAATTGAC	TTAGATGGTG	250
	AACTTCCTGC	GGATGTACAC	CGTGATCCAA	TTCACCGTCA	AGCACCTGCA	300
	TTCGAAGAAT	TATCTACTAA	AGTAGAAATT	CTTGAAACTG	GTATTAAAGT	350
	AGTAGACTTA	CTTGCTCCTT	ACATTAAGGG	TGGTAAGATC	GGCCTATTCTG	400

	GTGGTGCCGG	CGTAGGTAAA	ACAGTATTAA	TTCAGGAATT	AATCAATAAC	450
	ATCGCACAAAG	AGCACGGTGG	TATCTCTGTA	TTCGCTGGTG	TAGGTGAGCG	500
	TACTCGTGAG	GGTAATGACT	TATACCACGA	AATGAGCGAT	TCTGGCGTAA	550
	TCAAGAAAAC	TGCGATGGTA	TTCGGACAAA	TGAACGAGCC	ACCTGGAGCA	600
5	CGTCAACGTG	TTGCATTAAAC	AGGTTTAACA	ATGGCTGAGC	ATTTCCGTGA	650
	TGAGCAAGGA	CAAGACGTAC	TTCTGTTTCAT	CGATAACATC	TTCCGTTTCA	700
	CGCAAGCGGG	TTCTGAAGTA	TCTGCCCTTC	TTGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AACCAACACT	TGCAACAGAA	ATGGGTCAAT	TACAAGAGCG	800
10	TATTACATCT	ACAAATAAAG	GGTCTATCAC	GTC		833

2) INFORMATION FOR SEQ ID NO: 1263

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 25 (B) STRAIN: BGSC 4Q1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263

	CGAAAACGGA	AGCATGAACT	TAACATTTGA	AGTTGCACTT	CATTTAGGTG	50
30	ATGATACAGT	TCGTACAGTT	GCGATGTCTT	CCACAGATGG	ACTTGTTTCGT	100
	GGCACAGAAG	TAGAAGATAC	TGGTAAAGCA	ATTTCTGTAC	CAGTTGGTGA	150
	TGTAACACTT	GGACGTGTAT	TCAACGTATT	AGGTGATGCA	ATTGACTTAG	200
	ATGGTGAAC	TCCTGCGGAT	GTACACCGTG	ATCCAATTCA	CCGTCAAGCA	250
	CCTGCATTCTG	AAGAATTATC	TACTAAAGTA	GAAATTCTTG	AACTGGTAT	300
35	TAAAGTAGTA	GACTTACTTG	CTCCTTACAT	TAAGGGTGGT	AAGATCGGCC	350
	TATTCGGTGG	TGCCGGTGTA	GGTAAACAG	TATTAATTCA	GGAATTAATT	400
	AACAACATCG	CACAAGAGCA	CGGTGGTATC	TCTGTATTCTG	CTGGTGTAGG	450
	TGAGCGTACT	CGTGAGGGTA	ATGACTTATA	CCACGAAATG	AGCGATTCTG	500
	GCGTAATCAA	GAAAACTGCG	ATGGTATTCTG	GACAAATGAA	CGAGCCACCT	550
40	GGAGCACGTC	AACGTGTTGC	ATTAACAGGT	TTAACAATGG	CTGAGCATTT	600
	CCGTGATGAG	CAAGGACAAG	ACGTACTTCT	GTTTCATCGAT	AACATCTTCC	650
	GTTTCACGCA	AGCGGGTTCT	GAAGTATCTG	CCCTTCTTGG	TCGTATGCCA	700
	TCTGCGGTAG	GTTACCAACC	AACACTTGCA	ACAGAAATGG	GTCAATTACA	750
45	AGAGCGTATT	ACATCTACAA	ATAAAGGGTC	TATCACGTCT		790

2) INFORMATION FOR SEQ ID NO: 1264

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264

10 AGTTGCACTT CATTTAGGTG ATGATACAGT TCGTACAGTT GCGATGTCTT 50
 CCACAGATGG ACTTGTTTCGT GGCACAGAAG TAGAAGATAC TGGTAAACCA 100
 ATCTCTGTAC CAGTTGGTGA TGTAACACTT GGTCGCGTAT TTAACGTATT 150
 AGGTGATGCA ATTGACTTAG ATGGTGAGGT TCCTGCAGAT GTACATCGTG 200
 15 ATCCAATTCA CCGTCAAGCA CCTGCATTCG AAGAATTATC TACTAAAGTA 250
 GAAATTCTTG AAACCTGGTAT TAAAGTAGTA GACTTACTTG CTCCTTACAT 300
 TAAGGGTGGT AAGATCGGCC TATTCGGTGG TGCCGGCGTA GGTAACACAG 350
 TATTAATTCA GGAATTAATT AACAACATCG CACAAGAGCA CCGTGGTATC 400
 TCTGTATTCG CTGGTGTAGG TGAGCGTACT CGTGAGGGTA ATGACTTATA 450
 20 CCACGAAATG AGCGATTCTG GCGTAATCAA GAAACTGCG ATGGTATTCG 500
 GACAAATGAA CGAGCCACCT GGAGCACGTC AACGTGTTGC ATTAACAGGT 550
 TTAACAATGG CTGAGCATT TCCGTGATGAG CAAGGACAAG ACGTACTTCT 600
 GTTCATCGAT AACATCTTCC GTTTCACGCA AGCGGGTTCT GAAG 644

25

2) INFORMATION FOR SEQ ID NO: 1265

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: ATCC 4229

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265

GGCGGAAAGC TACCAGAAAT CTACAACGCC CTTACGGTAA AACAGAGCAA 50
 CGAAAACGGA ACAAGCATTA ACTTAACATT TGAAGTTGCA CTTCAATTTAG 100
 45 GTGATGACAC AGTTCGTACA GTTGCAATGT CTTCCACAGA TGGACTTGTT 150
 CGTGGCACAG AAGTAGAAGA TACTGGTAAA GCAATCTCTG TACCAAGTTGG 200
 TGATGCAACA CTTGGTCGTG TATTTAACGT ATTAGGTGAT GCAATTGACT 250
 TAGATGGTGA GGTTCCCTGCG GATGTACGTC GTGATCCAAT TCACCGTCAA 300
 GCACCTGCAT TCGAAGAATT ATCTACTAAA GTAGAAATTC TTGAAACTGG 350
 50 TATTAAAGTA GTAGACTTAC TTGCTCCTTA CATTAAAGGT GGTAAGATCG 400
 GTCTATTCGG TGGTGCCGGT GTAGGTAAAA CGGTATTAAT TCAGGAATTA 450
 ATCAATAACA TCGCACAAGA ACACGGTGGT ATCTCTGTAT TCGCTGGTGT 500
 AGGTGAGCGT ACTCGTGAGG GTAATGACTT ATACCACGAA ATGAGCGATT 550

	CTGGCGTAAT	TAAGAAAAC	GCGATGGTAT	TCGGACAAAT	GAACGAGCCA	600
	CCTGGAGCAC	GTCAACGTGT	TGCGTTAACA	GGTTTAACAA	TGGCTGAGCA	650
	TTTCCGTGAT	GAGCAAGGAC	AAGATGTACT	TCTGTTTCATC	GATAATATCT	700
	TCCGTTTCAC	GCAAGCAGGT	TCTGAAGTAT	CTGCCCTTCT	TGGCCGTATG	750
5	CCATCTGCGG	TAGGTTACCA	ACCAACACTT	GCAACAGAAA	TGGGTCAATT	800
	ACAAGAGCGT	ATTACATCTA	CAA			823

10 2) INFORMATION FOR SEQ ID NO: 1266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266

25	TGGTCCGAGR	CCCGATTCTMA	TGAAATTATC	AAGGAAACCT	CCAAYTTCAT	50
	TAAGAAGGTC	GGATATAACC	CCAAGACTGT	TCCTTTCGTT	CCCATTTCTG	100
	GTTTCCAGGG	TGACAACATG	ATCGATSCCT	CTGCCAACTG	CCCATGGTAC	150
	AAGGGCTGGT	ACMAKGAGAC	TGCCGACAGG	CAAGYACTCT	GGCAAGACCC	200
30	TTCTTGAGGC	CATTGACGSC	ATTGAGCCCC	CCAMSCGTCC	TWCCGATAAA	250
	CCTCTCCGTC	TTCCTCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGMAC	300
	TGTTCTGTG	GGACGTRTTG	AGACTGGAGT	CATCAAGCCC	GGTATGGTCG	350
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAAATG	400
	CACCACCAGC	AGCTTTCCGA	CGGTAWCCCC	GGTGACAACG	TCGGCTTCAA	450
35	CGTCAAGAAT	GTTTCCGTCA	AAGAAGTCCG	CCGTGGTAAC	GTTGCCTGGT	500
	GACTCTAAGA	ATGATCCCCG	MAWGGGCTGC	GATTCCTTCA	ATGCYCAGGT	550
	CATCGTCCCT	AACCACCCTG	GTCAGGTTGG	CGCTGGTTAT	GCCCCAGTCC	600
	TCGAYTGCCA	TACTGCCCAC	ATTGCTGTGA	ARTTCGCTGA	GMTCMAGKAG	650
	AAGATTGAYC	GCCGAACCGG	MAAGTCTGTT	GAGAACGCCC	CCAAGTTCAT	700
40	CAAGTCCGGT	GATGC				715

2) INFORMATION FOR SEQ ID NO: 1267

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 56220

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267

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GAGTCCTCTT ATTTACTTTT GTCATGACTA CCTTACTAAT CTGTCATAGA      50
TCGTTACAAC GAAATCGTCA AGGAGACTTC CAACTTCATC AAGAAGGTCG      100
GATACAACCC CAAGAACGTT CCTTTCGTTT CTATCTCCGG TTTCAACGGC      150
10 GACAACATGC TTGAGCCCTC CCCCAGCTGC CCCTGGTACA AGGGTTGGGA      200
GAAGGAGACC AAGGCCGGTA AGGTCACTGG TAAGACCCTC CTCGAGGCCA      250
TCGACGCCAT TGAGCCCCCT ACCCGTCCCG CCAACAAGGT CAGTACTACC      300
TCAATTACTT GAACTCTCTT CATACTGTTT GATTACTGAC TGCTTCACAG      350
CCCCCTCCGTC TTCCCCTCCA GGACGTTTAC AAGATCGGTG GTATTGGAAC      400
15 GGTGCCCCGTC GGTTCGTGTTG AGACCGGTAC CATCTCCCTT GGTATGGTCG      450
TTACCTTGTA TGTATCCTGA CCATCCCCCT TGGCAATCAT TACGTACTAA      500
CTCACTCTTC AGCGCTCCCG CCAACGTCAC CACTGAAGTC AAGAGTGTG      550
AAATGCACCA CCAGCAGCTC GCTGCCGGTC AGCCCGGTGA CAACGTTGGT      600
TTCAACGTGA AGAACGTCTC CGTCAAGGAA ATCCGTCGTG GTAACGTTGC      650
20 TGGTGATAGC AAGAACGACC CCCCTGCCGG TGCTGCTTCC TTCAACGCCC      700
AGGTCATCGT CCTCAACCAC CCGGTCAGG TCGGTGCTGG TTACGCCCCA      750
GTCCTTGACT GCCACACTGC CCACATTGCT TGCAAGTTCT CTGAACTCCT      800
TGAGAAGATT GACCGTCGTA CCGGAAAGTC TGTTGAGGAC CACCCCAAGT      850
TCATCAAGTC CGGTGACGCT GCCAT                                     875

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25

2) INFORMATION FOR SEQ ID NO: 1268

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: WSA-377

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268

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GTGAGCGTGG TATCACCATC GATATTGCCC TCTGGAAATT CGAGACCCCG      50
45 AAGTACAGTG TCACTGTCAT TGGTGAGTGC TTTTACCCC TCTTAAGCAG      100
ATTTCAACTT CCAGAGTATC TACTCTAACA TATCCGCTTA GATGCTCCCG      150
GCCATCGTGA CTTCATCAAG AACATGATCA CTGGTACCTC CCAGGCTGAC      200
TGCGCTATCC TCATCATTGC TGCCGGTACT GGTGAGTTCG AGGCTGGTAT      250
CTCCAAGGAT GGCCAGACTC GTGAGCACGC TCTGCTTGCT TTCACCCCTG      300
50 GTGTGAGGCA ACTCATCGTT GCCATCAACA AGATGGACAC CACCAAGTGG      350
TCCGAGTCCC GTTTCAACGA AATCATCAAG GAGGTTTCCA ACTTCATCAA      400
GAAGGTCGGA TATAACCCCA AGGCTGTTCC CTTCGTGCCA ATCTCTGGTT      450
TCGAGGGTGA CAACATGATT GAACCCTCCC CCAACTGCAC CTGGTACAAG      500

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GGCTGGAACA AGGAGACTGC CTCTGGCAAG TCTTCTGGTA AAACCCTTCT 550
CGATGCCATT GACGCCATTG AACCCCCAAC CCGTCCTACC GATAAGCCTC 600
TCCGTCTTCC CCTCCAGGAT GTTTACAAAA TCTCTGGTAT TGGCACTGTT 650
CCCGTCGGAC GTGTTGAGAC TGGTGTGATC AAGCCCGGTA TGGTCGTGAC 700
5 TTTCGCTCCC TCCAACGTCA CCACTGAAGT CAAGTCCGTC GAGATGCACC 750
ACCAACAACCT CCAGGCTGGT TACCCTGGTG ACAACGTCGG CTTCAACGTC 800
AAGAACGTTT CAGTCAAGGA AGTCCGCCGT GGCAACGTTG CTGGCGACTC 850
CAAAAATGAT CCCCCAAGG GCTGCGAATC CTTCAATGCC CAGGTCATCG 900
TCCTTAACCA CCCCAGGCCAG GTTGGCGCTG GTTATGCCCC AGTCCTCGAC 950
10 TGCCACACTG CCCACATTGC TTGCAAGTTC TCTGAACTCA TTGAGAAGAT 1000
CGACCGCCGT ACTGGAAAGT CTGTTGAGAA CAACCCCAAG TTCATCAAGT 1050
CTGGTGATGC TGCTATCGTC AAGATGGTTC CCTCCAAGCC CATGTGCGTG 1100
GAGCCCTTCA CTGACTATCC CCCT 1124

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15

2) INFORMATION FOR SEQ ID NO: 1269

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20 (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1043 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: Genomic DNA

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      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Trichophyton rubrum
            (B) STRAIN: WSA-224

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30

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      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269

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GTGAGCGTGG TATCACCATC GATATCGCCC TCTGGAAGTT CGAGACCCCC 50
AAGTACAATG TCACCGTCAT TGGTATGTTT CTTTGCCTTG TTCCCTCATG 100
35 TGGTTGTACC ATATCTAACG AGAGTAGACG CCCCCGGTCA CCGTGACTTC 150
ATCAAGAACA TGATCACTGG TACCTCCAG GCTGACTGCG CTATTCTCAT 200
CATTGCTGCC GGTACTGGTG AGTTCGAGGC TGGTATCTCC AAGGATGGCC 250
AGACCCGTGA GCACGCTCTG CTCGCCTTCA CCCTCGGTGT CAAGCAGCTC 300
ATCGTTGCCA TCAACAAGAT GGACACCACC GGCTGGTCCG AGGATCGTTT 350
40 CAAGGAAATT ATCAAGGAAG TCACCAACTT CATCAAGAAG GTTGGCTACG 400
ACCCAAGGGG TGTTCCATTC GTTCCAATCT CTGGTTTCAA CCGTGACAAC 450
ATGATTGAGG CCTCCACCAA CTGCCCATGG TACAAGGGAT GGAACAAGGA 500
GACCAAGGCC GGTGGTGCCA AGTCCGGCAA GACCCTCCTC GAGGCCATCG 550
ATGCCATCGA CATGCCAACC CGTCCTACCG ACAAGCCCCC CCGTCTCCCA 600
45 CTCCAGGATG TCTACAAGAT CTCTGGTATC GGAAGTGTGC CAGTCGGTCG 650
TGTTGAGACC GGTATCATCA AGCCCGGTAT GGTCGTCACC TTNGCCCCCG 700
CCAACGTCAC CACTGAAGTC AAGTCCGTYK AAATGCACCA CCAGCAGCTT 750
CAGCAGGGTG TCCCCGGTGA CAACGTCGGC TTCAATGTCA AGAACGTTT 800
CGTCAAGGAA GTCCGCCGTG GTAACGTTGC CCGTGACTCC AAGAACGACC 850
50 CACCATCCGG CTGTGCCTCC TTCAACGCCC AGGTCATYGT CCTCAACCAC 900
CCCGGCCAGA TCGGTGCTGG TTACGSTCCA GTCCTCGACT GCCACACTGS 950
TCACATTGCT TGCAAGTTCT CTGAGCTCCT CGAGAAGATT GACCGCCGTA 1000
CCGGTAAATC CGTCGAAGCC AACCCCAAGT TCGTCAAGTC TGG 1043

```

2) INFORMATION FOR SEQ ID NO: 1270

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1105 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium canis*
(B) STRAIN: WSA-217

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270

GCTGAGCGTG AGCGTGGTAT CACCATTGAT ATCGCCCTCT GGAAGTTCGA 50
GACCCCCAAG TACATGGTCA CCGTCATCGG TATGCTTTAT CTGTTTCCCA 100
TTTATAGTTG CGACCAGTAA CTAACAAAAA GTAGATGCCC CCGGGCACCG 150
20 TGACTTCATC AAGAACATGA TTACTGGTAC CTCCCAGGCC GACTGCGCTA 200
TTCTCATCAT TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG 250
GATGGCCAGA CTCGTGAGCA CGCCCTGCTC GCTTTCACCC TCGGTGTCAA 300
GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAC TGGTCTGAGT 350
CCCGTTTCGG TGAAATCATC AAGGAAGTCA CCAACTTCAT CAAGAAGGTC 400
25 GGCTACGACC CCAAGGGTGT CCCATTGCTC CCAATCTCTG GCTTCAACGG 450
TGACAACATG ATTGAGCCCT CCACCAACTG CCCATGGTAC AAGGGATGGA 500
ACAAGGAGAC CAAGGCCGGT GGCAAATCCT CTGGTAAGAC CCTCCTTGAG 550
GCCATCGATG CCATTGACAT GCCCACTCGT CCCACCGACA AGCCTCTCCG 600
TCTCCCACTC CAGGATGTCT ACAAGATCTC TGGTATCGGA ACAGTACCAG 650
30 TCGGTCTGTG TGAGACTGGT ATCATCAAGC CTGGTATGGT TGTCACCTTY 700
GCCCCCGCCA ACGTCACCAC TGAAGTCAAG TCCGTCGAAA TGCACCACCA 750
GCAGCTYGTC CAGGGTGTTC CCGGTGACAA CGTTGGCTTC AACGTCAAGA 800
ACGTYTCTGT CAAGGAAGTC CGCCGTGGTA ACGTTGCCGG TGATTCCAAG 850
AACGACCCAC CAGCTGGCTG CGCCTCTTTC AAGGCCCAGG TCATCGTCCT 900
35 CAACCACCCC GGCCAGATCG GTGCTGGTTA CGCCCCAGTC CTTGACTGCC 950
ACACTGCCCC CATTGCTTGC AAGTTCTCTG AGCTTCTTGA GAAGATTGAC 1000
CGCCGTA CTG GTAAATCCGT CGAAACCAGC CTAAGTTCG TCAAGTCTGG 1050
TGATGCCGCT ATTGCCACCA TGGTTCCATC CAAGCCCATG TCGGTTGAGG 1100
CTTTC 1105

40

2) INFORMATION FOR SEQ ID NO: 1271

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus versicolor*

(B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271

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5   GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA AGTTCCAGAC      50
    CCCTAAGTAT GAGGTCACCG TCATTGGTAT GTTGTCTTTC TTGTGTTACC      100
    ATCGAAACAT ATCTAACCTA CAACTGCAGA CGCCCCCGGT CACCGTGACT      150
    TCATCAAGAA CATGATCACT GGTACCTCCC AGGCCGACTG CGCTATTCTC      200
10  ATCATTGCTT CCGGTACTGG TGAATTCGAG GCTGGTATCT CCAAGGATGG      250
    CCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTCGGT GTCCGTCAGC      300
    TCATCGTTGC CCTCAACAAG ATGGACACTG CTGGCTGGGC TGAGGCTCGT      350
    TACAACGAAA TCGTCAAGGA AACTTCCGGT TTCATCAAGA AGGTCGGCTA      400
    CAACCCCAAG TCGGTTCCCT TCGTCCCAT CTCCGGTTTC AACGGTGACA      450
15  ACATGCTTGA GCCCTCCTCC AACTGCCCCT GGTACAAGGG TTGGGAGAAG      500
    GAGACCAAGG CTGGTAAGGC CACTGGTAAG ACCCTCCTCG AGGCCATCGA      550
    CGCCATTGAG CCTCCCGTCC GTCCCTCCAA CAAGCCTCTC CGTCTTCCCC      600
    TCCAGGATGT CTACAAGATC TCTGGTATTG GAACTGTCCC CGTCGGCCGT      650
    GTCGAGACCG GTACCATCGT CCCCGGTATG GTCGTCACCT TCGCTCCCGC      700
20  CAACGTCACC ACTGAAGTCA AGTCCGTTGA GATGCACCAC CAGCAGCTCA      750
    AGGAGGGTGT TCCCGGTKAC AACGTTGGTT TCAACGTGAA GAACGTTTCC      800
    GTCAAGGAAG TCCGCCGTGG TAACGTCGCT GGTGACTCCA AGAACGACCC      850
    CCCTGCCGGT GCTGCCTCTT TCACCGCCCA GGTCATCGTC CTCAACCACC      900
    CCGGTCAGGT CGGCGCTGGT TACGCTCCCG TCCTCGACTG CCACACCGCT      950
25  CACATTGCCT GCAAGTTCGC TGAGCTCCAG GAGAAGATCG ACCGCCGTAC      1000
    CGGAAAGTCT GTCGAATYTG CCCCCAAGTT CATCAAGTCT GGTGACGCCG      1050
    CTATCGTCAA GATGATTCCC TCCAAGCCCA TGTGTGTCGA GTCTTTCACT      1100
    GACTACCCTC CTYTCGGCCG TTTCGCCGTC CGTGACGTAA GTTCTTTCCC      1150
    CAGCTTTTCG ATGCTACCTT TCTMTGAATC ACGTGTCATG TCTTGGCACC      1200
30  CGCCCATCAC ATGACCACGC AACCCTATAC CCCGCCACAC CCTT          1244

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2) INFORMATION FOR SEQ ID NO: 1272

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1032 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Exophiala moniliae*

(B) STRAIN: WSA-219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272

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50  GCTGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT GGAAGTTCGA      50
    GACCCCAAG TACTATGTCA CCGTCATCGA CGCCCCCGGT CATCGTGACT      100
    TCATCAAGAA CATGATCACT GGTACTTCCC AAGCTGACTG CGCCATTCTC      150
    ATCATTGCTG CCGGTACTGG TGAATTCGAA GCCGGTATCT CCAAGGATGG      200

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	TCAGACCCGT	GAGCACGCTC	TGCTTGCCTA	CACCCTGGGT	GTCAAGCAGC	250
	TCATTGTCGC	CATCAACAAG	ATGGACACTA	CCAAGTGGTC	TGAGGACCGT	300
	TTCAACGAAA	TCATCAAGGA	GACTTCCAGC	TTCATCAAGA	AGGTCGGCTA	350
	CAACCCCAAG	TCCGTTCCCT	TCGTCCCCAT	CTCCGGCTTC	AACGGTGACA	400
5	ACATGATCGA	CGTCTCCACC	AACTGCCCCCT	GGTACAAGGG	CTGGGAGAAG	450
	GAGACCAAGG	CTGGCAAGGC	CTCTGGCAAG	ACTCTCCTTG	AGGCCATCGA	500
	CGCCATTGAC	CCCCCCTCTC	GTCCCACCGA	CAAGCCTYTC	CGTCTCCCTC	550
	TCCAGGATGT	GTACAAGATC	TCTGGTATCG	GAACGGTGCC	CGTCGGTCGT	600
	GTCGAGACTG	GATCATCAA	GGCCGGTATG	GTCGTTACCT	TCGCTCCTGC	650
10	CAACGTCACC	ACTGAAGTCA	AGTCCGTCGA	AATGCACCAC	GAACAGCTCG	700
	CCGAGGGTGT	TCCAGGTGAC	AACGTCGGTT	TCAACGTCAA	GAACGTYTCC	750
	GTCAAGGAGG	TTCGTCTGG	AAACGTTTGC	GGTGACTCCA	AGAACGACCC	800
	ACCCAAGGGC	GCTGATTCCCT	TCAACGCCCA	GGTCATCGTC	TTGAACCACC	850
	CTGGTCAAGT	TGGTGCTGGC	TACGCCCCAG	TGTTGGATTG	CCCACTGCC	900
15	CACATTGCTT	GCAAGTTCTC	TGAGCTTCTC	GAGAAGATCG	ATCGTCGKAC	950
	CGGAAAGTCG	ATCGAAAACA	ACCCCAAGTT	CATCAAGTCT	GGTGACGCTG	1000
	CCATCGTCAA	GATGGTTCCC	AGCAAGCCCA	TG		1032

20

2) INFORMATION FOR SEQ ID NO: 1273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hortaea werneckii*
 (B) STRAIN: ATCC 34944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273

	TAACAGCCCG	TGCGACCGTC	TCGTCCAATA	ACTAATGATT	CGCAGGTACT	50
	ATGTCGTGAG	TATCCGGTCC	TTTTTTGTTA	ATTTACCAGA	AATGACGAAA	100
	TTTTTGACTA	ATTAACACAC	TCAGACCGTC	ATTGACGCC	CGGGTCACCG	150
40	TGACTTCATC	AAGAACATGA	TCACTGGTAC	CTCCCAGGCC	GACTGCGCTG	200
	TCCTCATCAT	TGCTGCCGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	250
	GATGGCCAGA	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	300
	GCAGCTCATC	GTCGCCATCA	ATAAGATGGA	CACCACCAAG	TGGTCCGAGG	350
	AGCGTTACGG	CGAGATCATC	AAGGAGACCT	CTGCCTTCAT	CAAGAAGGTC	400
45	GGTTTCAACC	CGAAGCACGT	CCCGTTTCGT	CCGATCTCCG	GTTTCAACGG	450
	TGACAACATG	ATCGAGGCCCT	YCACCAACTG	CCCGTGGTAC	AAGGGCTGGG	500
	AGAAGGAGAC	CAAGGCCAAG	GTCACCGGCA	AGACCCTYCT	TGAGGCCATT	550
	GACAACATCG	ACCCGCCGAG	CCGTCCTTCC	GACAAGCCGC	TCCGTCTTCC	600
	CCTCCAGGAT	GTCTACAAGA	TCGGTGGTAT	TGGGACAGTC	CCAGTCGGCC	650
50	GTGTCGAGAC	CGGTACCATC	AAGGCCGGCA	TGGTCGTTAC	CTTCGCTCCG	700
	GCTGGTGTCA	CCACTGAAGT	GAAGTCCGTT	GARATGCACC	ACGAGCAGCT	750
	CGCTGAGGGT	YTGCCGGGTG	ACAACGTCGG	CTTCAACGTC	AAGAACGTTT	800
	CCGTCAAGGA	GATCCGTCGT	GGCAACGTTG	CTGGTGACAG	CAAGGCTGAC	850

	CCGCCGAAGG	GCTGCGACAG	CTTCAACGCC	CAGGTCATCG	TCCTGAACCA	900
	CCCTGGCCAG	GTCGGTGCTG	GTTACGCTCC	AGTCCTGGAC	TGCCACACTG	950
	CCCACATTGC	CTGCAAGTTC	GGCGAGCTCC	TCGAGAAGAT	CGACCGTCGC	1000
	TYTGGCAAGT	CCATTGAAGC	CTYGCCTAAG	TACATCAAGT	CTGGTGACGC	1050
5	TGCCATYGTC	AAGATGATTC	CGTCCAAGCC	GATGTGCGTT	GAGCCATTCA	1100
	CTGAGT					1106

10 2) INFORMATION FOR SEQ ID NO: 1274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
 (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274

25	CTCAAGGCCG	AGCGTGAGCG	TGGTATCACC	ATCGACATTG	CCCTCTGGAA	50
	GTTCGAGACT	CCCCGCTACT	ATGTCACCGT	CATTGGTATG	TTGCTGTCAC	100
	CTCTCTCACA	CATGTCTCAC	CACTAACAAT	CAACAGACGC	CCCCGGCCAC	150
	CGTGATTTC	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGACTGCGC	200
30	CATTCTCATC	ATTGCCGCCG	GTA CTGGTGA	GTTCGAGGCT	GGTATCTCCA	250
	AGGATGGCCA	GACCCGTGAG	CACGCCCTGC	TCGCCTACAC	CCTCGGTGTC	300
	AAGAACCTCA	TTGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCCGA	350
	GTCCC GTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAACTTC	ATCAAGAAGG	400
	TCGGCTACAA	CCCCAAGGCT	GTCGCTTTCG	TCCCCATCTC	CGGTTTCAAC	450
35	GGCGACAACA	TGCTTACTCC	CTCCACCAAC	TGCCCCCTGGT	ACAAGGGCTG	500
	GGAGCGTGAG	ATCAAGTCCG	GCAAGCTCAC	TGGCAAGACC	CTCCTCGAGG	550
	CCATTGACTC	CATCGAGCCC	CCCAAGCGTC	CCGTCGACAA	GCCCC TYCGA	600
	CTTCCCCTCC	AGGATGTCTA	CAAGATCGGT	GGTATTGGCA	CGGTTCCCGT	650
	CGGCCGTATC	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTMG	700
40	CCCCCTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	750
	CAGCTCTYTG	AGGGTCTTCC	CGGTGACAAC	GTCGGCTTCA	ACGTGAAGAA	800
	CGTYTCCGTC	AAGGAGATCC	GACGTGGCAA	CGTCGCTGGT	GA CTCCAAGA	850
	ACGACCCCCC	TYTGGGTGCC	GCCTCTTTCA	CCGCCCAGGT	CATTGTCCTC	900
	AACCACCCTG	GCCAGGTCGG	TGCCGGTTAC	GCCCCCGTTY	TGGACTGCCA	950
45	CACTGCCCCAC	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	1000
	GCCGA ACTGG	TAAGGCTGTT	GAGTCCGCCC	CCAAGTTCAT	CAAGTCTGGT	1050
	GACTCCGCCA	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GCGTTGAGGC	1100
	TTTCACTGAC	TACCCCCCT				1119

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2) INFORMATION FOR SEQ ID NO: 1275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
 (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275

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15 CTGAAGTCTG AGCGTGAGCG TGGTATCACT ATCGATATCG CCCTCTGGAA      50
   GTTCGAGACC CCCAAGTACA TGGTCACCGT CATCGATGCC CCCGGTCACC      100
   GTGATTTTCAT CAAGAACATG ATCACTGGTA CCTCCCAGGC TGA CTGCGCC      150
   ATTCTCATCA TTGCTGCCGG TACTGGTGAG TTCGAGGCTG GTATCTCCAA      200
   GGATGGCCAG ACTCGTGAGC ACGCTCTCCT CGCCTACACC CTTGGTGTCA      250
20 AGCAGCTCAT CGTTGCCATC AACAAGATGG ACACCACCAA GTGGTCTGAG      300
   GCCCGTTACC AGGAGATCAT CAAGGAGACC TCCGGTTTCA TCAAGAAGGT      350
   CGGCTACAAC CCCAAGCACG TTCCCTTCGT CCCCATCTCC GGCTTCAACG      400
   GAGACAACAT GATCGAGGTC AGCTCCAAC TCCCTTGGTA CAAGGGTTGG      450
   GAGAAGGAGA CCAAGGCCAA GGCCACTGGC AAGACCCTCC TCGAGGCCAT      500
25 TGACGCCATC GACCCTCCTT CCCGTCTAC CGACAAGCCC CTCCGTCTTC      550
   CCCTCCAGGA TGTCTACAAG ATCGGTGGTA TTGGCACGGT GCCCGTCGGT      600
   CGTGTTGAGA CCGGTAAGAT CATGGGTGGT ATGGTTGTCA CCTTCGCCCC      650
   CGCTGGTGTC ACCACCGAGG TCAAGTCCGT CGAGATGCAC CACGAGCAGC      700
   TCACCGAGGG TCTTCCCGGT GACAACGTCG GCTTCAACGT CAAGAACGTY      750
30 TCCGTCAAGG AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA      800
   CCCCCCAAG GGTGTGACT CTTTCAACGC CCAGGTCATC GTCCTGAACC      850
   ACCCTGGTCA GGTCCGGTGCT GGTTACGCAC CCGTCCTCGA CTGCCACACT      900
   GCCCACATTG CTTGCAAGTT YTCCGAGCTT GTTGAGAAGA TTGACCGCAG      950
   AACCGGCAAG TCCGTTGAGG CTGCCCCCAA GTTCATCAAG TCTGGTGACG      1000
35 CCGCCATCGT CAAGATGGTT CCCTCCAAGC CCATGTGTGT TGAGGCTTTC      1050
   ACCGACTACC CTCCTYTCGG TCGTTTCGCC GTCCGGTATG TTTTCTTCT      1100
   TCAATCATTC TTC                                     1113

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2) INFORMATION FOR SEQ ID NO: 1276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastomyces dermatitidis*
 (B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276

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5   GGTCTGAGAC CCGTTTCAAC GAAATTATCA AGGAAGTCAG CAACTTCATC   50
    AAGAAGGTCG GATACAACCC CAAGTCTGTT CCCTTCGTGC CAATCTCCGG   100
    TTTCGAGGGT GACAACATGA TTGAGCCTTC CCCCAACTGC CCTTGGTACA   150
    AGGGCTGGAA CAAGGAGACT GCTGCTGGCA AGGCCGCCGG TAAGACTCTT   200
    CTCGATGCCA TTGACGCCAT CGACCCCCCC GTCCGTCCTA CCGAGAAGCC   250
    TCTCCGTCTT CCCCTCCAGG ATGTGTACAA GATCTCCGGT ATTGGCACTG   300
10  TTCCCGTTGG ACGTGTGCGAG ACTGGTGTCA TCAAGCCTGG TATGGTCGTG   350
    ACCTTCGCCC CTGCCAACGT CACCACTGAA GTCAAGTCCG TTGAAATGCA   400
    CCACCAGCAG CTCCAGGCTG GTTACCCTGG TGACAACGTC GGCTTCAACG   450
    TCAAGAACGT TTCCGTCAAG GAAGTCCGCC GTGGCAACGT TGCCGGTGAC   500
    TCCAAGAACG ACCCCCCCAA GGGCTGCGAG TCCTTCAACG CCCAGGTCAT   550
15  CGTCCTCAAC CACCCCGGCC AGGTTGGCGC TGGTTATGCC CCAGTCCTCG   600
    ACTGCCACAC TGCCACATT GCTTGCAAGT TCTCTGAGCT CATCGAGAAG   650
    ATTGACCGCC GTACCGGAAA GTCTGTTGAG GACAACCCCA AGTTCATCAA   700
    GTCCGGTGAT GCTGCTATCG TCAAGATGAT T              731

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2) INFORMATION FOR SEQ ID NO: 1277

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 1046 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Exophiala dermatitidis
    (B) STRAIN: ATCC 76088

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277

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    CCGAGCGTGA GCGTGGTATC ACCATCGATA TCGCCCTCTG GAAGTTCGAG   50
    ACCCCCAAGT ACTATGTCAC CGTCATCGAC GCCCCGGGTC ATCGTGA CTT   100
40  TATCAAGAAC ATGATCACTG GTACCTCGCA GGCCGACTGC GCCATCTTGA   150
    TCATTGCCGC CGGTACCGGT GAATTCGAAG CCGGTATCTC CAAGGATGGT   200
    CAGACCCGTG AGCACGCTCT GCTCGCTTAC ACCTTGGGTG TCAAGCAGCT   250
    CATCGTCGCC ATCAACAAGA TGGACACCAC CAAGTGGTCC GAGGAGCGTT   300
    TCAACGAAAT CATCAAGGAG ACTTCCAAC TCAATCAAGAA GGTCGGCTAC   350
45  AACCCCAAGG CCGTTCCTTT CGTCCCCATC TCCGGCTTCA ACGGTGACAA   400
    CATGATTGAG GTCTCCACCA ACTGCCCCGTG GTACAAGGGA TGGGAGAAGG   450
    AGTCCAAGGC TGGCAAGGCC ACCGGCAAGA CCCTCCTCGA GGCCATTGAC   500
    GCCATCGACC CACCCACCCG TCCCACCGAC AAGCCTCTCC GTCTCCCTCT   550
    CCAGGATGTC TACAAGATCT CTGGTATCGG AACGGTTCCT GTCGGTCGTG   600
50  TCGAGACCGG TACCATCAAG GCCGGTATGG TCGTCACCTT CGCTCCGGCC   650
    AACGTCACCA CTGAAGTCAA GTCCGTCGAA ATGCACCACG AGCAGCTCGC   700
    CGAGGGTYTG CCAGGTGACA ACGTTGGCTT CAACGTCAAG AACGTYTCCG   750
    TCAAGGAGGT TCGTCGTGGT AACGTTGCCG GTGACTCCAA GAACGACCCG   800

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	CCCAAGGGTG	CCGAGTCCTT	CAACGCCCAG	GTCATTGTCC	TCAACCACCC	850
	TGGTCAGATC	GGTGCCGGCT	ACGCTCCAGT	CTTGGATTGC	CACACTGCCC	900
	ACATTGCTTG	CAAGTTCGCC	GAGTTGCTCG	AGAAGATCGA	CCGTCGTACC	950
	GGAAAGTCCA	TCGAGAACAA	CCCCAAGTTC	ATCAAGTCTG	GTGATGCTGC	1000
5	CATCGTCAAG	ATGATTCCCA	GCAAGCCCAT	GTGTGTCGAG	GCTTTC	1046

2) INFORMATION FOR SEQ ID NO: 1278

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
 (B) STRAIN: WSA-213

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278

25	CGTGAGCGTG	GTATCACCAT	CGATATTGCT	CTCTGGAAGT	TCGAGACTCC	50
	TCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GTCGCTCATA	CCTCATCCTA	100
	CTTCCTCATA	CTAACACATC	ATTCAGACGC	TCCCGGTCAC	CGTGATTTC	150
	TCAAGAACAT	GATCACTGGT	ACTTCCCAGG	CCGATTGCGC	CATTCTCATC	200
	ATTGCCGCGG	GTA CTGGTGA	GTTCGAGGCT	GGTATCTCCA	AGGATGGCCA	250
30	GACCCGTGAG	CACGCTCTTC	TTGCCTACAC	CCTTGGTGTC	AAGAACCTCA	300
	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AGTGGTCTGA	GGCCCGTTAC	350
	CAGGAGATCA	TCAAGGAGAC	CTCCTCTTTC	ATCAAGAAGG	TCGGCTACAA	400
	CCCCAAGGCT	GTCGCTTTTC	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	450
	TGCTTACCCC	CTCCACCAAC	TGCCCCTGGT	ACAAGGGTTG	GGAGCGTGAG	500
35	ATCAAGTCCG	GCAAGCTCTC	CGGCAAGACC	CTCCTCGAGG	CCATTGACTC	550
	CATCGAGCCT	CCCAAGCGTC	CCGTTGACAA	GCCCCTCCGT	CTTCCCCCTCC	600
	AGGATGTCTA	CAAGATCGGT	GGTATTGGAA	CGGTTCCCGT	CGGCCGTATT	650
	GAGACTGGTG	TCATCAAGCC	CGGTATGGTC	GTTACCTTCG	CTCCCTCCAA	700
	CGTCACCACT	GAAGTCAAGT	CCGTCGARAT	GCACCACGAG	CAGYTCAGTK	750
40	AGGGCCAGCC	CGGTGACAAC	GTTGGTTTCA	ACGTGAAGAA	CGTTTCCGTC	800
	AAGGACATCC	GACGTGGTAA	CGTCGCTGGT	GA CTCCAAGA	ACGACCCCCC	850
	CCAGGGTGCC	GCTTCTTTCA	CCGCCCAGGT	CATCGTCCTC	AACCACCCCG	900
	GCCAGGTCGG	TGCTGGTTAC	GCTCCTGTCC	TCGATTGCCA	CACTGCCCAC	950
	ATTGCCTGCA	AGTTCGCCGA	GATCCAGGAG	AAGATCGACC	GCCGAACCGG	1000
45	TAAGGCTACT	GAGGCCGCTC	CCAAGTTCAT	CAAGTCTGGT	GA CTCCGCCA	1050
	TCGTCAAGAT	GGTTCCCTCC	AAGCCCATGT	GTGTGCGAGG	TTTCACTGAC	1100
	TACCCTCCT					1109

50

2) INFORMATION FOR SEQ ID NO: 1279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus terreus*
 (B) STRAIN: WSA-174

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279

15 CCTGCAAGTG GTCTGAGGAC CGTTACAACG AAATCGTGAA GGAGACCTCC 50
 AACTTCATCA AGAAGGTCGG CTACAACCCC AAGGCCGTTC CTTTCGTCCC 100
 CATCTCCGGT TTCAACGGTG ACAACATGCT TGAGCCTTCC CCCAACTGCC 150
 CCTGGTACAA GGGTTGGGAG AAGGAGGGCA AGTCCGGCAA GGTCACCGGT 200
 AAGACTCTCC TCGAGGCCAT CGATGCCATC GAGCCCCCGG TCCGTCCTGC 250
 CAACAAGCCT CTCCGTCTTC CCCTCCAGGA TGTGTACAAG ATCTCTGGTA 300
 20 TCGGAAGTGT CCCCCTCGGC CGTGTGCGAGA CTGGTGTCAT CACCCCCGGC 350
 ATGGTTGTTA CTTTCGCTCC TTCCAACGTC ACCACTGAAG TGAAGTCCGT 400
 TGAGATGCAC CACCAGCAGC TCAAGGAGGG TCTCCCCGGT GACAACGTTG 450
 GTTTCAACGT CAAGAACGTC TCCGTCAAGG AGGTCCGTCG TGGTAACGTC 500
 GCTGGTGACT CCAAGAACGA CCCCCCTGCT GGCGCTGCCT CTTTCACCGC 550
 25 CCAGGTCATC GTTCTCAACC ACCCCGGTCA GGTCGGCGCT GGCTACGCCC 600
 CCGTCCTCGA CTGCCACACT GCCCACATTG CCTGCAAGTT CGCTGAGCTC 650
 CAGGAGAAGA TTGACCGCCG TACCGGAAAG TCTGTTGAGT CTTCTCCCAA 700
 GTTCATCAAG TCTGGTGATG CTGCCATCGT CAAGATGATC CCTYCAAAGC 750
 CCATGTGCGT CGAAG 765
 30

2) INFORMATION FOR SEQ ID NO: 1280

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280

50 GCGTGGTATC ACCATCGACA TTGCCCTCTG GAAGTTCCAG ACTCCCAAGT 50
 ATGAGGTCAC TGTCATCGGT AAGCTCGACT CGCCCCGATA TGTTTTGGTG 100
 CTGTAGCTAA CACGATCTGA AGATGCCCCC GGTCACCGTG ACTTCATCAA 150
 GAACATGATC ACTGGTACCT CCCAGGCTGA CTGCGCTATC CTCATCATTTG 200
 CCTCCGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACC 250

	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	GGTGTCAAGC	AGCTCATCGT	300
	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	GTCCGAGGAT	CGTTACAACG	350
	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	AGAAGGTCGG	CTACAACCCC	400
	AAGGCCGTTT	CCTTCGTMCC	CATCKCTGGC	TTC AACGGTG	ACAACATGCT	450
5	TGAGCCCTCC	TCCAAC TGCC	CCTGGTACAA	GGGATGGGAG	AAGGAGACCA	500
	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	TCGAGGCCAT	YGACGCCATT	550
	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	CTYCGTCTTC	CCCTCCAGGA	600
	TGTYTACAAG	ATCTCTGGTA	TCGGAACGGT	CCCTGTCGGC	CGTGTCGAGA	650
	CCGGTATCAT	CAAGCCCGGC	ATGGTCGTCA	CCTTTGCCCC	CGCCAACGTC	700
10	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	CACCAGCAGC	TCCAGGAGGG	750
	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	CAAGAACGTT	TCCGTCAAGG	800
	AAGTCCSCCG	TGGTAACGTT	TGCGGTGACT	CCAAGAACGA	TCCCCCTCAG	850
	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	GTCTCTCAACC	ACCCCGGTCA	900
	GGTCGGCGCT	GGTTACGCCC	CCGTCTCTGA	CTGCCACACT	GCCACATTG	950
15	CTTGCAAGTT	CTYTGAGCTG	CTTGAGAAGA	TTGACCGCCG	TACCGGCAAG	1000
	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	TCCGGTGAWG	CCGCCATCGT	1050
	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	CGAGTCCTTC	ACTGACTACC	1100
	CCCCT					1105

20

2) INFORMATION FOR SEQ ID NO: 1281

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 1343 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus laurentii*
(B) STRAIN: ATCC 44096
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281

	GCCGAGCGAG	AGCGAGGTAT	CACCATCGAC	ATTGCTCTCT	GGAAGTTCTGA	50
	GACCCCCAAG	TACAACGTCA	CCGTCAATTGA	CGCCCCCGGA	CACCGAGACT	100
40	TCATCAAGAA	CATGATCACC	GGTACCTCCC	AGGCCGACTG	CGCCATCCTT	150
	ATCATTGCCA	CCGGTATCGG	AGAGTTTCGAG	GCCGGTATCT	CTAAGGACGG	200
	TCAGACCCGA	GAGCACGCTT	TGCTCGCCTT	CACCCTCGGT	GTCAGGCAGC	250
	TCATCGTTGC	TTGCAACAAG	ATGGACACCT	GCAAGTGGTC	CGAGGACCGA	300
	TTCAACGAGA	TCGTCAAGGA	GACCAACGGT	TTCATCAAGA	AGGTCGGATA	350
45	CAACCCCAAG	GCTGTTCCCT	TCGTCCCCAT	CTCTGGATGG	CACGGAGACA	400
	AGTGAGTGCC	GTTCTTTGCG	TTGAGCCCTC	TTTGTCGCTC	CCCCCTCCCTC	450
	TCAAGTGGCG	GCGGCGGTCT	CCACCCACAA	ATCGGGTGGC	GAATCCGCCA	500
	CACCCACCAC	TTCTCGCCAC	CGAGTGTGGC	ACTTCTTCCA	ACTCCTCTTT	550
	CCACTCCTCC	TCGTCTCGTC	TCTTTTTTTC	TCCGTTGTCT	TTGACAAGGG	600
50	GAGTGTGCTG	ATAGTAAAGC	ATGCTTGAGG	AGACCACCAA	CATGCCGTGG	650
	TACAAGGGAT	GGACCAAGGA	GACCAAGTCC	GGTGTCGTTA	AGGGTAAGAC	700
	CCTCCTCGAC	GCCATCGACG	CCATCGAGCC	TCCTCAACGA	CCCACCGACA	750
	AGCCCCCTCCG	ACTTCCCCTC	CAGGATGTCT	ACAAGATCGG	TGGTATCGGT	800

	ACGGTGCCCCG	TCGGCCGAGT	CGAGACCGGT	GTCATCAAGG	CCGGGTAAAGT	850
	CACGGGAGCC	TGACGGCTGT	TGTTGCCACA	CCCAACTTAT	ATCCAGTATG	900
	GTCGTACACT	TCGCTCCTAC	CAACGTCACC	ACTGAGGTTA	AGTCCGTTGA	950
	GATGCACCAC	GAGCAGATCC	CTGAGGGTCT	TCCCGGAGAC	AACGTTGGTT	1000
5	TCAACGTGAA	GAACGTTTCC	ATCAAGGACA	TCCGACGAGG	AAACGTYTGC	1050
	TCCGACTCCA	AGAACGACCC	CGCTAAGGAG	GCCGCTTCTT	TCAACGCCCCA	1100
	GGTCATTGTC	CTCAACCACC	CTGGACAGAT	TGGTGCCGGT	TACACCCCCG	1150
	TCCTCGACTG	CCACACCGCC	CACATTGCCT	GCAAGTTCGC	CGAGCTCATC	1200
	GAGAAGATCG	ACCGACGAAC	TGGTAAGACC	ATGGAGGCCG	CCCCCAAGTT	1250
10	CGTCAAGTCC	GGAGACGCCG	CCATTGTCAA	GCTCGTTGCC	CAGAAGCCCCA	1300
	TCTGTGTCGA	GTCTTACTCT	GACTACCCTC	CCCTTGGACG	ATT	1343

15 2) INFORMATION FOR SEQ ID NO: 1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282

30	TGGTCCGAGG	CTCGTTTCAA	CGAAATCATC	AAGGAAGTCA	CCAACTTCAT	50
	CAAGAAGGTC	GGATACAACC	CCAAGTCTGT	TCCCTTCGTG	CCAATCTCTG	100
	GTTTCGAGGG	TGATAACATG	ATTGAGCCCT	CCACCAACTG	CCCCTGGTAC	150
	AAGGGCTGGA	CCAAGGAGAC	CGCTGCCGGC	AAGTCAACCG	GTAAGACTCT	200
35	TCTTGACGCC	ATTGATGCCA	TCGATCAACC	CTCCCCTCCT	ACCGACAAGC	250
	CCCTCCGTCT	TCCCCTCCAG	GATGTGTACA	AGATCTCCGG	TATTGGCACT	300
	GTTCCCCTTG	GACGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTCGT	350
	GACCTTCGCT	CCCTCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	400
	ACCACCAACA	GCTCTTGGCT	GGTAACCCCG	GTGACAACGT	CGGTTTCAAC	450
40	GTCAAGAACG	TTTCCGTCAA	GGAAGTCCGC	CGTGGCAACG	TTGCTGGTGA	500
	CTCAAAGAAC	GACCCCCCCA	AGGGCTGCGA	CTCCTTCAAC	GCCCAGGTCA	550
	TCGTCTCTCA	TCACCCCGGT	CAAGTTGGCG	CTGGTTATGC	CCCAGTCCTC	600
	GACTGCCACA	CTGCCCACAT	TGCTTGCAAG	TTCTCTGAGC	TCCTCGAGAA	650
	GATTGACCGC	CGTACCGGAA	AGTCCACTGA	GAACAACCCC	AAGTTCATCA	700
45	AGTCTGGTGA	CGCCGCTATC	GTCAAGATGG	TTCC		734

2) INFORMATION FOR SEQ ID NO: 1283

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 62877

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283

	CGTGAGCGTG	GTATCACCAT	CGACATTGCC	CTCTGGAAGT	TCGAGACTCC	50
	CCGCTACTAT	GTCACCGTCA	TTGGTATGTT	GCTGTCACCT	CTCTCACACA	100
	TGTCTCACCA	CTAACAATCA	ACAGACGCCC	CCGGCCACCG	TGACTTCATC	150
15	AAGAACATGA	TCACTGGTAC	TTCCCAGGCC	GACTGCGCCA	TTCTCATCAT	200
	TGCCGCTGGT	ACTGGTGAGT	TCGAGGCTGG	TATCTCCAAG	GATGGCCAGA	250
	CCCGTGAGCA	CGCCCTGCTC	GCCTACACCC	TCGGTGTCAA	GAACCTCATT	300
	GTCGCCATCA	ACAAGATGGA	CACCACCAAG	TGGTCCGAGT	CCCGTTACCA	350
	GGAGATCATC	AAGGAGACCT	CCAACTTCAT	CAAGAAGGTC	GGCTACAACC	400
20	CCAAGGCTGT	CGCTTTCGTC	CCCATCTCCG	GTTTCAACGG	CGACAACATG	450
	CTTACTCCCT	CCACCAACTG	CCCCTGGTAC	AAGGGCTGGG	AGCGTGAGAT	500
	CAAGTCCGGC	AAGCTCACTG	GCAAGACCCT	CCTCGAGGCC	ATTGACTCCA	550
	TCGAGCCCCC	CAAGCGTCCC	GTCGACAAGC	CCCTCCGACT	TCCCCCTCCAG	600
	GATGTCTACA	AGATCGGTGG	TATTGGCACG	GTTCCCGTCG	GCCGTATCGA	650
25	GACTGGTGTC	ATCAAGCCCC	GTATGGTCGT	TACCTTCGCC	CCCTCCAACG	700
	TCACCACTGA	AGTCAAGTCC	GTCGAGATGC	ACCACGAGCA	GCTCTYTGAG	750
	GGTCTTCCCC	GTGACAACGT	CGGCTTCAAC	GTKAAGAACG	TYTCCGTCAA	800
	GGAGATCCGA	CGTGGCAACG	TCGCTGGTGA	CTCCAAGAAC	GACCCCCCTY	850
	TGGGTGCCGC	CTCTTTCACC	GCCCAGGTCA	TTGTCCCTCAA	CCACCCTGGC	900
30	CAGGTCGGTG	CCGGTTACGC	CCCCGTTYTG	GACTGCCACA	CTGCCCACAT	950
	TGCCTGCAAG	TTCGCCGAGA	TCCAGGAGAA	GATCGACCGC	CGAACTGGTA	1000
	AGGCTGTTGA	GTCCGCCCCC	AAGTTCATCA	AGTCTGGTGA	CTCCGCCATC	1050
	GTCAAGATGG	TTCCCTCCAA	GCCCATGTGC	GTTGAGGCTT	TCACTGACTA	1100
	CCCCCCT					1107

35

2) INFORMATION FOR SEQ ID NO: 1284

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1045 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
(B) STRAIN: ATCC 14285

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284

	GCTCAAGGCC	GAGCGTGAGC	GCGGTATCAC	CATCGATATT	GCTCTGTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	TACGTCACCG	TCATTGACGC	CCCCGGTCAT	100
	CGCGATTTCA	TCAAGAACAT	GATCACTGGT	ACCTCGCAGG	CCGACTGCGC	150
	CATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTCGAGGCT	GGTATCTCCA	200
5	AGGATGGCCA	GACTCGTGAG	CACGCTCTGC	TCGCCTACAC	CCTGGGTGTG	250
	CGGCAGCTGA	TCGTCGCCAT	CAACAAGATG	GACACGGCCA	AGTGGGCTGA	300
	GGCTCGTTAC	CAGGAGATCA	TCAAGGAGAC	CTCCAAC TTC	ATCAAGAAGG	350
	TCGGCTACAA	CCCCAAGACT	GTTGCCTTCG	TCCCCATCTC	GGGCTTCAC	400
	GGCGACAACA	TGCTTACTCC	CTCGACCAAC	TGCCCCCTGGT	ACAAGGGCTG	450
10	GGAGAAGGAG	GGCAAGAGCG	GCAAGGTTAC	CGGTAAGACT	CTGCTGGACG	500
	CCATTGACGC	CGTCGAGCCC	CCCAAGCGCC	CCACGGACAA	GCCCCTGCGT	550
	CTGCCCCCTCC	AGGATGTCTA	CAAGATCGGC	GGTATCGGCA	CTGTCCCTGT	600
	CGGCCGTATC	GAGACTGGTG	TCCTGAAGCC	CGGCATGGTC	GTCACCTTTG	650
	CCCCGTCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAGAT	GCACCACGAG	700
15	CAGCTTGTTG	AGGGTGTTCC	CGGCGACAAC	GTGGGCTTCA	ACGTCAAGAA	750
	CGTYTCCGTC	AAGGAGATCC	GTYGTGGCAA	CGTTGCCGGT	GA CTCCAAGA	800
	ACGACCCCCC	CTCGGGCGCC	GCCACCTTCA	ACGCCCAGGT	CATTGTCCTG	850
	AACCACCCCG	GCCAGGTCGG	CAACGGCTAC	GCCCCGGTTY	TGGACTGCCA	900
	CACCGCCAC	ATTGCCTGCA	AGTTCACCGA	GATCCTTGAG	AAGATCGACC	950
20	GCCGTACCGG	CAAGTCGGTT	GAGAACAACC	CCAAGTTCAT	CAAGTCGGGT	1000
	GACGCCGCCA	TTGTCAAGCT	GACGCCCTYG	AAGCCCATGT	GCGTT	1045

25 2) INFORMATION FOR SEQ ID NO: 1285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285

40	TTGCCAGTGG	TCCGAGGCC	GTTACAACGA	AATCGTCAAG	GAGACTTCCG	50
	GTTTCATCAA	GAAGGTCGGA	TACAACCCCA	AGTCCGTTGC	CTTCGTCCCC	100
	ATCTCCGGTT	TCAACGGTGA	CAACATGCTC	GAGGCCTCTA	CCAACTGCCC	150
	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	GGCCGGTAAG	GCCACTGGTA	200
45	AGACCCTCCT	TGAGGCCATC	GACGCCATTG	AGCCCCCCAC	CCGTCCCTCC	250
	AACAAGCCCC	TCCGTCTTCC	CCTCCAGGAT	GTCTACAAGA	TCTCCGGTAT	300
	TGGAAGTGTC	CCCGTCGGCC	GTGTCGAGAC	TGGTGTTATC	ACCCCCGGCA	350
	TGGTCGTCAC	CTTCGCTCCT	GCCAACGTCA	CCACTGAAGT	CAAGTCCGTT	400
	GAGATGCACC	ACCAGCAGCT	CAAGGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
50	TTTCAACGTC	AAGAACGTTT	CCGTCAAGGA	AATCCGTCGT	GGTAACGTTG	500
	CCTCCGACTC	CAAGAACGAC	CCCGCCTCCG	GCGCTGCCTC	TTTCAACGCC	550
	CAGGTCATCG	TTCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	GTTACGCCCC	600
	CGTCCTCGAC	TGCCACACCG	CCCACATTGC	TTGCAAGTTC	TCTGAGCTTC	650

TTGAGAAGAT	TGACCGCCGT	ACCGGAAAGG	CTGTTGAAAC	CAGCCCCAAG	700
TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	CTTCCAAGCC	750
CATGTGCGKT	CCGA				764

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2) INFORMATION FOR SEQ ID NO: 1286

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 971 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 16264

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286

ACCATCGATA	TCGCGCTCTG	GAAGTTCGAG	ACTCCCAAGT	ACTTCGTCAC	50
CGTCATCGAT	GCCCCTGGTC	ATCGTGACTT	CATCAAGAAC	ATGATCACTG	100
25 GTACCTCCCA	GGCTGATTGT	GCTATTCTCA	TCATTGCCGC	TGGTACTGGT	150
GAGTTCGAGG	CCGGTATCTC	CAAGGATGGC	CAGACCCGTG	AGCATGCTCT	200
GCTCGCCTAC	ACCCTGGGCG	TGAAGCAGCT	TATCGTCGCC	ATCAACAAGA	250
TGGACACCAC	CAAATGGTCT	GAGGATCGTT	TCAACGAAAT	CATCAAGGAG	300
ACTTCCAAC	TCATCAAGAA	GGTCGGATAC	AACCCCAAGT	CCGTTCATT	350
30 CGTGCCCATC	TCCGGCTTCA	ACGGTGACAA	CATGATCGAC	GTCTCCACCA	400
ATGCCCCCTG	GTACAAGGGC	TGGGAAAAGG	AGTCCAAGGC	TGGCAAGGCC	450
ACCGGCAAGA	CCCTCCTTGA	GGCTATCGAC	TCCATCGACC	CTCCTGCTCG	500
TCCCACCGAC	AAGCCTCTCC	GTCTCCCACT	CCAGGATGTC	TACAAGATTT	550
CTGGTATCGG	CACGGTGCCC	GTCGGTCGTG	TTGAGACTGG	TACCATCAAG	600
35 GCCGGTATGG	TCGTACCTT	TGCCCCCGCC	AACGTCACCA	CTGAAGTCAA	650
GTCCGTGCAA	ATGCACCACG	AACAGCTYGC	CGAGGGCGTT	CCGGGTGACA	700
ACGTCGGCTT	CAACGTCAAG	AACGTYTCCG	TGAAGGAGGT	TCGTCTGTTG	750
AACGTTGCTG	GTGACTCCAA	GAACGACCCC	CCCAAGGGTG	CCGACTCCTT	800
CAACGCCCAG	GTCATCGTCC	TCAACCACCC	TGGTCAGGTC	GGTGCTGGCT	850
40 ACGCCCCGGT	CTTGGATTGC	CACACTGCCC	ACATTGCCTG	CAAGTTCTYT	900
GAGCTCCTCG	AGAAGATCGA	TCGTGCKACC	GGCAAGTCCA	TGGAAAACAA	950
CCCCAAGTTC	ATCAAGTCTG	G			971

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2) INFORMATION FOR SEQ ID NO: 1287

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
 5 (B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287

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10 GGTCTGAGGA CCGTTACCAG GAGATCATCA AGGAGACCTC CAACTTCATC 50
    AAGAAGGTCG GCTACAACCC CAAGCACGTT CCCTTCGTCC CCATCTCCGG 100
    TTTCAACGGA GACAACATGA TCGAGGCCTC CAGCAACTGC CCCTGGTACA 150
    AGGGTTGGGA GAAGGAGACC AAGGCCAAGG CCACTGGTAA GACCCTCCTT 200
    GAGGCCATTG ACGCCATCGA CCCTCCCAGC CGTCCTACCG ACAAGCCCCT 250
    CCGTCTTCCC CTCCAGGATG TCTACAAGAT TGGTGGTATT GGCACGGTTC 300
15 CCGTCGGTCG TGTCGAGACC GGTATCATCA AGGCCGGTAT GGTCGTCACC 350
    TTCGCCCCCG CTGGTGTAC CACTGAAGTC AAGTCCGTCG AGATGCACCA 400
    CGAGCAGCTT ACCGAGGGTG TCCCCGGTGA CAACGTCGGC TTCAACGTCA 450
    AGAACGTCTC CGTCAAGGAG ATCCGTCGTG GTAACGTTGC CGGTGACTCC 500
    AAGAACGACC CCCCCAAGGG CTGCGAGTCT TTCAACGCTC AGGTCATTGT 550
20 CCTCAACCAC CTTGGTCAGG TCGGTGCCGG TTACGCGCCA GTCCTCGACT 600
    GCCACACCGC CCACATTGCC TGCAAGTTCT CTGAGCTCCT CGAGAAGATT 650
    GACCGCCGTA CCGGAAAGTC TGTCGAAGCC TCTCCCAAGT TCATCAAGTC 700
    TGGTGACGCG GCCATCGTCA AGATGGTTCC CT 732
  
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2) INFORMATION FOR SEQ ID NO: 1288

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
 40 (B) STRAIN: HER 1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288

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    AATGGATCCT GTATACGCAC AAAAATTAGG CGTTAACATA GATGAATTTC 50
    TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA 100
45 CTTGTACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC 150
    TCTTGTAACG AAAGCAGAGA TTGAAGGCGA TATGGGTGAC TCACACGTAG 200
    GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA 250
    ATCAACAAAT CARRARCAAT WGCAATCTTT ATTAACCAAA TTCGWGAAAA 300
    AGTTGGGGTT ATGTTTCGGAA ACCCAGAAAC AACTCCA 337
50
  
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2) INFORMATION FOR SEQ ID NO: 1289

700

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10 (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: HER 1232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289

15 AATGGATCCT GTATATGCAC AAAAATTAGG CGTTAACATA GATGAATTTC 50
TATTATCACA GCCTGATACA GGGGAGCAAG GATTGGAAAT CGCGGAAGCA 100
CTTGTAACGAA GTGGTGCGGT TGACATTATC GTAATTGACT CTGTAGCAGC 150
TCTTGTAACCG AAAGCAGAGA TTGAAGGCCA TATGGGTGAC TCACACGTAG 200
20 GTTTACAAGC ACGTTTAATG TCACAAGCAC TTMGTAAGCT TTCAGGAGCA 250
ATCAACAAAT CARAARCAAT TGCAATCTTT ATTAACCAAA TTCGTGAAAA 300
AGTTGGGGTT ATGTTCTGGAA ACCCAGAAAC AACTCC 336

25 2) INFORMATION FOR SEQ ID NO: 1290

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
30 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290

GAYTAYGCIA TGISIGTIAT HGT 23

40 2) INFORMATION FOR SEQ ID NO: 1291

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291

GCIYTICCG AYGTIMGIGA YGG

23

5 2) INFORMATION FOR SEQ ID NO: 1292

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292

ARISCYTCIA RIATRTGIGC

20

20

2) INFORMATION FOR SEQ ID NO: 1293

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293

ATGGCTGAAT TACCTCAATC

20

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2) INFORMATION FOR SEQ ID NO: 1294

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294

ATGATTGTTG TATATCTTCT TCAAC

25

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2) INFORMATION FOR SEQ ID NO: 1295

702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295
- CAGAAAGTTT GAAGCGTTGT 20
- 15
- 2) INFORMATION FOR SEQ ID NO: 1296
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296
- AACGATTCGT GAGTCAGATA 20
- 30
- 2) INFORMATION FOR SEQ ID NO: 1297
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297
- CGGTCAACAT TGAGGAAGAG CT 22
- 45
- 2) INFORMATION FOR SEQ ID NO: 1298
- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298

ACGAAATCGA CCGTCTCTTT TTC

23

10

2) INFORMATION FOR SEQ ID NO: 1299

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 2711 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: 601055
(C) ACCESSION NUMBER: X71437

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299

	ATGGCTGAAT	TACCTCAATC	AAGAATAAAT	GAACGAAATA	TTACCAGTGA	50
	AATGCGTGAA	TCATTTT TAG	ATTATGCGAT	GAGTGTTATC	GTTGCTCGTG	100
30	CATTGCCAGA	TGTTTCGTGAC	GGTTTAA AAC	CAGTACATCG	TCGTATACTA	150
	TATGGATTAA	ATGAACAAGG	TATGACACCG	GATAAATCAT	ATAAAAAATC	200
	AGCACGTATC	GTTGGTGACG	TAATGGGTAA	ATATCACCCCT	CATGGTGACT	250
	CATCTATTTA	TGAAGCAATG	GTACGTATGG	CTCAAGATTT	CAGTTATCGT	300
	TATCCGCTTG	TTGATGGCCA	AGGTAACTTT	GGTTCAATGG	ATGGAGATGG	350
35	CGCAGCAGCA	ATGCGTTATA	CTGAAGCGCG	TATGACTAAA	ATCACACTTG	400
	AACTGTTACG	TGATATTAAT	AAAGATACAA	TAGATTTTAT	CGATAACTAT	450
	GATGGTAATG	AAAGAGAGCC	GTCAGTCTTA	CCTGCTCGAT	TCCCTAATTT	500
	ATTAGCCAAT	GGTGCATCAG	GTATCGCGGT	AGGTATGGCA	ACGAATATTC	550
	CACCACATAA	CTTAACAGAA	TTAATCAATG	GTGTACTTAG	CTTAAGTAAG	600
40	AACCCTGATA	TTTCAATTGC	TGAGTTAATG	GAAGATATTG	AAGGTCCTGA	650
	TTTCCCAACT	GCTGGACTTA	TTTTAGGTAA	GAGTGGTATT	AGACGTGCAT	700
	ATGAAACAGG	TCGTGGTTCA	ATTCAAATGC	GTTCTCGTGC	AGTTATTGAA	750
	GAACGTGGAG	GCGGACGTCA	ACGTATTGTT	GTCAGTAAA	TTCCCTTTCCA	800
	AGTGAATAAG	GCTCGTATGA	TTGAAAAAAT	TGCAGAGCTC	GTTTCGTGACA	850
45	AGAAAATTGA	CGGTATCACT	GATTTACGTG	ATGAAACAAG	TTTACGTACT	900
	GGTGTGCGTG	TCGTTATTGA	TGTGCGTAAG	GATGCAAATG	CTAGTGTCAT	950
	TTTAAATAAC	TTATACAAAC	AAACACCTCT	TCAAACATCA	TTTGGTGTGA	1000
	ATATGATTGC	ACTTGTAAT	GGTAGACCGA	AGCTTATTAA	TTTAAAAGAA	1050
	GCGTTGGTAC	ATTATTTAGA	GCATCAAAAG	ACAGTTGTTA	GAAGACGTAC	1100
50	GCAATATAAC	TTACGTAAAG	CTAAAGATCG	TGCCCCATATT	TTAGAAGGGT	1150
	TACGTATCGC	ACTTGACCAT	ATCGATGAAA	TTATTTCAAC	GATTCGTGAG	1200
	TCAGATACAG	ATAAAGTTGC	AATGGAAAGC	TTGCAACAAC	GCTTCAAAC	1250
	TTCTGAAAAA	CAAGCTCAAG	CTATTTTAGA	CATGCGTTTA	AGACGTCTAA	1300

	CAGGTTTAGA	GAGAAACAAA	ATTGAAGCTG	AATATAATGA	GTTATTAAAT	1350
	TATATTAGTG	AATTAGAAGC	CATCTTAGCT	GATGAAGAAG	TGTTATTACA	1400
	GTTAGTTAGA	GATGAATTGA	CTGAAATTAG	AGATCGTTTC	GGTGATGAGC	1450
	GTCGTACAGA	AATTCAATTA	GGTGGATTG	AAGACTTAGA	GGACGAAGAC	1500
5	TTAATTCCAG	AAGAACAAAT	AGTAATTACT	TTGAGCCATA	ATAACTACAT	1550
	TAAACGTTTG	CCGGTATCTA	CATATCGTGC	TCAAAACCGT	GGTGGTCGTG	1600
	GTGTTCAAGG	TATGAATACA	TTGGAAGAAG	ATTTTGTGAG	TCAATTGGTA	1650
	ACTTTAAGTA	CACATGACCA	TGTATTGTTC	TTTACTAACA	AAGGTCGTGT	1700
	ATACAAACTA	AAAGGTTATG	AAGTGCCTGA	GTTATCAAGA	CAGTCTAAAG	1750
10	GTATTCCTGT	AGTGAATGCT	ATTGAACTTG	GAAATGATGA	AGTCATTAGT	1800
	ACAATGATTG	CTGTTAAAGA	CCTTGAAAGT	GAAGACAACT	TCTTAGTGTT	1850
	TGCAACTAAA	CGTGGTGTTG	TTAAACGTTT	AGCATTAAAGT	AACTTCTCAA	1900
	GAATAAATAG	AAATGGTAAG	ATTGCGATT	CGTTCAGAGA	AGATGATGAG	1950
	TTAATTGCAG	TTCGTTTAAAC	AAGTGGTCAA	GAAGATATCT	TGATTGGTAC	2000
15	ATCACATGCA	TCATTAATTC	GATTCCCTGA	ATCAACATTA	CGTCCTTTAG	2050
	GCCGTACAGC	AACGGGTGTG	AAAGGTATTA	CACTTCGTGA	AGGTGACGAA	2100
	GTTGTAGGGC	TTGATGTAGC	TCATGCAAAC	AGTGTTGATG	AAGTATTAGT	2150
	AGTTACTGAA	AATGGTTATG	GTAAACGTAC	GCCAGTTAAT	GACTATCGTT	2200
	TATCAAATCG	TGGTGGTAAA	GGTATTAAAA	CAGCTACGAT	TACTGAGCGT	2250
20	AATGGTAATG	TTGTATGTAT	CACTACAGTA	ACTGGTGAAG	AAGATTTAAT	2300
	GATTGTTACT	AATGCCGGTG	TCATTATTCG	ACTAGATGTT	GCAGATATTT	2350
	CTCAAATGG	TCGTGCAGCA	CAAGGTGTTT	GCTTAATTCG	CTTAGGCGAT	2400
	GATCAATTTG	TTTCAACGGT	TGCTAAAGTA	AAAGAGGATG	CAGATGAAGT	2450
	AAATGAAGAT	GAACAATCTA	CTGTATCTGA	AGATGGTACT	GAACAACAAC	2500
25	GTGAAGCGGT	TGTAATGAT	GAAACACCAG	GAAATGCAAT	TCATACTGAA	2550
	GTGATTGATT	CAGAAGAAAA	TGATGAAGAT	GGACGTATTG	AAGTAAGACA	2600
	AGATTTTCATG	GATCGTGTTG	AAGAAGATAT	ACAACAATCA	TCAGATGAAG	2650
	ATGAAGAATA	A				2711

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2) INFORMATION FOR SEQ ID NO: 1300

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2628 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: K12
 45 (C) ACCESSION NUMBER: X57174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300

	ATGAGCGACC	TTGCGAGAGA	AATTACACCG	GTCAACATTG	AGGAAGAGCT	50
50	GAAGAGCTCC	TATCTGGATT	ATGCGATGTC	GGTCATTGTT	GGCCGTGCGC	100
	TGCCAGATGT	CCGAGATGGC	CTGAAGCCGG	TACACCGTCG	CGTACTTTAC	150
	GCCATGAACG	TACTAGGCAA	TGACTGGAAC	AAAGCCTATA	AAAAATCTGC	200
	CCGTGTCGTT	GGTGACGTAA	TCGGTAAATA	CCATCCCCAT	GGTGACTCGG	250

	CGGTCTATGA	CACGATCGTC	CGCATGGCGC	AGCCATTCTC	GCTGCGTTAT	300
	ATGCTGGTAG	ACGGTCAGGG	TAACTTCGGT	TCTATCGACG	GCGACTCTGC	350
	GGCGGCAATG	CGTTATACGG	AAATCCGTCT	GGCGAAAATT	GCCCATGAAC	400
	TGATGGCCGA	TCTCGAAAAA	GAGACGGTCG	ATTTTCGTTGA	TAACATATGAC	450
5	GGCACGGAAA	AAATTCCGGA	CGTCATGCCA	ACCAAAATTC	CTAACCTGCT	500
	GGTGAACGGT	TCTTCCGGTA	TCGCCGTAGG	TATGGCAACC	AACATCCCGC	550
	CGCACAACTT	GACGGAAGTC	ATCAACGGTT	GTCTGGCGTA	TATTGATGAT	600
	GAAGACATCA	GCATTGAAGG	GCTGATGGAA	CACATCCCGG	AGCCGGACTT	650
	CCCGACGGCG	GCAATCATT	ACGGTCGTCG	CGGTATTGAA	GAAGCTTACC	700
10	GTACCGGTCG	CGGCAAGGTG	TATATCCGCG	CTCGCGCAGA	AGTGGAAGTT	750
	GACGCCAAAA	CCGGTCGTGA	AACCATTATC	GTCCACGAAA	TTCCGTATCA	800
	GGTAAACAAA	GCGCGCCTGA	TCGAGAAGAT	TGCGGAACTG	GTAAAAGAAA	850
	AACGCGTGGA	AGGCATCAGC	GCGCTGCGTG	ACGAGTCTGA	CAAAGACGGT	900
	ATGCGCATCG	TGATTGAAGT	GAAACGCGAT	GCGGTCGGTG	AAGTTGTGCT	950
15	CAACAACCTC	TACTCCCAGA	CCCAGTTGCA	GGTTTCTTTC	GGTATCAACA	1000
	TGGTGGCATT	GCACCATGGT	CAGCCGAAGA	TCATGAACCT	GAAAGACATC	1050
	ATCGCGGCGT	TTGTTTCGTCA	CCGCCGTGAA	GTGGTGACCC	GTCGTACTAT	1100
	TTTCGAACTG	CGTAAAGCTC	GCGATCGTGC	TCATATCCTT	GAAGCATTAG	1150
	CCGTGGCGCT	GGCGAACATC	GACCCGATCA	TCGAACTGAT	CCGTTCATGCG	1200
20	CCGACGCCTG	CAGAAGCGAA	AACTGCGCTG	GTTGCTAATC	CGTGGCAGCT	1250
	GGGCAACGTT	GCCGCGATGC	TCGAACGTGC	TGGCGACGAT	GCTGCGCGTC	1300
	CGGAATGGCT	GGAGCCAGAG	TTGCGCGTGC	GTGATGGTCT	GTAACCTG	1350
	ACCGAACAGC	AAGCTCAGGC	GATTCTGGAT	CTGCGTTTGC	AGAAACTGAC	1400
	CGGTCTTGAG	CACGAAAAAC	TGCTCGACGA	ATACAAAGAG	CTGCTGGATC	1450
25	AGATCGCGGA	ACTGTTGCGT	ATTCTTGGA	GCGCCGATCG	TCTGATGGAA	1500
	GTGATCCGTG	AAGAGCTGGA	GCTGGTTCGT	GAACAGTTCG	GTGACAAACG	1550
	TCGTAAGTAA	ATCACCGCCA	ACAGCGCAGA	CATCAACCTG	GAAGATCTGA	1600
	TCACCCAGGA	AGATGTGGTC	GTGACGCTCT	CTCACCAGGG	CTACGTAAAG	1650
	TATCAGCCGC	TTTCTGAATA	CGAAGCGCAG	CGTCGTGGCG	GGAAAGGTAA	1700
30	ATCTGCCGCA	CGTATTAAAG	AAGAAGACTT	TATCGACCGA	CTGCTGGTGG	1750
	CGAACACTCA	CGACCATATT	CTGTGCTTCT	CCAGCCGTGG	TCGCGTCTAT	1800
	TCGATGAAAG	TTTATCAGTT	GCCGGAAGCC	ACTCGTGGCG	CGCGCGGTGC	1850
	TCCGATCGTC	AACCTGCTGC	CGCTGGAGCA	GGACGAACGT	ATCACTGCGA	1900
	TCCTGCCAGT	GACCGAGTTT	GAAGAAGGCG	TGAAAGTCTT	CATGGCGACC	1950
35	GCTAACGGTA	CCGTGAAGAA	AACTGTCCTC	ACCGAGTTCA	ACCGTCTGCG	2000
	TACCGCCGGT	AAAGTGGCGA	TCAAACCTGGT	TGACGGCGAT	GAGCTGATCG	2050
	GCGTTGACCT	GACCAGCGGC	GAAGACGAAG	TAATGCTGTT	CTCCGCTGAA	2100
	GGTAAAGTGG	TGCGCTTTAA	AGAGTCTTCT	GTCCGTGCGA	TGGGCTGCAA	2150
	CACCACCGGT	GTTCGCGGTA	TTGCTTAGG	TGAAGGCGAT	AAAGTCGTCT	2200
40	CTCTGATCGT	GCCTCGTGCG	GATGGCGCAA	TCCTCACC GC	AACGCAAAAC	2250
	GGTTACGGTA	AACGTACCGC	AGTGGCGGAA	TACCCAACCA	AGTCGCGTGC	2300
	GACGAAAGGG	GTTATCTCCA	TCAAGGTTAC	CGAACGTAAC	GGTTTAGTTG	2350
	TTGGCGCGGT	ACAGGTAGAT	GACTGCGACC	AGATCATGAT	GATCACCAGT	2400
	GCCGGTACGC	TGGTACGTAC	TCGCGTTTCG	GAAATCAGCA	TCGTGGGCCC	2450
45	TAACACCCAG	GGCGTGATCC	TCATCCGTAC	TGCGGAAGAT	GAAAACGTAG	2500
	TGGGTCTGCA	ACGTGTTGCT	GAACCGGTTG	ACGAGGAAGA	TCTGGATACC	2550
	ATCGACGGCA	GTGCCGCGGA	AGGGGACGAT	GAAATCGCTC	CGGAAGTGGA	2600
	CGTTGACGAC	GAGCCAGAAG	AAGAATAA			2628

50

2) INFORMATION FOR SEQ ID NO: 1301

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301
10 GTIMGIAWIM GICCIGSIAT GTA 23
- 15 2) INFORMATION FOR SEQ ID NO: 1302
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302
 TAIADIGGIG GIKKIGCIAT RTA 23
- 30 2) INFORMATION FOR SEQ ID NO: 1303
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303
 GGIGAIGAID YIMGIGARGG 20
- 45 2) INFORMATION FOR SEQ ID NO: 1304
- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1304

5

CIARYTTIKY ITTIGTYTG

19

10 2) INFORMATION FOR SEQ ID NO: 1305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305

ATGGTGACTG CATTGTCAGA TG

22

25

2) INFORMATION FOR SEQ ID NO: 1306

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306

GTCTACGGTT TTCTACAACG TC

22

40

2) INFORMATION FOR SEQ ID NO: 1307

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1923 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: M86227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307

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5  ATGGTGA CTG CATTGTCAGA TGTAACAAC ACGGATAATT ATGGTGCTGG      50
   GCAAATACAA GTATTAGAAG GTTTAGAAGC AGTACGTAAA AGACCAGGTA      100
   TGTATATAGG ATCGACTCAG AGAGAGTTGC ACATTAGTGT GGAAATTGTC      150
   GATAATAGTA TCGATGAAGC ATTAGCTGGT TATGCAAATA AAATTGAAGT      200
   TGTTATTGAA AAAGATAACT GGATTAAAGT AACGGATAAC GGACGTGGTA      250
10  TCCCAGTTGA TATTCAAGAA AAAATGGGAC GTCCAGCTGT CGAAGTTATT      300
   TTAAGTGTTC TACATGCTGG TGGTAAATTC GGCGGTGGCG GATACAAAGT      350
   ATCTGGTGGT TTACATGGTG TTGGTTCATC AGTTGTAAAC GCATTGTCAC      400
   AAGACTTAGA AGTATATGTA CACAGAAATG AGACTATATA TCATCAAGCA      450
   TATAAAAAAG GTGTACCTCA ATTTGACTTA AAAGAAGTTG GCACAACTGA      500
15  TAAGACAGGT ACTGTCATTC GTTTTAAAGC AGATGGAGAA ATCTTCACAG      550
   AGACAACTGT ATACAACTAT GAAACATTAC AGCAGCGTAT TAGAGAGCTT      600
   GCTTTCTTAA ACAAAGGAAT TCAAATCACA TTAAGAGATG AACGTGATGA      650
   AGAAAACGTT AGAGAAGACT CCTATCACTA TGAGGGCGGT ATTAAATCGT      700
   ACGTTGAGTT ATTGAACGAA AATAAAGAAC CTATTCATGA TGAGCCAATT      750
20  TATATTCATC AATCTAAAGA TGATATTGAA GTAGAAATTG CGATTCAATA      800
   TAACTCAGGA TATGCCACAA ATCTTTTAAAC TTACGCAAT AACATTCATA      850
   CGTACGAAGG TGGTACGCAT GAAGACGGAT TCAAACGTGC ATTAACCGCT      900
   GTCTTAAATA GTTATGGTTT AAGTAGCAGA TATGAAGAAG AAAAGATAGC      950
   TTCTGGTGAA GATACACGAG AAGGTATGAC AGCAATTATA TCTATCAAAC      1000
25  ATGGTGATCC TCAATTCGAA GGTCAAACGA AGACAAAATT AGGTAATTCT      1050
   GAAGTGCGTC AAGTTGTAGA TAAATTATTC TCAGAGCACT TTGAACGATT      1100
   TTTATATGAA AATCCACAAG TCGCACGTAC AGTGGTTGAA AAAGGTATTA      1150
   TGGCGGCACG TGCACGTGTT GCTGCGAAAA AAGCGCGTGA AGTAACACGT      1200
   CGTAAATCAG CGTTAGATGT AGCAAGTCTT CCAGGTAAAT TAGCCGATTG      1250
30  CTCTAGTCAA AGTCCTGAAG AATGTGAGAT TTTCTTAGTC GAAGGGGACT      1300
   CTGCCGGAGG GTCTACAAAA TCTGGTCGTG ACTCTAGAAC GCAGGCGATT      1350
   TTACCATTAC GAGGTAAGAT ATTAAATGTT GAAAAAGCAC GATTAGATAG      1400
   AATTTTGAAT AACAATGAAA TTCGTCAAAT GATCACAGCA TTTGGTACAG      1450
   GAATCGGTGG CGACTTTGAT CTAGCGAAAG CAAGATATCA CAAAATCGTC      1500
35  ATTATGACTG ATGCCGATGT GGATGGAGCG CATATTAGAA CATTGTTATT      1550
   AATATTCTTC TATCGATTTA TGAGACCGTT AATTGAAGCA GGCTATGTGT      1600
   ATATTGCACA GCCACCGTTG TATAAACTGA CACAAGGTAA ACAAAGTAT      1650
   TATGTATACA ATGATAGGGA ACTTGATAAA CTTAAATCTG AATTGAATCC      1700
   AACACCAAAA TGGTCTATTG CGCTATACAA AGGTCTTGGA GAAATGAATG      1750
40  CAGATCAATT ATGGGAAACA ACAATGAACC CTGAGCACCG CGCTCTTTTA      1800
   CAAGTAAAC TTGAAGATGC GATTGAAGCG GACCAACAT TTGAAATGTT      1850
   AATGGGTGAC GTTGTAGAAA ACCGTAGACA ATTTATAGAA GATAATGCAG      1900
   TTTATGCAAA CTTAGACTTC TAA                                     1923

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45

2) INFORMATION FOR SEQ ID NO: 1308

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308

5

ATGTAYGTIA TIATGGAYMG IGC

23

10 2) INFORMATION FOR SEQ ID NO: 1309

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309

ATIATYTTT TICCYTTICC YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1310

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310

ATIATITSIA TIACYTCRTC

20

40

2) INFORMATION FOR SEQ ID NO: 1311

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311

GARATGAARA TIMGIGGIGA RCA

23

5 2) INFORMATION FOR SEQ ID NO: 1312

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312

AARTAYATIA TICARGARMG IGC

23

20

2) INFORMATION FOR SEQ ID NO: 1313

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313

AMIAIYICKRT GIGGITTITT YTT

23

35

2) INFORMATION FOR SEQ ID NO: 1314

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314

TAIGAITYYA CIGAISMICA RGC

23

50

2) INFORMATION FOR SEQ ID NO: 1315

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315
- ACIATIGCIT CIGCYTGIKS YTC 23
- 15
- 2) INFORMATION FOR SEQ ID NO: 1316
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316
- GTGAGTGAAA TAATTCAAGA TT 22
- 30
- 2) INFORMATION FOR SEQ ID NO: 1317
- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317
- CACCAAAATC ATCTGTATCT AC 22
- 45
- 2) INFORMATION FOR SEQ ID NO: 1318
- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318

ACCTAYTCSA TGTACGTRAT CATGGA

26

10

2) INFORMATION FOR SEQ ID NO: 1319

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319

AGRTCCTCIA CCATCGGYAG YTT

23

25

2) INFORMATION FOR SEQ ID NO: 1320

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 2259 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Escherichia coli*
(B) STRAIN: K-12 MG1655
(C) ACCESSION NUMBER: AE000384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320

ATGAGCGATA	TGGCAGAGCG	CCTTGCGCTA	CATGAATTTA	CGGAAAACGC	50
45	CTACTTAAAC	TACTCCATGT	ACGTGATCAT	GGACCGTGCG	100
	TTGGTGATGG	TCTGAAACCT	GTTCAGCGCC	GCATTGTGTA	150
	GAACTGGGCC	TGAATGCCAG	CGCCAAATTT	AAAAAATCGG	200
	CGGTGACGTA	CTGGGTAAAT	ACCATCCGCA	CGGCGATAGC	250
	AAGCGATGGT	CCTGATGGCG	CAACCGTTCT	CTTACCGTTA	300
50	GATGGTCAGG	GGAAGTGGGG	CGCGCCGGAC	GATCCGAAAT	350
	AATGCGTTAC	ACCGAATCCC	GGTTGTGCGA	ATATTCCGAG	400
	GCGAGCTGGG	GCAGGGGACG	GCTGACTGGG	TGCCAAACTT	450
	TTGCAGGAGC	CGAAAATGCT	ACCTGCCCGT	CTGCCAAACA	500
	TTTGCTTAA				

	CGGCACCACC	GGTATTGCCG	TCGGCATGGC	GACCGATATT	CCACCGCATA	550
	ACCTGCGTGA	AGTGGCTCAG	GCGGCAATCG	CATTAATCGA	CCAGCCGAAA	600
	ACCACGCTCG	ATCAGCTGCT	GGATATCGTG	CAGGGGCCGG	ATTATCCGAC	650
	TGAAGCGGAA	ATTATCACTT	CGCGCGCCGA	GATCCGTAAA	ATCTACGAGA	700
5	ACGGACGTGG	TTCAGTGCGT	ATGCGCGCGG	TGTGGAAGAA	AGAAGATGGC	750
	GCGGTGGTTA	TCAGCGCATT	GCCGCATCAG	GTTTCAGGTG	CGCGCGTACT	800
	GGAGCAAATT	GCTGCGCAAA	TGCGCAACAA	AAAGCTGCCG	ATGGTTGACG	850
	ATCTGCGCGA	TGAATCTGAC	CACGAGAACC	CGACCCGCCT	GGTGATTGTG	900
	CCGCGTTCCA	ACCGCGTGGA	TATGGATCAG	GTGATGAACC	ACCTCTTCGC	950
10	TACCACCGAT	CTGGA AAAAGA	GCTATCGTAT	TAACCTTAAT	ATGATCGGTC	1000
	TGGATGGTCG	TCCGGCGGTG	AAAAACCTGC	TGGAATCCT	CTCCGAATGG	1050
	CTGGTGTTCC	GCCGCGATAC	CGTGCGCCGC	CGACTGAACT	ATCGTCTGGA	1100
	GAAAGTCCTC	AAGCGCCTGC	ATATCCTCGA	AGGTTTGCTG	GTGGCGTTTC	1150
	TCAATATCGA	CGAAGTGATT	GAGATCATTC	GTAATGAAGA	TGAACCGAAA	1200
15	CCGGCGCTGA	TGTCGCGGTT	TGGCCTTACG	GAAACCCAGG	CGGAAGCGAT	1250
	CCTCGAACTG	AAACTGCGTC	ATCTTGCCAA	ACTGGAAGAG	ATGAAGATTC	1300
	GCGGTGAGCA	GAGTGAACTG	GAAAAAGAGC	GCGACCA GTT	GCAGGGCATT	1350
	TTGGCTTCCG	AGCGTAA AAT	GAATAACCTG	CTGAAGAAAG	AACTGCAGGC	1400
	AGACGCGCAA	GCCTACGGTG	ACGATCGTCG	TTCGCCGTTG	CAGGAACGCG	1450
20	AAGAAGCGAA	AGCGATGAGC	GAGCACGACA	TGCTGCCGTC	TGAACCTGTC	1500
	ACCATTGTGC	TGTCGCAGAT	GGGCTGGGTA	CGCAGCGCTA	AAGGCCATGA	1550
	TATCGACGCG	CCGGGCCTGA	ATTATAAAGC	GGGTGATAGC	TTCAAAGCGG	1600
	CGGTGAAAGG	TAAGAGCAAC	CAACCGGTAG	TGTTTGTTGA	TTCCACCGGT	1650
	CGTAGCTATG	CCATTGACCC	GATTACGCTG	CCGTCGGCGC	GTGGTCAGGG	1700
25	CGAGCCGCTC	ACCGGCAAAT	TAACGTTGCC	GCCTGGGGCG	ACCGTTGACC	1750
	ATATGCTGAT	GGAAAGCGAC	GATCAGAAAC	TGCTGATGGC	TTCCGATGCG	1800
	GGTTACGGTT	TCGTCTGCAC	CTTTAACGAT	CTGGTGGCGC	GTAACCGTGC	1850
	AGGTAAGGCT	TTGATCACCT	TACCGGAAAA	TGCCCATGTT	ATGCCGCCGG	1900
	TGGTGATTGA	AGATGCTTCC	GATATGCTGC	TGGCAATCAC	TCAGGCAGGC	1950
30	CGTATGTTGA	TGTTCCCGGT	AAGTGATCTG	CCGCAGCTGT	CGAAGGGCAA	2000
	AGGCAACAAG	ATTATCAACA	TTCCATCGGC	AGAAGCCGCG	CGTGGAGAAG	2050
	ATGGTCTGGC	GCAATTGTAC	GTTCTGCCGC	CGCAAAGCAC	GCTGACCATT	2100
	CATGTTGGGA	AACGCAAAAT	TAAACTGCGC	CCGGAAGAGT	TACAGAAAGT	2150
	CACTGGCGAA	CGTGGACGCC	GCGGTACGTT	GATGCGCGGT	TTGCAGCGTA	2200
35	TCGATCGTGT	TGAGATCGAC	TCTCCTCGCC	GTGCCAGCAG	CGGTGATAGC	2250
	GAAGAGTAA					2259

40 2) INFORMATION FOR SEQ ID NO: 1321

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 2403 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: KMP9
 (C) ACCESSION NUMBER: D67074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321

	GTGAGTGAAA	TAATTCAAGA	TTTATCACTT	GAAGATGTTT	TAGGTGATCG	50
5	CTTTGGAAGA	TATAGTAAAT	ATATTATTCA	AGAGCGTGCA	TTGCCAGATG	100
	TTCGTGATGG	TTTAAAACCA	GTACAACGTC	GTATTTTATA	TGCAATGTAT	150
	TCAAGTGGTA	ATACACACGA	TAAAAATTTT	CGTAAAAGTG	CGAAAACAGT	200
	CGGTGATGTT	ATTGGTCAAT	ATCATCCACA	TGGAGACTTC	TCAGTGTACA	250
	AAGCAATGGT	CCGTTTAAGT	CAAGACTGGA	AGTTACGACA	TGTCTTAATA	300
10	GAAATGCATG	GTAATAATGG	TAGTATCGAT	AATGATCCGC	CAGCGGCAAT	350
	GCGTTACACT	GAAGCTAAGT	TAAGCTTACT	AGCTGAAGAG	TTATTACGTG	400
	ATATTAATAA	AGAGACAGTT	TCTTTCATT	CAAACATGA	TGATACGACA	450
	CTCGAACC	TGGTATTGCC	ATCAAGATTT	CCTAACTTAC	TAGTGAATGG	500
	TTCTACAGGT	ATATCTGCAG	GTTACGCGAC	AGATATACCA	CCACATAATT	550
15	TAGCTGAAGT	GATTCAAGCA	ACACTTAAAT	ATATTGATAA	TCCGGATATT	600
	ACAGTCAATC	AATTAATGAA	ATATATTAAA	GGTCTTGATT	TTCCAACCTG	650
	TGGTATTATT	CAAGGTATTG	ATGGTATTAA	AAAAGCTTAT	GAATCAGGTA	700
	AAGGTAGAAT	TATAGTTCGT	TCTAAAGTTG	AAGAAGAAAC	TTTACGCAAT	750
	GGACGTAAAC	AGTTAATTAT	TACTGAAATT	CCATATGAAG	TGAACAAAAG	800
20	TAGCTTAGTA	AAACGTATCG	ATGAATTACG	TGCTGACAAA	AAAGTCGATG	850
	GTATCGTTGA	AGTACGTGAT	GAAACTGATA	GAAGTGGTTT	ACGAATAGCA	900
	ATTGAATTGA	AAAAAGATGT	GAACAGTGAA	TCAATCAAAA	ATTATCTTTA	950
	TAAAACTCT	GATTTACAGA	TTTCATATAA	TTTCAACATG	GTGCTATTA	1000
	GTGATGGTCG	TCCAAAATTG	ATGGGTATT	GTCAAATTAT	AGATAGTTAT	1050
25	TTGAATCATC	AAATTGAGGT	TGTTGCAAAT	AGAACGAAGT	TTGAATTAGA	1100
	TAATGCTGAA	AAACGTATGC	ATATCGTTGA	AGGTTTGATT	AAAGCGTTGT	1150
	CAATTTTAGA	TAAAGTAATT	GAATTGATTC	GTAGCTCTAA	AAACAAGCGT	1200
	GACGCTAAAG	AAAACCTTAT	CGAAGTATTC	GAGTTCACAG	AAGAACAGGC	1250
	TGAAGCAATT	GTAATGTTAC	AGTTATATCG	TTTAACAAAC	ACTGACATAG	1300
30	TTGCGCTTGA	AGGTGAACAT	AAAGAACTTG	AAGCATTAAT	CAAACAATTA	1350
	CGTCATATTC	TTGATAACCA	TGATGCATTA	TTGAATGTCA	TAAAAGAAGA	1400
	ATTGAATGAA	ATTAAAAAGA	AATTCAAATC	TGAACGACTG	TCTTTAATTG	1450
	AAGCAGAAAT	TGAAGAAATT	AAAATTGACA	AAGAAGTTAT	GGTGCCTAGT	1500
	GAAGAAGTTA	TTTTAAGTAT	GACACGTCAT	GGATATATTA	AACGTACTTC	1550
35	TATTCGTAGC	TTTAATGCTA	GCGGTGTTGA	GGATATTGGT	TTAAAAGATG	1600
	GTGACAGTTT	ACTTAAACAT	CAAGAAGTAA	ATACGCAAGA	TACCGTACTA	1650
	GTATTTACAA	ATAAAGGTCG	TTATCTATTT	ATACCGGTTT	ATAAATTAGC	1700
	AGATATTCGT	TGGAAGAAGT	TGGGGCAACA	TGTATCACAA	ATAGTTCCTA	1750
	TCGAAGAAGA	TGAAGTGGTT	ATTAATGTCT	TTAATGAAAA	GGACTTTAAT	1800
40	ACAGATGCAT	TTTATGTTTT	TGCGACTCAA	AATGGCATGA	TTAAGAAAAG	1850
	TACAGTGCCT	CTATTTAAAA	CAACGCGTTT	TAATAAACCT	TTAATTGCTA	1900
	CTAAAGTTAA	AGAAAATGAT	GATTTGATTA	GTGTTATGCG	CTTTGAAAAA	1950
	GATCAATTAA	TTACCGTCAT	TACTAATAAA	GGTATGTCAT	TAACGTATAA	2000
	TACAAGTGAA	CTATCAGATA	CCGGATTAA	GGCAGCTGGT	GTTAAATCAA	2050
45	TAAATCTTAA	AGCTGAAGAT	TTCGTTGTTA	TGACAGAAGG	TGTTTCTGAA	2100
	AATGATACTA	TATTGATGGC	CACACAACGC	GGCTCGTTAA	AACGTATTAG	2150
	TTTTAAAATC	TTACAAGTTG	CTAAAAGAGC	ACAACGTGGA	ATAACTTTAT	2200
	TAAAAGAATT	AAAGAAAAAT	CCACATCGTA	TTGTAGCTGC	ACATGTAGTG	2250
	ACAGGTGAAC	ATAGTCAATA	TACATTATAT	TCAAAAATCAA	ATGAAGAACA	2300
50	TGGTTTAATT	AATGATATTC	ATAAATCTGA	ACAATATACA	AATGGCTCAT	2350
	TCATTGTAGA	TACAGATGAT	TTTGGTGAAG	TAATAGACAT	GTATATTAGC	2400
	TAA					2403

2) INFORMATION FOR SEQ ID NO: 1322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322

RTIGAIAAYI SIGTIGAYGA RG

22

2) INFORMATION FOR SEQ ID NO: 1323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323

ACIAWRSAIG GIGGIACICA YG

22

2) INFORMATION FOR SEQ ID NO: 1324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324

CCICCIGCIS WRTCICCYTC

20

2) INFORMATION FOR SEQ ID NO: 1325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325

RTTCATYTCI CCIARICCYT T

21

10

2) INFORMATION FOR SEQ ID NO: 1326

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326

TGATTCAATA CAGGTTTTAG AG

22

25

2) INFORMATION FOR SEQ ID NO: 1327

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327

40

CTAGATTTC TCCTCATCAA AT

22

2) INFORMATION FOR SEQ ID NO: 1328

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1992 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: RN4220

(C) ACCESSION NUMBER: D67075

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328

	ATGAATAAAC	AAAATAATTA	TTCAGATGAT	TCAATACAGG	TTTtagaggg	50
	GTTAGAAGCA	GTTCGTAAAA	GACCTGGTAT	GTATATTGGA	TCAACTGATA	100
10	AACGGGGATT	ACATCATCTA	GTATATGAAA	TTGTCGATAA	CTCCGTCGAT	150
	GAAGTATTGA	ATGGTTACGG	TAACGAAATA	GATGTAACAA	TTAATAAAGA	200
	TGGTAGTATT	TCTATAGAAG	ATAATGGACG	TGGTATGCCA	ACAGGTATAC	250
	ATAAATCAGG	TAAACCGACA	GTCGAAGTTA	TCTTTACTGT	TTTACATGCA	300
	GGAGGTAAAT	TTGGACAAGG	CGGCTATAAA	ACTTCAGGTG	GTCTTCACGG	350
15	TGTTGGTGCT	TCAGTTGTAA	ATGCATTGAG	TGAATGGCTT	GAAGTTGAAA	400
	TCCATCGAGA	TGGTAATATA	TATCATCAAA	GTTTTAAAAA	CGGTGGTTTCG	450
	CCATCTTCTG	GTTTAGTGAA	AAAAGGTAAA	ACTAAGAAAA	CAGGTACCAA	500
	AGTAACATTT	AAACCTGATG	ACACAATTTT	TAAAGCATCT	ACATCATTTA	550
	ATTTTGATGT	TTTAAGTGAA	CGACTACAAG	AGTCTGCGTT	CTTATTGAAA	600
20	AATTTAAAAA	TAACGCTTAA	TGATTTACGC	AGTGGTAAAG	AGCGTCAAGA	650
	GCATTACCAT	TATGAAGAAG	GAATCAAAGA	GTTTGTTAGT	TATGTCAATG	700
	AAGGAAAAGA	AGTTTTGCAT	GACGTGGCTA	CATTTTCAGG	TGAAGCAAAT	750
	GGTATAGAGG	TAGACGTAGC	TTTCCAATAT	AATGATCAAT	ATTCAGAAAG	800
	TATTTTAAGT	TTTGTAATAA	ATGTACGTAC	TAAAGATGGT	GGTACACATG	850
25	AAGTTGGTTT	TAAAACAGCA	ATGACACGTG	TATTTAATGA	TTATGCACGT	900
	CGTATTAATG	AACTTAAAC	AAAAGATAAA	AACTTAGATG	GTAATGATAT	950
	TCGTGAAGGT	TTAACAGCTG	TTGTGTCTGT	TCGTATTCCA	GAAGAATTAT	1000
	TGCAATTTGA	AGGACAAACG	AAATCTAAAT	TGGGTACTTC	TGAAGCTAGA	1050
	AGTGCTGTTG	ATTCAGTTGT	TGCAGACAAA	TTGCCATTCT	ATTTAGAAGA	1100
30	AAAAGGACAA	TTGTCTAAAT	CACTTGTGAA	AAAAGCGATT	AAAGCACAAAC	1150
	AAGCAAGGGA	AGCTGCACGT	AAAGCTCGTG	AAGATGCTCG	TTCAGGTAAG	1200
	AAAAACAAGC	GTAAAGACAC	TTTGCTATCT	GGTAAATTAA	CACCTGCACA	1250
	AAGTAAAAAC	ACTGAAAAAA	ATGAATTGTA	TTAGTCGAA	GGTGATTCTG	1300
	CGGGAGGTTT	AGCAAACTT	GGACGAGACC	GCAAATTCCA	AGCGATATTA	1350
35	CCATTACGTG	GTAAGGTAAT	TAATACAGAG	AAAGCACGTC	TAGAAGATAT	1400
	TTTTAAAAAT	GAAGAAATTA	ATACAATTAT	CCACACAATC	GGGGCAGGCG	1450
	TTGGTACTGA	CTTTAAAATT	GAAGATAGTA	ATTATAATCG	TGTAATTATT	1500
	ATGACTGATG	CTGATACTGA	TGGTGCGCAT	ATTCAGTGTC	TATTGTTAAC	1550
	ATTCTTCTTC	AAATATATGA	AACCGCTTGT	TCAAGCAGGT	CGTGTATTTA	1600
40	TTGCTTTACC	TCCACTTTAT	AAATTGGAAA	AAGGTAAAGG	CAAAACAAAG	1650
	CGAGTTGAAT	ACGCTTGGAC	AGACGAAGAG	CTTAATAAAT	TGCAAAAAGA	1700
	ACTTGGTAAA	GGCTTCACGT	TACAACGTTA	CAAAGGTTTG	GGTGAAATGA	1750
	ACCCTGAGCA	ATTATGGGAA	ACGACGATGA	ACCCAGAAAC	ACGAACCTTA	1800
	ATTCGTGTAC	AAGTTGAAGA	TGAAGTGCCT	TCATCTAAAC	GTGTAACAAC	1850
45	ATTAATGGGT	GACAAAGTAC	AACCTAGACG	TGAATGGATT	GAAAAGCATG	1900
	TTGAGTTTGG	TATGCAAGAG	GACCAAAGTA	TTTtagataa	TTCTGAAGTA	1950
	CAAGTGCTTG	AAAATGATCA	ATTTGATGAG	GAGGAAATCT	AG	1992

50

2) INFORMATION FOR SEQ ID NO: 1329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329

10 TGTAGAGCGC GGTATCATCA AAGTA

25

2) INFORMATION FOR SEQ ID NO: 1330

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330

25

AGATTCGAAC TTGGTGTGCG GG

22

30 2) INFORMATION FOR SEQ ID NO: 1331

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331

40

GCCCTTGAGG TACAGAATGG TAATGAAGTT

30

45

2) INFORMATION FOR SEQ ID NO: 1332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332

5 GACCGCGGCG CAGACCATCA 20

2) INFORMATION FOR SEQ ID NO: 1333

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333

20

TCATGGTGAC TTATCTATTT ATG 23

25 2) INFORMATION FOR SEQ ID NO: 1334

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334

CATCTATTTA TAAAGCAATG GTA 23

40

2) INFORMATION FOR SEQ ID NO: 1335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335

CTATTTATGG AGCAATGGT 19

2) INFORMATION FOR SEQ ID NO: 1336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336

TGGAGACTAC TCAGTGT

17

2) INFORMATION FOR SEQ ID NO: 1337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337

TGGAGACTTC TCAGTGT

17

2) INFORMATION FOR SEQ ID NO: 1338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338

GTGTACGGAG CAATG

15

2) INFORMATION FOR SEQ ID NO: 1339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339

CCAGCGGAAA TCGGT

15

10

2) INFORMATION FOR SEQ ID NO: 1340

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340

GAACAAGGTA TGACACCGGA TAAAT

25

25

2) INFORMATION FOR SEQ ID NO: 1341

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341

GATAACTGAA ATCCTGAGCC ATACG

25

40

2) INFORMATION FOR SEQ ID NO: 1342

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342

GATGTTATTG GTCAATATCA TCCA

24

5

2) INFORMATION FOR SEQ ID NO: 1343

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 29 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343

AAGAAACTGT CTCTTTATTA ATATCACGT

29

20

2) INFORMATION FOR SEQ ID NO: 1344

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344

35 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1345

40

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345

50

CCCGCCGAGC ATTTCAACTA TTG

23

2) INFORMATION FOR SEQ ID NO: 1346

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346

GATGTTACGC AGCAGGGCAG TC

22

15

2) INFORMATION FOR SEQ ID NO: 1347

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347

ACCAAGCAGG TTCGCAGTCA AGTA

24

30

2) INFORMATION FOR SEQ ID NO: 1348

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: Unidentified bacterium
 (C) ACCESSION NUMBER: X04555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348

ATGCGCTCAC	GCAACTGGTC	CAGAACCTTG	ACCGAACGCA	GCGGTGGTAA	50
50 CGGCGCAGTG	GCGGTTTTCA	TGGCTTGTTA	TGACTGTTTT	TTTGTACAGT	100
CTATGCCTCG	GGCATCCAAG	CAGCAAGCGC	GTTACGCCGT	GGGTCGATGT	150
TTGATGTTAT	GGAGCAGCAA	CGATGTTACG	CAGCAGGGCA	GTCGCCCTAA	200
AACAAAGTTA	GGCCGCATGG	ACACAACGCA	GGTCACATTG	ATACACAAAA	250

	TTCTAGCTGC	GGCAGATGAG	CGAAATCTGC	CGCTCTGGAT	CGGTGGGGGC	300
	TGGGCGATCG	ATGCACGGCT	AGGGCGTGTA	ACACGCAAGC	ACGATGATAT	350
	TGATCTGACG	TTTCCCGGCG	AGAGGCGCGG	CGAGCTCGAG	GCAATAGTTG	400
	AAATGCTCGG	CGGGCGCGTC	ATGGAGGAGT	TGGACTATGG	ATTCTTAGCG	450
5	GAGATCGGGG	ATGAGTTACT	TGACTGCCAA	CCTGCTTGGT	GGGCAGACGA	500
	AGCGTATGAA	ATCGCGGAGG	CTCCGCAGGG	CTCGTGCCCA	GAGGCGGCTG	550
	AGGGCGTCAT	CGCCGGGCGG	CCAGTCCGTT	GTAACAGCTG	GGAGGCGATC	600
	ATCTGGGATT	ACTTTTACTA	TGCCGATGAA	GTACCACCAG	TGGACTGGCC	650
	TACAAAGCAC	ATAGAGTCCT	ACAGGCTCGC	ATGCACCTCA	CTCGGGGCGG	700
10	AAAAGGTTGA	GGTCTTGCGT	GCCGCTTTCA	GGTCGCGATA	TGCGGCCTAA	750

2) INFORMATION FOR SEQ ID NO: 1349

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349

25

CAGCCGACCA ATGAGTATCT TGCC

24

2) INFORMATION FOR SEQ ID NO: 1350

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350

40

TAATCAGGGC AGTTGCGACT CCTA

24

2) INFORMATION FOR SEQ ID NO: 1351

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Pseudomonas aeruginosa*
(B) STRAIN: Stone 130
(C) ACCESSION NUMBER: L06157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351

```
10 ATGTTATGGA GCAGCAACGA TGTTACGCAG CAGGGCAGTC GCCCTAAAAC      50
   AAAGTTAGGT GGCTCAATGA GCATCATTGC AACCGTCAAG ATCGGCCCTG      100
   ACGAAATTTC AGCCATGAGG GCTGTGCTCG ATCTCTTCGG CAAAGAGTTT      150
   GAGGACATTC CAACCTACTC TGATCGCCAG CCGACCAATG AGTATCTTGC      200
   CAATCTTCTG CACAGCGAGA CGTTCATCGC GCTCGCTGCT TTTGACCGCG      250
15 GAACAGCAAT AGGTGGGCTC GCCGCCTACG TTCTACCCAA GTTCGAGCAA      300
   GCGCGAAGCG AGATCTACAT TTATGACTTG GCAGTCGCTT CCAGCCATCG      350
   AAGGCTAGGA GTCGCAACTG CCCTGATTAG CCACCTGAAG CGTGTGGCGG      400
   TTGAACTTGG CGCGTATGTA ATCTATGTGC AAGCAGACTA CGGTGACGAT      450
   CCGGCAGTCG CTCTCTACAC AAAGCTTGGG GTTCGGGAAG ACGTCATGCA      500
20 CTTGACATT GATCCAAGAA CCGCCACCTA A                      531
```

2) INFORMATION FOR SEQ ID NO: 1352

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352

35

CCACGCTGAC AGAGCCGCAC CG

22

40 2) INFORMATION FOR SEQ ID NO: 1353

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353

GGCCAGCTCC CATCGGACCC TG

22

2) INFORMATION FOR SEQ ID NO: 1354

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354

CACGCTGACA GAGCCGCACC G

21

15

2) INFORMATION FOR SEQ ID NO: 1355

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355

ATGCCGTTGC TGTCGAAATC CTCG

24

30

2) INFORMATION FOR SEQ ID NO: 1356

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M97172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356

50 ATGAACACGA TCGAATCGAT CACGGCGGAC CTGCACGGAC TGGGCGTCCG 50
 GCCCGGCGAC CTGATCATGG TCCATGCATC GCTGAAAGCC GTCGGCCCCG 100
 TCGAGGGAGG TGCGGCCTCG GTGGTGTGCG CCCTTCGCGC CGCGGTCGGG 150
 TCCGCAGGGA CCCTGATGGG TTATGCCTCA TGGGACCGCT CGCCCTATGA 200
 GGAGACGCTG AACGGCGCGC GGATGGACGA AGAACTGCGC CGCCGGTGCC 250

	CACCCCTTCGA	TCTGGCCACA	TCCGGTACCT	ATCCCGGCTT	CGGCCTGCTC	300
	AACCGGTTTC	TGCTTGAGGC	GCCCGACGCA	CGGCGCAGCG	CGCATCCCGA	350
	CGCCTCCATG	GTCGCGGTCG	GCCCCCTTGC	CGCCACGCTG	ACAGAGCCGC	400
	ACCGGCTTGG	GCAGGCGCTG	GGCGAAGGCT	CGCCGCTGGA	GCGCTTCGTC	450
5	GGGCATGGCG	GAAAGGTCCT	GCTTCTGGGA	GCGCCGCTCG	ACTCCGTCAC	500
	CGTGCTGCAT	TACGCCGAGG	CCATCGCCCC	CATCCCGAAC	AAACGCCGCG	550
	TGACCTATGA	AATGCCGATG	CTCGGCCCGG	ATGGCAGGGT	CCGATGGGAG	600
	CTGGCCGAGG	ATTTGACAG	CAACGGCATT	CTCGATTGCT	TCGCGGTCGA	650
	TGGGAAGCCG	GATGCCGTCG	AGACGATCGC	CAAGGCTTAT	GTCGAACTGG	700
10	GCCGGCATCG	GGAAGGCATC	GTCGGTCGCG	CACCCCTCCTA	TCTGTTTGAA	750
	GCGCAGGATA	TCGTCTCGTT	CGGCGTCACC	TATCTCGAAC	AGCATTTTCGG	800
	CGCGCCCTGA					810

15

2) INFORMATION FOR SEQ ID NO: 1357

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357

GCCCATCCAT TTGCCTTTGC

20

30

2) INFORMATION FOR SEQ ID NO: 1358

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358

GCGTACCAAC TTGCCATCCT GAAG

24

45

2) INFORMATION FOR SEQ ID NO: 1359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359

TGCCCCTGCC ACCTCACTC

19

10

2) INFORMATION FOR SEQ ID NO: 1360

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360

CGTACCAACT TGCCATCCTG AAGA

24

25

2) INFORMATION FOR SEQ ID NO: 1361

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 786 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X01385

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361

GTGCAATACG AATGGCGAAA AGCCGAGCTC ATCGGTCAGC TTCTCAACCT 50
TGGGGTTACC CCCGGCGGTG TGCTGCTGGT CCACAGCTCC TTCCGTAGCG 100
45 TCCGGCCCCCT CGAAGATGGG CCACTTGGAC TGATCGAGGC CCTGCGTGCT 150
GCGCTGGGTC CGGGAGGGAC GCTCGTCATG CCCTCGTGGT CAGGTCTGGA 200
CGACGAGCCG TTCGATCCTG CCACGTCGCC CGTTACACCG GACCTTGGAG 250
TTGTCTCTGA CACATTCTGG CGCCTGCCAA ATGTAAAGCG CAGCGCCCAT 300
CCATTTGCCT TTGCGGCAGC GGGGCCACAG GCAGAGCAGA TCATCTCTGA 350
50 TCCATTGCCC CTGCCACCTC ACTCGCCTGC AAGCCCGGTC GCCCGTGTCC 400
ATGAACTCGA TGGGCAGGTA CTTCTCCTCG GCGTGGGACA CGATGCCAAC 450
ACGACGCTGC ATCTTGCCGA GTTGATGGCA AAGGTTCCCT ATGGGGTGCC 500
GAGACACTGC ACCATTCTTC AGGATGGCAA GTTGGTACGC GTCGATTATC 550

TCGAGAATGA CCACTGCTGT GAGCGCTTTG CCTTGGCGGA CAGGTGGCTC 600
AAGGAGAAGA GCCTTCAGAA GGAAGGTCCA GTCGGTCATG CCTTTGCTCG 650
GTTGATCCGC TCCCGCGACA TTGTGGCGAC AGCCCTGGGT CAACTGGGCC 700
GAGATCCGTT GATCTTCCTG CATCCGCCAG AGGGCGGGAT GCGAAGAATG 750
5 CGATGCCGCT CGCCAGTCGA TTGGCTGAGC TCATGA 786

2) INFORMATION FOR SEQ ID NO: 1362

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362

20

CGCCGCCATC GCCCAAAGCT GG

22

25 2) INFORMATION FOR SEQ ID NO: 1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363

35

CGGCATAATG GAGCGCGGTG ACTG

24

40

2) INFORMATION FOR SEQ ID NO: 1364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364

50

TTTCTCGCCC ACGCAGGAAA AATC

24

2) INFORMATION FOR SEQ ID NO: 1365

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365

CATCCTCGAC GAATATGCCG CG

22

15

2) INFORMATION FOR SEQ ID NO: 1366

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 900 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (C) ACCESSION NUMBER: M88012

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366

	ATGACTGATC	CCCGCAAAAA	CGGCGATTTG	CACGAACCCG	CGACGGCACC	50
	CGCGACGCC	TGGTCCAAAA	GCGAGCTGGT	CCGGCAATTG	CGCGACCTCG	100
35	GCGTGCGCTC	AGGCGATATG	GTGATGCCGC	ATGTGTCGTT	GCGCGCCGTC	150
	GGGCCGCTGG	CGGACGGACC	GCAGACACTT	GTCGATGCGC	TGATCGAGGC	200
	CGTCGGCCCC	ACCGGGAATA	TTCTCGCCTT	CGTCTCGTGG	CGCGATTTCG	250
	CCTATGAACA	GACGCTGGGT	CATGATGCGC	CGCCCGCCGC	CATCGCCCAA	300
	AGCTGGCCTG	CGTTCGACCC	CGACCATGCG	CCCGCCTACC	CCGGCTTTGG	350
40	CGCGATCAAC	GAATTTATCC	GAACCTATCC	GGGGTGTCGG	CGCACGGCCC	400
	ATCCCGACGC	ATCGATGGCG	GCGATCGGGC	CCGATGCGGC	GTGGCTGGTG	450
	GCGCCGCACG	AGATGGGCGC	CGCTTATGGC	CCCCGCTCGC	CGATCGCGCG	500
	TTTTCTCGCC	CACGCAGGAA	AAATCCTGTC	GATCGGCGCC	GGGCCCAGATG	550
	CAGTCACCGC	GCTCCATTAT	GCCGAAGCGG	TGGCGCGGAT	CGAGGGCAAG	600
45	CGCCGCGTCA	CTTATTCGAT	GCCCTTACTG	CGCGAAGGCA	AGCGCGTCTG	650
	GGTCACCACG	TCCGACTGGG	ATTCGAACGG	CATCCTCGAC	GAATATGCCG	700
	CGCCCGACGG	CCCCGACGCG	GTCGAACGGA	TCGCCCCGCA	CTATCTCGCC	750
	CGCACCAGGG	TTGCGCAAGG	CCCGGTGCGC	GGCGCGCAAT	CCCGGCTGAT	800
	CGACGCGGCC	GATATCGTTT	CCTTCGGCAT	CGAATGGCTC	GAGGCGCGCC	850
50	ACGCCGCGCC	AGCGGCGGCA	GCGCTGAAGC	CGAAACAACG	CCGCGACTGA	900

2) INFORMATION FOR SEQ ID NO: 1367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367

CAAATATACT AACAGAAGCG TTCA

24

2) INFORMATION FOR SEQ ID NO: 1368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368

AGGATCTTGC CAATACCTTT AT

22

2) INFORMATION FOR SEQ ID NO: 1369

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369

AAACCTTTGT TTCGGTCTGC TAAT

24

2) INFORMATION FOR SEQ ID NO: 1370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370

AAGCGATTCC AATAATACCT TGCT

24

10

2) INFORMATION FOR SEQ ID NO: 1371

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 558 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter diversus*
(C) ACCESSION NUMBER: M18967

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371

ATGAATTATC AAATTGTGAA TATTGCGGAA TGCAGCAATT ATCAGTTAGA 50
AGCAGCAAAT AACTAACAG AAGCGTTCAA TGATCTTGGT AACAATTCAT 100
30 GGCCAGATAT GACGAGTGCA ACAAAGAAG TAAAAGAATG TATTGAGAGT 150
CCAAACCTTT GTTTCGGTCT GCTAATAAAT AACTCCTTAG TTGGCTGGAT 200
AGGCTTAAGG CCAATGTACA AGGAAACCTG GGAATTGCAT CCATTGGTTG 250
TCAGACCAGA TTATCAAAAT AAAGGTATTG GCAAGATCCT GCTTAAGGAA 300
TTAGAAAACA GAGCTAGAGA GCAAGGTATT ATTGGAATCG CTTTAGGAAC 350
35 AGATGATGAA TACTATAGAA CAAGTCTCTC TTTAATAACT ATAACAGAAG 400
ATAATATATT TGATTCAATA AAAAATATTA AAAATATTAA TAAACATCCA 450
TATGAGTTTT ATCAGAAGAA TGGTTATTAT ATTGTTGGAA TAATTCCAAA 500
TGCCAATGGT AAAACAAAC CAGATATTTG GATGTGGAAA AGTTTAATCA 550
AAGAGTAA 558

40

2) INFORMATION FOR SEQ ID NO: 1372

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372

GCTTTCGTTG CCTTTGCCGA GGTC

24

5

2) INFORMATION FOR SEQ ID NO: 1373

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373

CACCCCTGTT GCTTCGCCCA CTC

23

20

2) INFORMATION FOR SEQ ID NO: 1374

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374

AGATATTGGC TTCGCCGCAC CACA

24

35

2) INFORMATION FOR SEQ ID NO: 1375

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375

50 CCCTGTTGCT TCGCCCACTC CTG

23

2) INFORMATION FOR SEQ ID NO: 1376

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 441 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (C) ACCESSION NUMBER: M94066

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376

	ATGATCGTCA	TCTGCGACCA	CGACAACCTC	GACGCCTGGC	TGGCGCTGCG	50
	CACCGCGCTG	TGGCCCTCCG	GCTCGCCTGA	AGATCACCGC	GCGGAAATGC	100
	GCGAGATATT	GGCTTCGCCG	CACCACACCG	CGTTTATGGC	GCGGGGGCTG	150
20	GACGGCGCTT	TCGTTGCCTT	TGCCGAGGTC	GCGCTGCGCT	ACGATTACGT	200
	CAACGGCTGC	GAATCGTCGC	CGGTGGCGTT	TTTGGAAGGA	ATTTATACCG	250
	CCGAACGCGC	CCGCCGCCAG	GGCTGGGGCCG	CGCGCCTGAT	CGCGCAGGTG	300
	CAGGAGTGGG	CGAAGCAACA	GGGGTGCAGC	GAGCTGGCGT	CGGATACCGA	350
	TATCGCCAAT	CTGGACTCCC	AGCGCCTGCA	TGCGGCGCTG	GGCTTTGCCG	400
25	AAACGGAGCG	AGTAGTGTTT	TACCGCAAAA	CGCTGGGCTG	A	441

2) INFORMATION FOR SEQ ID NO: 1377

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377

40

GCCGTGGGTC GATGTTTGAT GTTA

24

45 2) INFORMATION FOR SEQ ID NO: 1378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378

GCTCGATGAC GCCAACTACC TCTG

24

5

2) INFORMATION FOR SEQ ID NO: 1379

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379

20 AGCAGCAACG ATGTTACGCA GCAG

24

2) INFORMATION FOR SEQ ID NO: 1380

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380

35

CGCTCGATGA CGCCAACTAC CTCT

24

40 2) INFORMATION FOR SEQ ID NO: 1381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: X02340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381

```

5  GTGGTAACGG CGCAGTGGCG GTTTTCATGG CTTCTTGTTA TGACATGTTT    50
   TTTTGGGGTA CAGTCTATGC CTCGGGCATC CAAGCAGCAA GCGCGTTACG    100
   CCGTGGGTCG ATGTTTGATG TTATGGAGCA GCAACGATGT TACGCAGCAG    150
   GGCAGTCGCC CTAAACAAA GTTAAACATC ATGAGGGAAG CCGTGATCGC    200
   CGAAGTATCG ACTCAACTAT CAGAGGTAGT TGGCGTCATC GAGCGCCATC    250
   TCGAACCGAC GTTGCTGGCC GTACATTGTG ACGGCTCCGC AGTGGATGGC    300
   GGCCTGAAGC CACACAGTGA TATTGATTG CTGGTTACGG TGACCGTAAG    350
10  GCTTGATGAA ACAACGCGGC GAGCTTTGAT CAACGACCTT TTGGAAACTT    400
   CGGCTTCCCC TGGAGAGAGC GAGATTCTCC GCGCTGTAGA AGTCACCATT    450
   GTTGTGCACG ACGACATCAT TCCGTGGCGT TATCCAGCTA AGCGCGAACT    500
   GCAATTTGGA GAATGGCAGC GCAATGACAT TCTTGCAAGT ATCTTCGAGC    550
   CAGCCACGAT CGACATTGAT CTGGCTATCT TGCTGACAAA AGCAAGAGAA    600
15  CATAGCGTTG CTTGGTAGG TCCAGCGGCG GAGGAACTCT TTGATCCGGT    650
   TCCTGAACAG GATCTATTTG AGGCGCTAAA TGAAACCTTA ACGCTATGGA    700
   ACTCGCCGCC CGACTGGGCT GGCGATGAGC GAAATGTAGT GCTTACGTTG    750
   TCCCGCATTG GGTACAGCGC AGTAACCGGC AAAATCGCGC CGAAGGATGT    800
   CGCTGCCGAC TGGGCAATGG AGCGCCTGCC GGCCCAGTAT CAGCCCGTCA    850
20  TACTTGAAGC TAGACAGGCT TATCTTGGAC AAGAAGAAGA TCGCTTGGCC    900
   TCGCGCGCAG ATCAGTTGGA AGAATTTGTC CACTACGTGA AAGGCGAGAT    950
   CACCAAGGTA GTCGGCAAAT AA                                972

```

25

2) INFORMATION FOR SEQ ID NO: 1382

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382

TAGATATGAT AGGCGGTAAA AAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1383

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383

CCCAAATTCG AGTAAGAGGT ATT

23

5 2) INFORMATION FOR SEQ ID NO: 1384

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384

GATATGATAG GCGGTAAAAA GC

22

20

2) INFORMATION FOR SEQ ID NO: 1385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385

TCCCAAATTC GAGTAAGAGG TA

22

35

2) INFORMATION FOR SEQ ID NO: 1386

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 477 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01282

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386

ATGAAAGAAA GATATGGAAC AGTATATAAA GGCTCTCAGA GGCTCATAGA

50

CGAGGAAAGT GGAGAAGTAA TAGAGGTAGA TAAGCTATAC CGTAAACAAA 100
 CGTCTGGTAA CTTTGTAATA GCGTATATCG TCCAATTAAT AAGTATGTTA 150
 GATATGATAG GCGGTAAAAA GCTCAAGATT GTTAATTATA TATTAGATAA 200
 TGTACATCTA AGTAATAACA CAATGATAGC AACTGTTAGA GAAATAGCAG 250
 5 AAGGAACAAA TACAAGCACG AAAACCGTAA ATACAACGCT TAAAATCTTA 300
 GAAGAAGGAA ATATCATTAA AAGAAGAACT GGAGCATTA TGGCTAAACCC 350
 AGAGCTACTC ATGAGAGGCG ATGACCAAAA ACAAAAATAC CTCTTACTCG 400
 AATTTGGGAA CTTTGAGCAA GAGGACGACC AAAAGCAAGA AAATGCTTTA 450
 TCAGAATATT ATTCTTTCAA GGAGTAG 477
 10

2) INFORMATION FOR SEQ ID NO: 1387

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387
 25 TTATGCCTCT TCCGACCATC AAGC 24

2) INFORMATION FOR SEQ ID NO: 1388

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 35 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388
 40 TACGCTCGTC ATCAAAATCA CTCG 24

45 2) INFORMATION FOR SEQ ID NO: 1389

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389

GAATAACGGT TTGGTTGATG CGAG

24

5

2) INFORMATION FOR SEQ ID NO: 1390

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390

20 ATGGCAAGAT CCTGGTATCG GTCT

24

2) INFORMATION FOR SEQ ID NO: 1391

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: J01839

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391

40	ATGAGCCATA TTCAACGGGA AACGTCTTGC TCGAGGCCGC GATTAAATTC	50
	CAACATGGAT GCTGATTTAT ATGGGTATAA ATGGGCTCGC GATAATGTCG	100
	GGCAATCAGG TGCGACAATC TATCGATTGT ATGGGAAGCC CGATGCGCCA	150
	GAGTTGTTTC TGAAACATGG CAAAGGTAGC GTTGCCAATG ATGTTACAGA	200
	TGAGATGGTC AGACTAAACT GGCTGACGGA ATTTATGCCT CTTCCGACCA	250
45	TCAAGCATTT TATCCGTACT CCTGATGATG CATGGTTACT CACCACTGCG	300
	ATCCCCGGGA AAACAGCATT CCAGGTATTA GAAGAATATC CTGATTCAGG	350
	TGAAAATATT GTTGATGCGC TGGCAGTGTT CCTGCGCCGG TTGCATTCTGA	400
	TTCCTGTTTG TAATTGTCCT TTTAACAGCG ATCGCGTATT TCGTCTCGCT	450
	CAGGCGCAAT CACGAATGAA TAACGGTTTG GTTGATGCGA GTGATTTTGA	500
50	TGACGAGCGT AATGGCTGGC CTGTTGAACA AGTCTGGAAA GAAATGCATA	550
	AGCTTTTGCC ATTCTCACCG GATTGATCGC TCACTCATGG TGATTCTCTCA	600
	CTTGATAACC TTATTTTGA CGAGGGGAAA TTAATAGGTT GTATTGATGT	650
	TGGACGAGTC GGAATCGCAG ACCGATACCA GGATCTTGCC ATCCTATGGA	700

ACTGCCTCGG TGAGTTTTCT CCTTCATTAC AGAAACGGCT TTTTCAAAAA 750
TATGGTATTG ATAATCCTGA TATGAATAAA TTGCAGTTTC ATTTGATGCT 800
CGATGAGTTT TTCTAA 816

5

2) INFORMATION FOR SEQ ID NO: 1392

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392

20 TGGGTGGAGA GGCTATTCGG CTAT 24

2) INFORMATION FOR SEQ ID NO: 1393

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393

35 CAGTCCCTTC CCGCTTCAGT GAC 23

2) INFORMATION FOR SEQ ID NO: 1394

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394

50 GACGTTGTCA CTGAAGCGGG AAGG 24

2) INFORMATION FOR SEQ ID NO: 1395

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1395

CTTGGTGGTC GAATGGGCAG GTAG

24

15

2) INFORMATION FOR SEQ ID NO: 1396

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (C) ACCESSION NUMBER: V00618

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396

ATGATTGAAC AAGATGGATT GCACGCAGGT TCTCCGGCCG CTTGGGTGGA 50
 GAGGCTATTC GGCTATGACT GGGCACAACA GACAATCGGC TGCTCTGATG 100
 35 CCGCCGTGTT CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG 150
 ACCGACCTGT CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGCGGCT 200
 ATCGTGGCTG GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTCGACGTTG 250
 TCACTGAAGC GGGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG 300
 GATCTCCTGT CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC 350
 40 TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCG 400
 ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC 450
 GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC 500
 AGCCGAACTG TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGAGGATC 550
 TCGTCGTGAC CCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAAT 600
 45 GGCCGCTTTT CTGGATTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG 650
 CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGGCG 700
 GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT 750
 TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGA 795

50

2) INFORMATION FOR SEQ ID NO: 1397

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397
10 GTGGGAGAAA ATGAAAACCT AT 22
- 15 2) INFORMATION FOR SEQ ID NO: 1398
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398
 ATGGAGTGAA AGAGCCTGAT 20
- 30 2) INFORMATION FOR SEQ ID NO: 1399
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399
 ACCTATGATG TGGAACGGGA AAAG 24
- 45 2) INFORMATION FOR SEQ ID NO: 1400
- (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400

5

CGATGGAGTG AAAGAGCCTG ATG

23

10 2) INFORMATION FOR SEQ ID NO: 1401

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
(C) ACCESSION NUMBER: V01547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401

25

ATGGCTAAAA	TGAGAATATC	ACCGGAATTG	AAAAAACTGA	TCGAAAAATA	50
CCGCTGCGTA	AAAGATACGG	AAGGAATGTC	TCCTGCTAAG	GTATATAAGC	100
TGGTGGGAGA	AAATGAAAAC	CTATATTTAA	AAATGACGGA	CAGCCGGTAT	150
AAAGGGACCA	CCTATGATGT	GGAACGGGAA	AAGGACATGA	TGCTATGGCT	200
30 GGAAGGAAAG	CTGCCTGTTC	CAAAGGTCCT	GCACTTTGAA	CGGCATGATG	250
GCTGGAGCAA	TCTGCTCATG	AGTGAGGCCG	ATGGCGTCCT	TTGCTCGGAA	300
GAGTATGAAG	ATGAACAAAG	CCCTGAAAAG	ATTATCGAGC	TGTATGCGGA	350
GTGCATCAGG	CTCTTTCACT	CCATCGACAT	ATCGGATTGT	CCCTATACGA	400
ATAGCTTAGA	CAGCCGCTTA	GCCGAATTGG	ATTACTTACT	GAATAACGAT	450
35 CTGGCCGATG	TGGATTGCGA	AAACTGGGAA	GAAGACACTC	CATTTAAAGA	500
TCCGCGCGAG	CTGTATGATT	TTTTAAAGAC	GGAAAAGCCC	GAAGAGGAAC	550
TTGTCTTTTC	CCACGGCGAC	CTGGGAGACA	GCAACATCTT	TGTGAAAGAT	600
GGCAAAGTAA	GTGGCTTTAT	TGATCTTGGG	AGAAGCGGCA	GGGCGGACAA	650
GTGGTATGAC	ATTGCCTTCT	GCGTCCGGTC	GATCAGGGAG	GATATCGGGG	700
40 AAGAACAGTA	TGTCGAGCTA	TTTTTTGACT	TACTGGGGAT	CAAGCCTGAT	750
TGGGAGAAAA	TAAATATTA	TATTTTACTG	GATGAATTGT	TTTAG	795

45 2) INFORMATION FOR SEQ ID NO: 1402

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402

5 TATTCAACAA TTTATCGGAA ACAG 24

2) INFORMATION FOR SEQ ID NO: 1403

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403

20 TCAGAGAGCC AACTCAACAT TTT 23

2) INFORMATION FOR SEQ ID NO: 1404

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404

35 AAACAGCGTT TTAGAGCCAA ATAA 24

40 2) INFORMATION FOR SEQ ID NO: 1405

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
45 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405

TTCTCAGAGA GCCAACTCAA CATT 24

2) INFORMATION FOR SEQ ID NO: 1406

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: BM2580
 (C) ACCESSION NUMBER: X07753
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406

	ATGGAATTGC	CCAATATTAT	TCAACAATTT	ATCGGAAACA	GCGTTTTAGA	50
	GCCAAATAAA	ATTGGTCAGT	CGCCATCGGA	TGTTTATTCT	TTTAATCGAA	100
20	ATAATGAAAC	TTTTTTTCTT	AAGCGATCTA	GCACTTTATA	TACAGAGACC	150
	ACATACAGTG	TCTCTCGTGA	AGCGAAAATG	TTGAGTTGGC	TCTCTGAGAA	200
	ATTAAAGGTG	CCTGAACTCA	TCATGACTTT	TCAGGATGAG	CAGTTTGAAT	250
	TCATGATCAC	TAAAGCGATC	AATGCAAAAC	CAATTTTCAGC	GCTTTTTTTA	300
	ACAGACCAAG	AATTGCTTGC	TATCTATAAG	GAGGCACTCA	ATCTGTAAAA	350
25	TTCAATTGCT	ATTATTGATT	GTCCATTTAT	TTCAAACATT	GATCATCGGT	400
	TAAAAGAGTC	AAAATTTTTT	ATTGATAACC	AACTCCTTGA	CGATATAGAT	450
	CAAGATGATT	TTGACACTGA	ATTATGGGGA	GACCATAAAA	CTTACCTAAG	500
	TCTATGGAAT	GAGTTAACCG	AGACTCGTGT	TGAAGAAAGA	TTGGTTTTTT	550
	CTCATGGCGA	TATCACGGAT	AGTAATATTT	TTATAGATAA	ATTCAATGAA	600
30	ATTTATTTTT	TAGATCTTGG	TCGTGCTGGG	TTAGCAGATG	AATTTGTAGA	650
	TATATCCTTT	GTTGAACGTT	GCCTAAGAGA	GGATGCATCG	GAGGAAACTG	700
	CGAAAATATT	TTTAAAGCAT	TTAAAAAATG	ATAGACCTGA	CAAAAGGAAT	750
	TATTTTTTAA	AACTTGATGA	ATTGAATTGA			780

35

2) INFORMATION FOR SEQ ID NO: 1407

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407

CCCTGTAATA GAAAAGCAAG TAGG

50

24

2) INFORMATION FOR SEQ ID NO: 1408

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408
- TTGTCGTATC CCTCAAATCA CC 22
- 15 2) INFORMATION FOR SEQ ID NO: 1409
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409
- TGGGATTACA ATGGCAATCA GCG 23
- 30 2) INFORMATION FOR SEQ ID NO: 1410
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410
- GGGGAATAGG TCACAAGATC TGCTT 25
- 45 2) INFORMATION FOR SEQ ID NO: 1411
- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 912 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(C) ACCESSION NUMBER: S46063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411

10 ATGCTTTTAT ATAAAATGTG TGACAATCAA AATTATGGGG TTA CTTACAT 50
 GAAGTTTTTA TTGGCATT TT CGCTTTTAAT ACCATCCGTG GTTTTTGCAA 100
 GTAGTTCAA GTTTCAGCAA GTTGAACAAG ACGTTAAGGC AATTGAAGTT 150
 TCTCTTTCTG CTCGTATAGG TGTTTCCGT CTTGATACTC AAAATGGAGA 200
 15 ATATTGGGAT TACAATGGCA ATCAGCGCTT CCCGTTAACA AGTACTTTTA 250
 AAACAATAGC TTGCGCTAAA TTACTATATG ATGCTGAGCA AGGAAAAGTT 300
 AATCCCAATA GTACAGTCGA GATTAAGAAA GCAGATCTTG TGACCTATTC 350
 CCCTGTAATA GAAAAGCAAG TAGGGCAGGC AATCACACTC GATGATGCGT 400
 GCTTCGCAAC TATGACTACA AGTGATAATA CTGCGGCAAA TATCATCCTA 450
 20 AGTGCTGTAG GTGGCCCCAA AGGCGTTACT GATTTTTTAA GACAAATTGG 500
 GGACAAAGAG ACTCGTCTAG ACCGTATTGA GCCTGATTTA AATGAAGGTA 550
 AGCTCGGTGA TTTGAGGGAT ACGACAAC TC AAGGCAAT AGCCAGTACT 600
 TTGAATAAAC TTTTATTTGG TTCCGCGCTA TCTGAAATGA ACCAGAAAAA 650
 ATTAGAGTCT TGGATGGTGA ACAATCAAGT CACTGGTAAT TTACTACGTT 700
 25 CAGTATTGCC GGCGGGATGG AACATTGCGG ATCGCTCAGG TGCTGGCGGA 750
 TTTGGTGCTC GGAGTATTAC AGCAGTTGTG TGGAGTGAGC ATCAAGCCCC 800
 AATTATTGTG AGCATCTATC TAGCTCAAAC ACAGGCTTCA ATGGCAGAGC 850
 GAAATGATGC GATTGT TAAA ATTGGTCATT CAATTTTGA CGTTTATACA 900
 TCACAGTCGC GC 912

30

2) INFORMATION FOR SEQ ID NO: 1412

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412

45 GAGAAAACGC TCCAGCAGGG C

21

2) INFORMATION FOR SEQ ID NO: 1413

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413

CATGAGGCTT TCACTGCGGG G

21

10

2) INFORMATION FOR SEQ ID NO: 1414

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414

TATCGTTAAT CGCACCATCA C

21

25

2) INFORMATION FOR SEQ ID NO: 1415

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415

40

ATGCAGTAAT GCGGCTTTAT C

21

2) INFORMATION FOR SEQ ID NO: 1416

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(B) STRAIN: HEL-1

(C) ACCESSION NUMBER: X91840

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416

	ATGATGAAAA	AATCGTTATG	CTGCGCTCTG	CTGCTGACAG	CCTCTTTCTC	50
	CACATTTGCT	GCCGCAAAAA	CAGAACAACA	GATTGCCGAT	ATCGTTAATC	100
10	GCACCATCAC	CCCGTTGATG	CAGGAGCAGG	CTATTCCGGG	TATGGCCGTT	150
	GCCGTTATCT	ACCAGGGAAA	ACCCTATTAT	TTACCTGGG	GTAAAGCCGA	200
	TATCGCCAAT	AACCACCCAG	TCACGCAGCA	AACGCTGTTT	GAGCTAGGAT	250
	CGGTAGTAA	GACGTTTAAC	GGCGTGTTGG	GCGGCGATGC	TATCGCCCGC	300
	GGCGAAATTA	AGCTCAGCGA	TCCGGTCACG	AAATACTGGC	CAGAACTGAC	350
15	AGGCAAACAG	TGGCAGGGTA	TCCGCCTGCT	GCACCTAGCC	ACCTATACGG	400
	CAGGCGGCCT	ACCGCTGCAG	ATCCCCGATG	ACGTTAGGGA	TAAAGCCGCA	450
	TTACTGCATT	TTTATCAAAA	CTGGCAGCCG	CAATGGACTC	CGGGCGCTAA	500
	GCGACTTTAC	GCTAACTCCA	GCATTGGTCT	GTTTGGCGCG	CTGGCGGTGA	550
	AACCCTCAGG	AATGAGTTAC	GAAGAGGCAA	TGACCAGACG	CGTCCTGCAA	600
20	CCATTAAAC	TGGCGCATAC	CTGGATTACG	GTTCCGCAGA	ACGAACAAAA	650
	AGATTATGCC	TGGGGCTATC	GCGAAGGGAA	GCCCCGTACAC	GTTTCTCCGG	700
	GACAACTTGA	CGCCGAAGCC	TATGGCGTGA	AATCCAGCGT	TATTGATATG	750
	GCCCCGCTGGG	TTCAGGCCAA	CATGGATGCC	AGCCACGTTC	AGGAGAAAAC	800
	GCTCCAGCAG	GGCATTGCGC	TTGCGCAGTC	TCGCTACTGG	CGTATTGGCG	850
25	ATATGTACCA	GGGATTAGGC	TGGGAGATGC	TGAACTGGCC	GCTGAAAGCT	900
	GATTTCGATCA	TCAACGGCAG	CGACAGCAAA	GTGGCATTGG	CAGCGCTTCC	950
	CGCCGTTGAG	GTAAACCCGC	CCGCCCCCGC	AGTGAAAGCC	TCATGGGTGC	1000
	ATAAAACGGG	CTCCACTGGT	GGATTTGGCA	GCTACGTAGC	CTTCGTTCCA	1050
	GAAAAAACC	TTGGCATCGT	GATGCTGGCA	AACAAAAGCT	ATCCTAACCC	1100
30	TGTCCGTGTC	GAGGCGGCCT	GGCGCATTCT	TGAAAAGCTG	CAATAA	1146

2) INFORMATION FOR SEQ ID NO: 1417

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417

45

TGGTTAACTA YAATCCSATT GCGGA

25

50 2) INFORMATION FOR SEQ ID NO: 1418

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418

10 ATGCTTTACC CAGCGTCAGA TT 22

2) INFORMATION FOR SEQ ID NO: 1419

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419

25 CGATGAATAA GCTGATTTCT CACG 24

2) INFORMATION FOR SEQ ID NO: 1420

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420

40 TGCTTTACCC AGCGTCAGAT TACG 24

45 2) INFORMATION FOR SEQ ID NO: 1421

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421

AATTAGAGCG GCAGTCGGGA GGAA

24

2) INFORMATION FOR SEQ ID NO: 1422

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422

GAAATCAGCT TATTCATCGC CACG

24

2) INFORMATION FOR SEQ ID NO: 1423

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 876 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
 (B) STRAIN: GRI-1
 (C) ACCESSION NUMBER: X92506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423

40	ATGGTTAAAA AATCACTGCG TCAGTTCACG CTGATGGCGA CGGCAACCGT	50
	CACGCTGTTG TTAGGAAGTG TGCCGCTGTA TGCGCAAACG GCGGACGTAC	100
	AGCAAAAAC T GCCGAATTA GAGCGGCAGT CGGGAGGAAG ACTGGGTGTG	150
	GCATTGATTA ACACAGCAGA TAATTCGCAA ATACTTTATC GTGCTGATGA	200
45	GCGCTTTGCG ATGTGCAGCA CCAGTAAAGT GATGGCCGTG GCCGCGGTGC	250
	TGAAGAAAAG TGAAAGCGAA CCGAATCTGT TAAATCAGCG AGTTGAGATC	300
	AAAAAATCTG ACTTGGTTAA CTATAATCCG ATTGCGGAAA AGCACGTCGA	350
	TGGGACGATG TCACTGGCTG AGCTTAGCGC GGCCGCGCTA CAGTACAGCG	400
	ATAACGTGGC GATGAATAAG CTGATTTCTC ACGTTGGCGG CCCGCTAGC	450
50	GTCACCGCGT TCGCCCGACA GCTGGGAGAC GAAACGTTCC GTCTCGACCG	500
	TACCGAGCCG ACGTTAAACA CCGCCATTCC GGGCGATCCG CGTGATACCA	550
	CTTCACCTCG GGCAATGGCG CAAACTCTGC GTAATCTGAC GCTGGGTAAA	600
	GCATTGGGTG ACAGCCAACG GGCGCAGCTG GTGACATGGA TGAAAGGCAA	650

TACCACCGGT GCAGCGAGCA TTCAGGCTGG ACTGCCTGCT TCCTGGGTTG 700
TGGGGGATAA AACCGGCAGC GGTGACTATG GCACCACCAA CGATATCGCG 750
GTGATCTGGC CAAAAGATCG TGCGCCGCTG ATTCTGGTCA CTTACTTCAC 800
CCAGCCTCAA CCTAAGGCAG AAAGCCGTCG CGATGTATTA GCGTCGGCGG 850
5 CTAAAATCGT CACCAACGGT TTGTAA 876

2) INFORMATION FOR SEQ ID NO: 1424

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424

20

GTTAACGGTG ATGGCGACGC TAC

23

25 2) INFORMATION FOR SEQ ID NO: 1425

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425

35

GAATTATCGG CGGTGTTAAT CAGC

24

40

2) INFORMATION FOR SEQ ID NO: 1426

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426

50

CACGCTCAAT ACCGCCATTC CA

22

2) INFORMATION FOR SEQ ID NO: 1427

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427

TTATCGCCCA CTACCCATGA TTTC

24

15

2) INFORMATION FOR SEQ ID NO: 1428

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 876 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: CAS-5
 30 (C) ACCESSION NUMBER: X92507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428

	ATGATGACTC	AGAGCATTCG	CCGCTCAATG	TTAACGGTGA	TGGCGACGCT	50
35	ACCCCTGCTA	TTTAGCAGCG	CAACGCTGCA	TGCGCAGGCG	AACAGCGTGC	100
	AACAGCAGCT	GGAAGCCCTG	GAGAAAAGTT	CGGGAGGTCG	GCTTGGCGTT	150
	GCGCTGATTA	ACACCGCCGA	TAATTCGCAG	ATTCTCTACC	GTGCCGATGA	200
	ACGTTTTGCG	ATGTGCAGTA	CCAGTAAGGT	GATGGCGGCC	GCGGCGGTGC	250
	TTAAACAGAG	CGAGAGCGAT	AAGCACCTGC	TAAATCAGCG	CGTTGAAATC	300
40	AAGAAGAGCG	ACCTGGTTAA	CTACAATCCC	ATTGCGGAGA	AACACGTTAA	350
	CGGCACGATG	ACGCTGGCTG	AGCTTGGCGC	AGCGGCGCTG	CAGTATAGCG	400
	ACAATACTGC	CATGAATAAG	CTGATTGCCC	ATCTGGGTGG	TCCCGATAAA	450
	GTGACGGCGT	TTGCTCGCTC	GTTGGGTGAT	GAGACCTTCC	GTCTGGACAG	500
	AACCGAGCCC	ACGCTCAATA	CCGCCATTCC	AGGCGACCCG	CGTGATACCA	550
45	CCACGCCGCT	CGCGATGGCG	CAGACCCTGA	AAAATCTGAC	GCTGGGTAAA	600
	GCGCTGGCGG	AAACTCAGCG	GGCACAGTTG	GTGACGTGGC	TTAAGGGCAA	650
	TACTACCGGT	AGCGCGAGCA	TTCGGGCGGG	TCTGCCGAAA	TCATGGGTAG	700
	TGGGCGATAA	AACCGGCAGC	GGAGATTATG	GCACCACCAA	CGATATCGCG	750
	GTTATCTGGC	CGGAAAACCA	CGCACCCTG	GTTCTGGTGA	CCTACTTTAC	800
50	CCAACCGGAG	CAGAAGGCGG	AAAGCCGTCG	GGATATTCTG	GCTGCGGCGG	850
	CGAAAATCGT	AACCCACGGT	TTCTGA			876

2) INFORMATION FOR SEQ ID NO: 1429

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429

TTTACGGCTA AAGATACTGA AAAGT

25

15

2) INFORMATION FOR SEQ ID NO: 1430

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430

GTTTAATAAA ACAACCACCG AATAAT

26

30

2) INFORMATION FOR SEQ ID NO: 1431

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431

45 TAATTGACAC TCCATTTACG GCTAA

25

2) INFORMATION FOR SEQ ID NO: 1432

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432

ACCGAATAAT ATTTTCCTTT CAGGCA

26

10

2) INFORMATION FOR SEQ ID NO: 1433

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 741 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: AJ223604

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433

	ATGAGCAAGT	TATCTGTATT	CTTTATATTT	TTGTTTTGCA	GCATTGCTAC	50
	CGCAGCAGAG	TCTTTGCCAG	ATTTAAAAAT	TGAAAAGCTT	GATGAAGGCG	100
30	TTTATGTTCA	TACTTCGTTT	GAAGAAGTTA	ACGGGTGGGG	CGTTGTTTCCT	150
	AAACATGGTT	TGGTGGTTCT	TGTAAATGCT	GAGGCTTACC	TAATTGACAC	200
	TCCATTTACG	GCTAAAGATA	CTGAAAAGTT	AGTCACTTGG	TTTGTGGAGC	250
	GTGGCTATAA	AATAAAAAGGC	AGCATTTCCT	CTCATTTTCA	TAGCGACAGC	300
	ACGGGCGGAA	TAGAGTGGCT	TAATTCTCGA	TCTATCCCCA	CGTATGCATC	350
35	TGAATTAACA	AATGAACTGC	TTAAAAAAGA	CGGTAAGGTT	CAAGCCACAA	400
	ATTCATTTAG	CGGAGTTAAC	TATTGGCTAG	TTAAAAATAA	AATTGAAGTT	450
	TTTTATCCAG	GCCCGGGACA	CACTCCAGAT	AACGTAGTGG	TTTGGTTGCC	500
	TGAAAGGAAA	ATATTATTCG	GTGGTTGTTT	TATTAAACCG	TACGGTTTAG	550
	GCAATTTGGG	TGACGCAAAT	ATAGAAGCTT	GGCCAAAGTC	CGCCAAATTA	600
40	TTAAAGTCCA	AATATGGTAA	GGCAAAACTG	GTTGTTCCAA	GTCACAGTGA	650
	AGTTGGAGAC	GCATCACTCT	TGAAACTTAC	ATTAGAGCAG	GCGGTTAAAG	700
	GGTTAAACGA	AAGTAAAAAA	CCATCAAAAC	CAAGCAACTA	A	741

45

2) INFORMATION FOR SEQ ID NO: 1434

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434

5 CACAATCAAG ACCAAGATTT GCGAT 25

2) INFORMATION FOR SEQ ID NO: 1435

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435

20

GAAAGGGCAG CTCGTTACGA TAGAG 25

25 2) INFORMATION FOR SEQ ID NO: 1436

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436

CAGCATCAAC ATTTAAGATC CCCA 24

40

2) INFORMATION FOR SEQ ID NO: 1437

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437

CTCCACTTGA TTAAGTGC GG AAATTC 26

2) INFORMATION FOR SEQ ID NO: 1438

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X06046
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438

```
ATGGCAATCC GAATCTTCGC GATACTTTTC TCCATTTTTT CTCTTGCCAC      50
TTTCGCGCAT GCGCAAGAAG GCACGCTAGA ACGTTCTGAC TGGAGGAAGT     100
TTTTCAGCGA ATTTCAAGCC AAAGGCACGA TAGTTGTGGC AGACGAACGC     150
20 CAAGCGGATC GTGCCATGTT GGTTTTTGAT CCTGTGCGAT CGAAGAAACG     200
CTACTCGCCT GCATCGACAT TCAAGATACC TCATACACTT TTTGCACTTG     250
ATGCAGGCGC TGTTTCGTGAT GAGTTCCAGA TTTTTCGATG GGACGGCGTT     300
AACAGGGGCT TTGCAGGCCA CAATCAAGAC CAAGATTTCG GATCAGCAAT     350
GCGGAATTCT ACTGTTTGGG TGTATGAGCT ATTTGCAAAG GAAATTGGTG     400
25 ATGACAAAGC TCGGCGCTAT TTGAAGAAAA TCGACTATGG CAACGCCGAT     450
CCTTCGACAA GTAATGGCGA TTA CTGGATA GAAGGCAGCC TTGCAATCTC     500
GGCGCAGGAG CAAATTGCAT TTCTCAGGAA GCTCTATCGT AACGAGCTGC     550
CCTTTCGGGT AGAACATCAG CGCTTGGTCA AGGATCTCAT GATTGTGGAA     600
GCCGGTCGCA ACTGGATACT GCGTGCAAAG ACGGGCTGGG AAGGCCGTAT     650
30 GGGTTGGTGG GTAGGATGGG TTGAGTGGCC GACTGGCTCC GTATTCTTCG     700
CACTGAATAT TGATACGCCA AACAGAATGG ATGATCTTTT CAAGAGGGAG     750
GCAATCGTGC GGGCAATCCT TCGCTCTATT GAAGCGTTAC CGCCCAACCC     800
GGCAGTCAAC TCGGACGCTG CGCGATAA      828
```

35

2) INFORMATION FOR SEQ ID NO: 1439

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 801 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*
(C) ACCESSION NUMBER: J03427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439

50

```
ATGAAAACAT TTGCCGCATA TGTAATTATC GCGTGTCTTT CGAGTACGGC      50
```

```

ATTAGCTGGT TCAATTACAG AAAATACGTC TTGGAACAAA GAGTTCTCTG      100
CCGAAGCCGT CAATGGTGTC TTCGTGCTTT GTAAAAGTAG CAGTAAATCC      150
TGCCTACCA ATGACTTAGC TCGTGCATCA AAGGAATATC TTCCAGCATC      200
AACATTTAAG ATCCCCAACG CAATTATCGG CCTAGAAACT GGTGTCATAA      250
5  AGAATGAGCA TCAGGTTTTT AAATGGGACG GAAAGCCAAG AGCCATGAAG      300
CAATGGGAAA GAGACTTGAC CTTAAGAGGG GCAATACAAG TTTCAGCTGT      350
TCCCGTATTT CAACAAATCG CCAGAGAAGT TGGCGAAGTA AGAATGCAGA      400
AATACCTTAA AAAATTTTCC TATGGCAACC AGAATATCAG TGGTGGCATT      450
GACAAATTCT GGTGGAAGG CCAGCTTAGA ATTTCCGCAG TTAATCAAGT      500
10 GGAGTTTCTA GAGTCTCTAT ATTTAAATAA ATTGTCAGCA TCTAAAGAAA      550
ACCAGCTAAT AGTAAAGAG GCTTTGGTAA CGGAGGCGGC ACCTGAATAT      600
CTAGTGCATT CAAAACTGG TTTTCTGGT GTGGGAACTG AGTCAAATCC      650
TGGTGTGCA TGGTGGGTTG GGTGGGTTGA GAAGGAGACA GAGGTTTACT      700
TTTTCGCCTT TAACATGGAT ATAGACAACG AAAGTAAGTT GCCGCTAAGA      750
15 AAATCCATTC CCACCAAAAT CATGGAAAGT GAGGGCATCA TTGGTGGCTA      800
A                                                                801

```

20 2) INFORMATION FOR SEQ ID NO: 1440

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440

AGACCGTTAT CGTAAACAGG GCTAAG

26

35

2) INFORMATION FOR SEQ ID NO: 1441

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441

TTTTTTGCTC AAACTTTTTC AGGATC

26

50

2) INFORMATION FOR SEQ ID NO: 1442

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: RNL-1
 (C) ACCESSION NUMBER: Z21957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442

15 ATGAATGTCA TTATAAAAGC TGTAGTTACT GCCTCGACGC TACTGATGGT 50
 ATCTTTTAGT TCATTCGAAA CCTCAGCGCA ATCCCCACTG TTAAAAGAGC 100
 AAATTGAATC CATAGTCATT GGAAAAAAG CCACTGTAGG CGTTGCAGTG 150
 TGGGGGCCTG ACGATCTGGA ACCTTTACTG ATTAATCCTT TTGAAAAATT 200
 20 CCCAATGCAA AGTGTATTTA AATTGCATTT AGCTATGTTG GTACTGCATC 250
 AGGTTGATCA GGGAAAGTTG GATTTAAATC AGACCGTTAT CGTAAACAGG 300
 GCTAAGGTTT TACAGAATAC CTGGGCTCCG ATAATGAAAG CGTATCAGGG 350
 AGACGAGTTT AGTGTTCCAG TGCAGCAACT GCTGCAATAC TCGGTCTCGC 400
 ACAGCGATAA CGTGGCCTGT GATTTGTTAT TTGAACTGGT TGGTGGACCA 450
 25 GCTGCTTTGC ATGACTATAT CCAGTCTATG GGTATAAAGG AGACCGCTGT 500
 GGTCGCAAAAT GAAGCGCAGA TGCACGCCGA TGATCAGGTG CAGTATCAAA 550
 ACTGGACCTC GATGAAAGGT GCTGCAGAGA TCCTGAAAAA GTTTGAGCAA 600
 AAAACACAGC TGTCTGAAAC CTCGCAGGCT TTGTTATGGA AGTGGATGGT 650
 CGAAACCACC ACAGGACCAG AGCGGTTAAA AGGTTTGTTA CCAGCTGGTA 700
 30 CTGTGGTCGC ACATAAAACT GGTACTTCGG GTATCAAAGC CGGAAAAACT 750
 GCGGCCACTA ATGATTTAGG TATCATCTCG TTGCCTGATG GACGGCCCTT 800
 GCTGGTTGCT GTTTTTGTGA AAGACTCAGC CGAGTCAAGC CGAACCAATG 850
 AAGCTATCAT TGCGCAGGTT GCTCAGACTG CGTATCAATT TGAATTGAAA 900
 AAGCTTTCTG CCCTAAGCCC AAATTAA 927
 35

2) INFORMATION FOR SEQ ID NO: 1443

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443

50 CTTCTGCTCT GCTGATGCTT GGC

23

2) INFORMATION FOR SEQ ID NO: 1444

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444

GGCGACCAGG TATTTTGTAA TACTGC

26

15

2) INFORMATION FOR SEQ ID NO: 1445

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 927 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
(B) STRAIN: JMC
30 (C) ACCESSION NUMBER: X93314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445

	ATGAATGTCA	TCACAAAATG	TGTTTTACCC	GCTTCTGCTC	TGCTGATGCT	50
35	TGGCTTAAAGT	TCATTTGTAG	TATCAGCCCA	ATCCCCTTTG	TTAAAAGAGC	100
	AGATTGAAAC	CATAGTGACG	GGTAAAAAGG	CCACTGTAGG	TGTAGCAGTG	150
	TGGGGGCCTG	ACGATCTGGA	ACCTTTGTTG	CTGAATCCAT	TTGAAAAGTT	200
	TCCGATGCAA	AGTGTGTTTA	AACTGCATTT	AGCTATGTTA	GTTCTGCATC	250
	AGGTCGATCA	GGGGAAACTG	GATTTAAATC	AGTCTGTTAC	TGTTAATCGT	300
40	GCTGCAGTAT	TACAAAATAC	CTGGTCGCCA	ATGATGAAAG	ATCATCAGGG	350
	CGATGAATTT	ACTGTTGCAG	TACAGCAGTT	ACTGCAGTAT	TCGGTGTCAC	400
	ACAGCGACAA	TGTGGCCTGC	GATTTGTTAT	TTGAACTGGT	GGGCGGGCCG	450
	CAAGCTTTGC	ATGCTTATAT	CCAGTCTTTA	GGCGTTAAAG	AAGCTGCCGT	500
	GGTAGCAAAT	GAAGCGCAAA	TGCATGCGGA	TGATCAGGTG	CAATATCAAA	550
45	ACTGGACGTC	GATGAAAGCC	GCAGCACAAG	TTCTGCAAAA	GTTTGAACAG	600
	AAAAAGCAGT	TGTCTGAAAC	CTCTCAGGCC	TTGTTATGGA	AATGGATGGT	650
	TGAAACCACC	ACAGGACCAC	AGCGGTAAA	AGGCTTGTTA	CCTGCTGGTA	700
	CTATAGTGGC	GCATAAAACC	GGTACTTCGG	GCGTCAGAGC	AGGAAAAACT	750
	GCGGCGACTA	ATGATGCGGG	CGTCATTATG	TTGCCTGATG	GACGGCCTTT	800
50	ATTGGTGGCG	GTATTTGTCA	AGGATTCGGC	TGAATCAGAA	CGAACCAATG	850
	AAGCTATTAT	TGCGCAGGTT	GCGCAAGCGG	CTTATCAGTT	TGAGCTGAAA	900
	AAACTCTCTG	CAGTGAGTCC	GGATTGA			927

2) INFORMATION FOR SEQ ID NO: 1446

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446

GGCCTGYGAT TTGTTATTTG AACTGGT

27

2) INFORMATION FOR SEQ ID NO: 1447

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447

CGCTSTGGTC CTGTGGTGGT TTC

23

2) INFORMATION FOR SEQ ID NO: 1448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448

GATCAGGTGC ARTATCAAAA CTGGAC

26

2) INFORMATION FOR SEQ ID NO: 1449

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449

AGCWGGTAAC AAYCCTTTTA ACCGCT

26

10

2) INFORMATION FOR SEQ ID NO: 1450

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450

ACCACTGGGA ATACACTTGT AATGGC

26

25

2) INFORMATION FOR SEQ ID NO: 1451

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451

40 ATCTACCTGG TCAATCATTG CTTCGT

26

2) INFORMATION FOR SEQ ID NO: 1452

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: BM10393
 (C) ACCESSION NUMBER: AF045472

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452

```

ATGACATTAT CAATAATTGT CGCTCACGAT AAACAAAGAG TCATTGGGTA      50
CCAAAATCAA TTACCTTGGC ACTTACCAA TGATTTAAAG CATATTAAAC      100
10 AACTGACCAC TGGGAATACA CTTGTAATGG CACGGAAAAC TTTTAATTCT      150
   ATAGGGAAGC CATTGCCAAA TAGACGTAAC GTCGTACTCA CTAACCAAGC      200
   TTCATTTTAC CATGAAGGGG TAGATGTTAT AAATCTCTCT GATGAAATTA      250
   AAGAGTTATC TGGTCATGTT TTTATATTTG GAGGACAAAC GTTATACGAA      300
   GCAATGATTG ACCAGGTAGA TGATATGTAT ATCACAGTAA TAGATGGAAA      350
15 GTTTCAAGGA GACACATTCT TTCCACCATA CACATTTCGAA AACTGGGAAG      400
   TCGAATCTTC AGTAGAAGGT CAACTAGATG AAAAAAATAC TATACCGCAT      450
   ACATTCTTAC ATTTAGTGCG TAGAAAAGGG AAATAG                    486

```

20

2) INFORMATION FOR SEQ ID NO: 1453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453

```

ATCGAAGAAT GGAGTTATCG GRAATG                                26

```

35

2) INFORMATION FOR SEQ ID NO: 1454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454

```

CCTAAAYTR CTGGGGATTT CWGGA                                25

```

50

2) INFORMATION FOR SEQ ID NO: 1455

764

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455

CAGGTGGTGG GGAGATATAC AAAA

24

15

2) INFORMATION FOR SEQ ID NO: 1456

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456

TATGTTAGAS RCGAAGTCTT GGKTAA

26

30

2) INFORMATION FOR SEQ ID NO: 1457

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457

CAAAGGTGAA CAGCTCCTGT TT

22

45

2) INFORMATION FOR SEQ ID NO: 1458

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458

TCCGTTATTT TCTTTAGGTT GGTTAAA

27

10

2) INFORMATION FOR SEQ ID NO: 1459

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1459

AAGGTGAACA GCTCCTGTTT

20

25

2) INFORMATION FOR SEQ ID NO: 1460

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460

GATCACTACG TTCTCATTGT CA

22

40

2) INFORMATION FOR SEQ ID NO: 1461

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: AJ238350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461

5 GTGAAACTAT CACTAATGGT AGCTATATCG AAGAATGGAG TTATCGGGAA 50
TGGCCCTGAT ATTCCATGGA GTGCCAAAGG TGAACAGCTC CTGTTTAAAG 100
CTATTACCTA TAACCAATGG CTGTTGGTTG GACGCAAGAC TTTTGAATCA 150
ATGGGAGCAT TACCCAACCG AAAGTATGCG GTCGTAACAC GTCCAAGTTT 200
10 TACATCTGAC AATGAGAACG TAGTGATCTT TCCATCAATT AAAGATGCTT 250
TAACCAACCT AAAGAAAATA ACGGATCATG TCATTGTTTC AGGTGGTGGG 300
GAGATATACA AAAGCCTGAT CGATCAAGTA GATACACTAC ATATATCTAC 350
AATAGACATC GAGCCGGAAG GTGATGTTTA CTTTCCTGAA ATCCCCAGCA 400
ATTTTAGGCC AGTTTTTACC CAAGACTTCG CCTCTAACAT AAATTATAGT 450
15 TACCAAATCT GGCAAAAGGG TTAA 474

2) INFORMATION FOR SEQ ID NO: 1462

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

25

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462

30

GCACTCCCYA ATAGGAAATA CGC

23

35 2) INFORMATION FOR SEQ ID NO: 1463

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463

AGTGTTGCTC AAAAACAAC TCG

23

50

2) INFORMATION FOR SEQ ID NO: 1464

(i) SEQUENCE CHARACTERISTICS:

767

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464

10 ACGTTYGAAT CTATGGGMGC ACT

23

2) INFORMATION FOR SEQ ID NO: 1465

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465

25

GTCGATAAGT GGAGCGTAGA GGC

23

2) INFORMATION FOR SEQ ID NO: 1466

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466

40

AAGCATTGAC CTACAATCAG TGT

23

2) INFORMATION FOR SEQ ID NO: 1467

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467

5 AATACAATA CATTGTCATC ATTTGAT

27

2) INFORMATION FOR SEQ ID NO: 1468

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468

20

CGTTACCCGC TCAGGTTGGA CATCAA

26

25 2) INFORMATION FOR SEQ ID NO: 1469

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1469

35

CATCCCCCTC TGGCTCGATG TCG

23

40 2) INFORMATION FOR SEQ ID NO: 1470

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: Z50804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470

```

5  TTGAAAGTAT CATTGATAGC TGCGAAACGA AAAAACGGCG TGATTGGTTG      50
   CGGTCCAGAC ATACCGTGGT CCGCGAAAGG GGAGCAGCTA CTTTTTAAAG      100
   CATTGACCTA CAATCAGTGT CTTCTGGTGG GTCGCAAGAC GTTTGAATCT      150
   ATGGGCGCAC TCCCAATAG GAAATACGCG GTCGTTACCC GCTCAGGTTG      200
   GACATCAAAT GATGACAATG TAGTTGTATT TCAGTCAATC GAAGAGGCCA      250
   TGGACAGGCT AGCTGAATTC ACCGGTCACG TTATAGTGTC TGGTGGCGGA      300
10  GAAATTTACC GAGAAACATT ACCCATGGCC TCTACGCTCC ACTTATCGAC      350
   GATCGACATC GAGCCAGAGG GGGATGTTTT CTTCCCGAGT ATTCCAAATA      400
   CCTTCGAAGT TGTTTTTGAG CAACACTTTA CTTCAAACAT TAACTATTGC      450
   TATCAAATTT GGAAAAGGG TTAA                                     474

```

15

2) INFORMATION FOR SEQ ID NO: 1471

```

20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471

```

30  GATAATGACA ACGTAATAGT ATTCCC                                     26

```

2) INFORMATION FOR SEQ ID NO: 1472

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 23 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472

```

45  GCTCAATATC AATCGTCGAT ATA                                     23

```

2) INFORMATION FOR SEQ ID NO: 1473

50

```

      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 bases
      (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473

TTAAAGCCTT GACGTACAAC CAGTGG

26

10

2) INFORMATION FOR SEQ ID NO: 1474

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474

TGGGCAATGT TTCTCTGTAA ATCTCC

26

25

2) INFORMATION FOR SEQ ID NO: 1475

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X12868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475

GTGAAAGTAT	CATTAATGGC	TGCAAAAGCG	AAAAACGGAG	TGATTGGTTG	50
45	CGGTCCACAC	ATACCCTGGT	CCGCGAAAGG	AGAGCAGCTA	100
	CCTTGACGTA	CAACCAGTGG	CTTTTGGTGG	GCCGCAAGAC	150
	ATGGGAGCAC	TCCCTAATAG	GAAATACGCG	GTCGTTACTC	200
	GACGGCCGAT	AATGACAACG	TAATAGTATT	CCCGTCGATC	250
	TGTACGGGCT	GGCTGAACTC	ACCGATCACG	TTATAGTGTC	300
50	GAGATTTACA	GAGAAACATT	GCCCATGGCC	TCTACGCTCC	350
	GATTGATATT	GAGCCGGAAG	GAGATGTTTT	CTTTCCGAAT	400
	CCTTCGAAGT	TGTTTTTGAG	CAACACTTTA	GCTCAAACAT	450
	TATCAAATTT	GGCAAAAGGG	TTAA		474

2) INFORMATION FOR SEQ ID NO: 1476

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476

GGCGAGCAGC TCCTATTCAA AG

22

2) INFORMATION FOR SEQ ID NO: 1477

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477

TAGGTAAGCT AATGCCGATT CAACA

25

2) INFORMATION FOR SEQ ID NO: 1478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478

GAGAATGGAG TAATTGGCTC TGGATT

26

2) INFORMATION FOR SEQ ID NO: 1479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479

GCGAAATACA CAACATCAGG GTCAT

25

10

2) INFORMATION FOR SEQ ID NO: 1480

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 474 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Proteus mirabilis*
- (B) STRAIN: J120
- (C) ACCESSION NUMBER: Z86002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480

ATGAAAATAT	CTCTTATGGC	AGCTGTTTCC	GAGAATGGAG	TAATTGGCTC	50
TGGATTGGAT	ATACCTTGGC	ATGTACAAGG	CGAGCAGCTC	CTATTCAAAG	100
CCATGACTTA	CAATCAATGG	CTTCTAGTTG	GTCGTAAAAC	CTTCGACTCA	150
ATGGGTAAAC	TTCCGAATAG	AAAATATGCA	GTGGTTACTC	GTTCTAAAAT	200
TATCTCGAAT	GACCCTGATG	TTGTGTATTT	CGCAAGTGTT	GAATCGGCAT	250
TAGCTTACCT	AAACAATGCG	ACAGCACATA	TCTTTGTTTC	TGGTGGTGGT	300
GAAATATATA	AAGCTTTAAT	CGATCAAGCA	GATGTTATCC	ATCTTTCAGT	350
GATTACAAG	CATATCTCTG	GCGATGTGTT	TTTTCCTCCA	GTTCCACAGG	400
GCTTCAAGCA	AACATTTGAG	CAAAGTTTCA	GTTCAAATAT	TGATTACACG	450
TACCAAATTT	GGGCAAAGGG	CTAA			474

40

2) INFORMATION FOR SEQ ID NO: 1481

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481

RTTACAGATC ATKTATATGT CTCT

24

5 2) INFORMATION FOR SEQ ID NO: 1482

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482

TAATTTATAT TAGACAWAAA AAAC TG

26

20

2) INFORMATION FOR SEQ ID NO: 1483

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483

CARYGTCAGA AAATGGCGTA ATC

23

35

2) INFORMATION FOR SEQ ID NO: 1484

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1484

TKCAAAGCRW TTTCTATTGA AGGAAA

26

50

2) INFORMATION FOR SEQ ID NO: 1485

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485

AAAATGGCGT AATCGGTAAT GGC

23

15

2) INFORMATION FOR SEQ ID NO: 1486

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486

CATTTGAGCT TGAAATTCCT TTCCTC

26

30

2) INFORMATION FOR SEQ ID NO: 1487

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487

AATCGAAAAT ATGCAGTAGT GTCGAG

26

45

2) INFORMATION FOR SEQ ID NO: 1488

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488

AGACTATTGT AGATTGACC GCCA

24

10

2) INFORMATION FOR SEQ ID NO: 1489

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 474 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*
(B) STRAIN: VA292
(C) ACCESSION NUMBER: U31119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489

30 TTGAAAATTT CATTGATTTC TGCAACGTCA GAAAATGGCG TAATCGGTAA 50
TGGCCCTGAT ATCCCATGGT CAGCAAAAGG TGAGCAGTTA CTCTTTAAAG 100
CGCTCACATA TAATCAGTGG CTCCTTGTTG GAAGGAAAAC ATTTGACTCT 150
ATGGGTGTTT TTCCAAATCG AAAATATGCA GTAGTGTCGA GGAAAGGAAT 200
TTCAAGCTCA AATGAAAATG TATTAGTCTT TCCTTCAATA GAAATCGCTT 250
TGCAAGAACT ATCGAAAATT ACAGATCATT TATATGTCTC TGGTGGCGGT 300
CAAATCTACA ATAGTCTTAT TGAAAAAGCA GATATAATTC ATTTGTCTAC 350
35 TGTTACGTT GAGGTTGAAG GTGATATCAA TTTTCCTAAA ATTCCAGAGA 400
ATTTCAATTT GGTTTTTGAG CAGTTTTTTT TGTCTAATAT AAATTACACA 450
TATCAGATTT GGAAAAAAGG CTA 474

40

2) INFORMATION FOR SEQ ID NO: 1490

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490

GACCTATGAG AGCTTGCCCG TCAA

25

2) INFORMATION FOR SEQ ID NO: 1491

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491

TCGCCTTCGT ACAGTCGCTT AACAAA

26

15

2) INFORMATION FOR SEQ ID NO: 1492

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492

CATTTTAGCT GCCACCGCCA ATGGTT

26

30

2) INFORMATION FOR SEQ ID NO: 1493

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493

45 GCGTCGCTGA CGTTGTTTAC GAAGA

25

2) INFORMATION FOR SEQ ID NO: 1494

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(B) STRAIN: BL26A
(C) ACCESSION NUMBER: U10186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494

ATGATCGAGC	TTCATGCCAT	TTTAGCTGCC	ACCGCCAATG	GTTGCATTGG	50
GAAGGACAAC	GCACTTCCCT	GGCCACCACT	AAAAGGCGAT	CTGGCCAGAT	100
15 TCAAAAAATT	GACCATGGGG	AAGGTGGTCA	TTATGGGGCG	CAAGACCTAT	150
GAGAGCTTGC	CCGTCAAATT	AGAAGGTCGC	ACCTGCATCG	TTATGACGCG	200
CCAAGCGCTG	GAGCTTCCGG	GTGTTCGTGA	CGCTAACGGC	GCTATCTTCG	250
TGAACAACGT	CAGCGACGCC	ATGCGGTTTCG	CTCAAGAAGA	GAGCGTGGGC	300
GATGTGGCCT	ACGTCATTGG	TGGCGCTGAG	ATATTCAAGC	GACTTGCCTT	350
20 GATGATCACG	CAGATTGAAT	TGACCTTTGT	TAAGCGACTG	TACGAAGGCG	400
ACACCTACGT	TGATCTGGCC	GAAATGGTCA	AAGACTACGA	GCAGAATGGC	450
ATGGAAGAAC	ATGACCTTCA	CACTTACTTC	ACTTACCGTA	AAAAGGAGCT	500
TACAGAATGA					510

2) INFORMATION FOR SEQ ID NO: 1495

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495

TCTCTAAACA TGATTGTCGC TGTC

24

2) INFORMATION FOR SEQ ID NO: 1496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496

CAGTGAGGCA AAAGTTTTTC TACC

24

5

2) INFORMATION FOR SEQ ID NO: 1497

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1497

CGGACGACTT CATGTGGTAG TCAGT

25

20

2) INFORMATION FOR SEQ ID NO: 1498

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498

TTTGTTTTCA GTAATGGTCG GGACCT

26

35

2) INFORMATION FOR SEQ ID NO: 1499

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 534 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: X57730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499

	ATGGCTTCTC	TAAACATGAT	TGTCGCTGTC	AATAAGACAG	GAGGTATCGG	50
	ATTTGAAAAT	CAGATTCCGT	GGCATGAACC	AGAAGATTTA	AAACACTTCA	100
	AAGCTGTTAC	AATGAACTCA	GTTTTGATTA	TGGGTAGAAA	AACTTTTGCC	150
	TCACTGCCTA	AAGTGCTGCC	CGGACGACTT	CATGTGGTAG	TCAGTAAAAC	200
5	AGTACCACCC	ACCCAGAACA	CTGATCAAGT	TGTGTATGTA	AGTACATACC	250
	AGATCGCAGT	AAGAACTGCA	AGCTTGTTGG	TTGACAAACC	AGAGTATTCT	300
	CAAATTTTGT	TAATTGGTGG	GAAGAGTGCG	TACGAGAACT	TAGCTGCCTA	350
	CGTGGACAAA	CTCTACTTAA	CTAGAGTACA	GCTCAACACA	CAACAAGACA	400
	CTGAACTGGA	TTTATCCCTA	TTCAAGTCAT	GGAAACTCGT	ATCTGAGGTC	450
10	CCGACCATTA	CTGAAAACAA	AACAAACTT	ATTTTCCAAA	TTTGGATTAA	500
	CCCTAACCCT	ATTAGTGAGG	AACCCACATG	TTAG		534

15 2) INFORMATION FOR SEQ ID NO: 1500

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

20 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500

ATCGGGTTAT TGGCAATGGT CCTA

24

30

2) INFORMATION FOR SEQ ID NO: 1501

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

35 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501

GCGGTAGTTA GCTTGGCGTG AGATT

25

45

2) INFORMATION FOR SEQ ID NO: 1502

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

50 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502

5

GCGGGCGGAG CTGAGATATA CA

22

10 2) INFORMATION FOR SEQ ID NO: 1503

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503

AACGGAGTGG GTGTACGGAA TTACAG

26

25

2) INFORMATION FOR SEQ ID NO: 1504

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(B) STRAIN: TKS84

(C) ACCESSION NUMBER: Z21672

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504

	ATGAACTCGG AATCAGTACG CATTATCTC GTTGCTGCGA TGGGAGCCAA	50
	TCGGGTTATT GGCAATGGTC CTAATATCCC CTGGAAAATT CCGGGTGAGC	100
45	AGAAGATTTT TCGCAGACTC ACTGAGGGAA AAGTCGTTGT CATGGGGCGA	150
	AAGACCTTTG AGTCTATCGG CAAGCCTCTA CCGAACCGTC ACACATTGGT	200
	AATCTCACGC CAAGCTAACT ACCGCGCCAC TGGCTGCGTA GTTGTTTCAA	250
	CGCTGTCGCA CGCTATCGCT TTGGCATCCG AACTCGGCAA TGAAGTCTAC	300
	GTCGCGGGCG GAGCTGAGAT ATACACTCTG GCACTACCTC ACGCCACGG	350
50	CGTGTTTCTA TCTGAGGTAC ATCAAACCTT CGAGGGTGAC GCCTTCTTCC	400
	CAATGCTCAA CGAAACAGAA TTCGAGCTTG TCTCAACCGA AACCATTCAA	450
	GCTGTAATTC CGTACACCCA CTCCGTTTAT GCGCGTCGAA ACGGCTAA	498

2) INFORMATION FOR SEQ ID NO: 1505

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505

ATTTTTCGCA GGCTCACCGA GAGC

24

15

2) INFORMATION FOR SEQ ID NO: 1506

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506

CGGATGAGAC AACCTCGAAT TCTGCTG

27

30

2) INFORMATION FOR SEQ ID NO: 1507

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 498 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: RA33.2
 (C) ACCESSION NUMBER: Z50802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507

50 ATGAACCCGG AATCGGTCCG CATTTATCTG GTCGCTGCCA TGGGTGCCAA 50
 TCGGGTTATT GGCAATGGTC CCGATATCCC CTGGAAAATC CCAGGTGAGC 100
 AGAAGATTTT TCGCAGGCTC ACCGAGAGCA AAGTGCTCGT TATGGGCCGC 150
 AAGACATTTG AGTCCATAGG CAAGCCCTTA CCAAACCGCC ACACAGTGGT 200

GCTCTCGCGC CAAGCTGGTT ATAGCGCTCC TGGTTGTGCA GTTGTTTCAA 250
CGCTGTCACA CGTATCGCCA TCGACAGCCG AACACGGCAA AGAACTCTAC 300
GTAGCGCGCG GAGCCGAGGT ATATGCGCTG GCGCTACCGC ATGCCAACGG 350
CGTCTTTCTA TCTGAGGTAC ATCAAACCTT TGAGGGTGAC GCCTTCTTCC 400
5 CAGTGCTTAA CGCAGCAGAA TTCGAGGTTG TCTCATCCGA AACCATTCAA 450
GGCACAATCA CGTACACGCA CTCCGTCTAT GCGCGTCGTA ACGGCTAA 498

10 2) INFORMATION FOR SEQ ID NO: 1508

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508

AGAATGTATT GGTATTTCCA TCTATCG

27

25

2) INFORMATION FOR SEQ ID NO: 1509

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
30 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509

CAATGTCGAT TGTTGAAATA TGTA AA

26

40

2) INFORMATION FOR SEQ ID NO: 1510

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases
45 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510

TGGAGTGCCA AAGGGGAACA AT

5 2) INFORMATION FOR SEQ ID NO: 1511

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511

CAGACACAAT CACATGATCC GTTATCG

27

20

2) INFORMATION FOR SEQ ID NO: 1512

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: UI14
 (C) ACCESSION NUMBER: Z83331

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512

	GTGAAACTAT CACTAATGGC AGCAATTTTCG AAGAATGGAG TTATCGGAAA	50
	TGGCCCAGAT ATTCCATGGA GTGCCAAAGG GGAACAATTA CTCTTCAAAG	100
40	CGATTACCTA TAATCAGTGG CTTTTGGTAG GCCGAAAGAC TTTCGAGTCA	150
	ATGGGGGCTT TACCCAACCG AAAATATGCC GTTGTAAGTTC GTTCAAGCTT	200
	CACTTCCAGT GATGAGAATG TATTGGTATT TCCATCTATC GATGAAGCGC	250
	TAAATCATCT GAAGACGATA ACGGATCATG TGATTGTGTC TGGTGGTGGT	300
	GAAATATACA AAAGCCTGAT CGATAAAGTT GATACTTTAC ATATTTCAAC	350
45	AATCGACATT GAGCCAGAAG GTGATGTCTA TTTTCCAGAA ATCCCCAGTA	400
	GTTTTAGGCC AGTTTTTAGC CAAGACTTCG TGTCTAACAT AAATTATAGT	450
	TACCAAATCT GGCAAAGGG TTAA	474

50

2) INFORMATION FOR SEQ ID NO: 1513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513

10 TTCAAGCTCA AATGAAAACG TCC

23

2) INFORMATION FOR SEQ ID NO: 1514

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514

25

GAAATTCTCA GGCATTATAG GGAAT

25

30 2) INFORMATION FOR SEQ ID NO: 1515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515

GTGGTCAGTA AAAGGTGAGC AAC

23

45

2) INFORMATION FOR SEQ ID NO: 1516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

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CTATGTCTCA	AGGCCGTGCA	ACATACTCTA	TGGAATTTGC	TAAATATGCT	50
GAAACTCCAC	GTAACGTGGC	TGAAGGCATC	ATTTCTAAAT	TTCAGTCTGG	100
CGGTAAAAAA	GGTGACGACG	AGTAA			125

5

2) INFORMATION FOR SEQ ID NO: 1519

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
- (B) STRAIN: CDCF 3697

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519

TCTTTTCGATT	ACTATAAGCC	CAAACAAATT	CATAGTTAAA	AACCAAGTGC	50
TCATGCAGTG	ATCCTGCATG	AGTAGTTTAA	AAAGGAAGAT	CTC	93

25

2) INFORMATION FOR SEQ ID NO: 1520

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
- (B) STRAIN: CDCF 3697

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520

45	ATGGCTAAGG	CTAAGTTTGA	ACGTAATAAG	CCACACGTTA	ACGTGGGCAC	50
	AATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACAGCT	GCAATTGCAA	100
	CTGTATGTGC	GAAGAAATTC	GGTGGCGAAG	CGAAAGACTA	CGCTGCAATT	150
	GACTCTGCAC	CAGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACTTCACA	200
	CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTA	GACTGCCCGG	250
50	GCCACGCCGA	TTATGTTAAA	AACATGATTA	CTGGTGCTGC	TCAGATGGAC	300
	GGCGCGATCC	TTGTATGTGC	TGCGACTGAT	GGTCCAATGC	CACAGACTCG	350
	TGAACACATC	CTTCTTTCTC	GTCAGGTTGG	TGTACCTTAC	ATTCTTGTAT	400
	TCCTTAACAA	GTGTGACCTT	GTTGATGATG	AAGAACTTCT	TGAGCTAGTG	450

GAAATGGAAG TTCGTGAACT TCTTTCTACT TATGACTTCC CAGGTGATGA 500
 CACTCCAGTT ATCCGTGGTT CAGCTCTTCT TGCACCTAAC GGTGACGCTG 550
 GTCAGTATGG CGAAGAAGCA GTTGTTCGCG TTGTTGACGC ACTTGACACT 600
 TACATTCCAG AGCCAGTACG TGCAATCGAC CAAGCATTCT TAATGCCAAT 650
 5 CGAAGACGTA TTCTCTATTT CTGGTCGTGG TACAGTAGTA ACTGGCCGTG 700
 TAGAAACTGG TATTGTGAAA GTAGGCGAAT CAGTTGAAAT CGTTGGTATC 750
 CGTGATACTC AAGTAACTAC AGTTACTGGC GTAGAAATGT TCCGTAAATT 800
 GCTTGACGAA GGTCGTGCGG GCGAGAACTG TGGTGTTCCT CTACGTGGTA 850
 CTAAGCGTGA AGACGTACAA CGTGGTCAAG TACTTGCTAA ACCAGGTGCA 900
 10 ATCAAGCCAC AACTAAATT CGATGCAGAA GTATACGTAC TTTCTAAAGA 950
 AGAAGGTGGT CGTCACACTC CATTCCCTTA CGGTTACCGT CCACAGTTCT 1000
 ACTTCCGTAC AACTGACGTA ACTGGCGCGA TCAAATTACA AGATGGCGTT 1050
 GAAATGGTTA TGCCTGGTGA CAACGTAGAA ATGTCAGTAG AATTAATCCA 1100
 CCCAAT 1106
 15

2) INFORMATION FOR SEQ ID NO: 1521

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Haemophilus influenzae*
 30 (B) STRAIN: ATCC 9006
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521

ACAAACCTCAA GGTCGTGCAT CTTACTCAAT GGAACCGTTA AAATATGCTG 50
 35 AAGCTCCAAC AAGTGTTCGCG GCTGCAGTAA TTGAAGCGCG TAAAAAATAA 100

2) INFORMATION FOR SEQ ID NO: 1522

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522

TTTTTGTAAG CCAGCGGTGT AAAATATGAT TGTTTTATAC CGCACTTCTT 50
 AGGAAACATT AGAA 64

5

2) INFORMATION FOR SEQ ID NO: 1523

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: ATCC 9006

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523

ATGTCTAAAG AAAAATTTGA ACGTACAAAA CCGCACGTAA ACGTGGGTAC 50
 AATCGGCCAC GTTGACCACG GTAAAACAAC TTAAACAGCA GCAATTACAA 100
 25 CCGTATTAGC AAAACACTAC GGTGGTGCAG CGCGTGCATT TGACCAAATC 150
 GATAACGCGC CAGAAGAAAA AGCGCGTGGT ATTACCATCA ACACTTCACA 200
 TGTTGAATAC GATACACCAA CTCGCCACTA TGCACACGTA GACTGTCCAG 250
 GACACGCCGA CTATGTTAAA AACATGATTA CCGGTGCGGC GCAAATGGAT 300
 GGTGCTATTT TAGTAGTAGC AGCAACAGAT GGTCCATATGC CACAACTCG 350
 30 TGAACATATC TTATTAGGTC GCCAAGTAGG TGTTCATAC ATCATCGTAT 400
 TCTTAAACAA ATGCGACATG GTAGATGATG AAGAGTTATT AGAATTAGTA 450
 GAAATGGAAG TGCGTGAAC TCTATCTCAA TATGACTTCC CAGGTGACGA 500
 TACACCAATC GTACGTGGTT CAGCATTACA AGCATTGAAC GGCGTAGCAG 550
 AATGGGAAGA AAAAATCCTT GAATTAGCTG GTCACCTAGA TACTTACATC 600
 35 CCAGAACCAG AACGTGCGAT TGACCAACCG TTCCTTCTTC CAATTGAAGA 650
 CGTATTCTCA ATTTCAGGTC GTGGTACAGT AGTAACTGGT CGTGTAGAAC 700
 GTGGTATCAT CCGTACTGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT 750
 ACAGCGAAAA CTACTGTAAC AGGTGTTGAA ATGTTCCGTA AATTACTTGA 800
 CGAAGGTCGT GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC 850
 40 GTGAAGAAAT CGAACGTGGT CAAGTATTAG CGAAACCAGG TTCAATCACA 900
 CCACACACTG ATTTTGAATC AGAAGTATAC GTATTATCAA AAGATGAAGG 950
 TGGTCGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACAA TTCTATTTCC 1000
 GTACAACAGA CGTAACTGGT ACAATTGAAT TACCAGAAGG CGTGGAATG 1050
 GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCCA 1098

45

2) INFORMATION FOR SEQ ID NO: 1524

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524

10

CAATGGAGTT CTTGAAGTAC AACGAAGCGC CTAGCAACGT CGCTCAGGCT 50
ATTATCGAAG CTCGTAAAGC GAAATAA 77

15

2) INFORMATION FOR SEQ ID NO: 1525

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 bases

20

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525

GATCCTTTTCG AGTTCAATTT AGTTTACGCT CCCTCTGTGA GAGGGAGCGA 50
TATTAAGGAA TATAGTC 67

35

2) INFORMATION FOR SEQ ID NO: 1526

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 1112 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 25933

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526

GTGTCTAAAG AAAAATTTGA ACGTTCAAAA CCGCACGTTA ACGTTGGTAC 50

	TATCGGCCAC	GTTGACCACG	GTAAAACAAC	TCTGACTGCT	GCAATCACTA	100
	CAGTTTTAGC	TAAAACTTAC	GGTGGTGCTG	CTCGTGCATT	CGACCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCGCGTGGT	ATCACCATCT	CTACTTCACA	200
	CGTAGAATAC	GATACTCCAA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
5	GTCACGCCGA	CTATGTTAAA	AACATGATCA	CTGGTGCTGC	GCAAATGGAC	300
	GGCGCTATTC	TGGTAGTAGC	AGCAACTGAT	GGTCCAATGC	CACAAACTCG	350
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTCCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGTGACATG	GATAGATGATG	AAGAGCTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	CAGGTGATGA	500
10	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCTTATATC	600
	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATCGAAGA	650
	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	CGTGTAAGAC	700
	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	TATCAAAGAA	750
15	ACCACCAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	800
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACAAAAC	850
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CAAAACCAGG	CTCAATCAAC	900
	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAC	ACACCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
20	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	CGTAGAAATG	1050
	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGAACTGA	TCCACCCAAT	1100
	CGCAATGGAC	GA				1112

25

2) INFORMATION FOR SEQ ID NO: 1527

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527

	ATCAACGAAG	CTATCGAGGT	TTATTTTGAG	GTTGAGGGCA	AGAAAAATAG	50
	ATTGATCCTG	GAGGTCGCGG	CTCACTTGGG	TGATAACCGC	GTCAGAACGA	100
	TCGCTATGGA	TATGAGTGAG	GGGCTTACTC	GCGGGCTTGA	AGCTACCGCT	150
45	CTTGGTGCGC	CTATTAGTGT	GCCGGTTGGC	GAGAAGGTTT	TGGGAAGAAT	200
	TTTTAACGTC	GTCGGCGATC	TCATCGACGA	GGGCGAGGGC	GTAAATTTTG	250
	ATAAACATTG	GTCTATCCAC	CGCGATCCGC	CACCATTTGA	AGAACAAAGC	300
	ACGAAAAGTG	AAATTTTGA	AACCGGTATA	AAGGTTGTGG	ATCTTCTTGC	350
	GCCTTACGCA	AAGGGCGGTA	AGGTGCGACT	ATTTGGCGGT	GCAGGTGTGC	400
50	GTAAAACGGT	CATCATCATG	GAGCTCATCC	ACAATGTCGC	CTTCAAACAC	450
	AGCGGATACT	CTGTATTTCG	AGGTGTTGGC	GAGAGGACGC	GCGAAGGAAA	500
	CGACCTTTAT	CACGAGATGA	AAGAAAGTAA	CGTTTTGGAT	AAAGTCGCCT	550
	TGTGCTACGG	ACAGATGAAC	GAGCCGCCAG	GGGCGAGAAA	TCGTATCGCA	600

CTGACTGGTC	TAACGATGGC	TGAGTATTTTC	CGCGATGAGA	TGGGACTTGA	650
TGTGCTTATG	TTTATCGACA	ACATCTTCCG	CTTCTCTCAA	TCTGGTGCAG	700
AGATGTCGGC	ACTCCTCGGA	CGTATCCCAT	CAGCCGTTGG	TTACCAGCCG	750
ACGCTGGCAA	GCGAGATGGG	TAAATTTCAA	GAAAGGATCA	CATCGACTAA	800

5

2) INFORMATION FOR SEQ ID NO: 1528

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528

20 AACTTGAGCG ATTTTCGGAT ACCCTG

26

2) INFORMATION FOR SEQ ID NO: 1529

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529

35

TTGCCGATGA AATAACCGCC GACT

24

40 2) INFORMATION FOR SEQ ID NO: 1530

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1035 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: M11277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530

```

      ATGCGATTGG TTTGGAAATG TGGGGCGATT CAGGCATCCC GGTATCTGA      50
      ATGGCTCAAC TCAACAGCCG GTGCTCATGA ACTTGAGCGA TTTTCGGATA      100
5     CCCTGACCTT TTCTGTGTAT GGCTCAGTGC TGATCTGGCT GAAATCATAT      150
      CTCCGCGAAT CAGGAAGAAA ACTGCAGTTA GTCGGAATCG CCTTACCCAA      200
      CACCCTGAAC CCAAGGGACG ACCTAGCGCA ATTGGCCGAA ATTATCCAGC      250
      TCATCGATCA CCTCATGAAA CCGCACGTTG ATATGTTGAC TCACTTGTTG      300
      GCGTCCATTG ATGGCCAGTC GGCGGTTATT TCATCGGCAA AATGGGGGGA      350
10    GCTAGAAACG GCTCGGCAGG AGAAAGCTAT CTCAGGGGTA ACCAGATTGA      400
      AGCTCCGCTT GGCGTCGCTT GCGCCCGTCC TGAAAAAACA CGTCAACAGC      450
      GATTTGTTCC GAAAAGCCTC TGATCGAATA GAGTCGATAG AGTATACGTT      500
      GGAAACCTTG CGTATAATGA AAACCTTCTT CGATGGTACC TCTCTTGAGG      550
      GAGATACTTC CGTACGTGAC TCGTATATGG CGGGCGTAGT AGATGGAATG      600
15    GTTCGAGCGA ATCCGGATGT GAAGATAATT CTGCTGGCGC ACAACAATCA      650
      TCTACAAAAA ACTCCAGTCT CTTTTTCAGG CGAGCTTACG GCTGTTCCCA      700
      TGGGGCAGCA CCTCGCAGAG AGGGTGAATT ACCGTGCGAT TGCATTACC      750
      CATCTTGGAC CCACCGTGCC GGAAATGCAT TTCCCATCGC CAAAAAGTCC      800
      TCTTGGATTG TCTGTTGTGA CCACGCCTGC CGATGCAATC CGTGAGGATA      850
20    GTATGGAACA GTATGTCATC GACGCCTGTG GTACGGAGAA TTCATGTCTG      900
      ACATTGACAG ATGCCCCCAT GGAAGCAAAG CGAATGCGGT CTCAAAGCGC      950
      CTCTGTAGAA ACGAAATTGA GCGAGGCATT TGATGCCATC GTCTGTGTTA      1000
      CAAGCGCCGG CAAGGACAGC CTGGTTGCC TATAG      1035

```

25

2) INFORMATION FOR SEQ ID NO: 1531

```

      (i) SEQUENCE CHARACTERISTICS:
30      (A) LENGTH: 25 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531

```

      TCTTTTGTGTT ACGACATACG CTTTT
40

```

25

2) INFORMATION FOR SEQ ID NO: 1532

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45      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532

AGTGCTTCTT TATCCGCTGT TCTA

24

5

2) INFORMATION FOR SEQ ID NO: 1533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533

CAGCGGATAA AGAAGCACTA CACATT

26

20

2) INFORMATION FOR SEQ ID NO: 1534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534

CCTCCTGAAA TAAAGCCCGA CAT

23

35

2) INFORMATION FOR SEQ ID NO: 1535

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: A15097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535

	ATGAGGTTTCG	AAGAATGGGT	CAAAGATAAG	CATATTCCTT	NCAAACNGAA	50
	TCACCCTGAT	GATAATTACG	ATGATTTTAA	GCCATTAAGA	AANATAATTG	100
	GAGATACCCG	AGTTGTAGCA	TTAGGTGAAA	ATTCTCATTT	CATAAAAGAA	150
	TTCTTTTGT	TACGACATAC	GCTTTTGCCT	TTTTTTATCG	AAGATCTAGG	200
5	TTTTACTACG	TTTGCTTTTG	AATTTGGTTT	TGCTGAGGGT	CAAATCATCA	250
	ATAACTGGAT	ACATGGACAA	GGAAGTACG	ATGAAATAGG	CAGATTCTTA	300
	AAACACTTCT	ATTATCCAGA	AGAGCTCAA	ACCACATTTT	TATGGCTAAG	350
	GGAGTACAAT	AAAGCAGCAA	AAGAAAAAAT	CACATTTCTT	GGCATTGATA	400
	TACCCAGAAA	TGGAGGTTCA	TACTTACCAA	ATATGGAGAT	AGTGCATGAC	450
10	TTTTTTAGAA	CAGCGGATAA	AGAAGCACTA	CACATTATCG	ATGATGCATT	500
	TAATATTGCA	AAAAAGATTG	ATTACTTCTC	CACATCACAG	GCAGCCTTAA	550
	ATTTACATGA	GCTAACAGAT	TCTGAGAAAT	GCCGTTTAAC	TAGCCAATTA	600
	GCTCGAGTAA	AAGTTCGCCT	TGAAGCTATG	GCTCCAATTC	ACATTGAAAA	650
	ATATGGGATT	GATAAATATG	AGACAATTCT	GCATTATGCC	AACGGTATGA	700
15	TATACTTGGA	CTATAACATT	CAAGCTATGT	CGGGCTTTAT	TTCAGGAGGC	750
	GGAATGCAGG	GCGATATGGG	TGCAAAAGAC	AAATACATGG	CAGATTCTGT	800
	GCTGTGGCAT	TTAAAAAACC	CACAAAGTGA	GCAGAAAGTG	ATAGTAGTAG	850
	CACATAATGC	ACATATTCAA	AAAACACCCA	TTCTGTATGA	TGGATTTCTA	900
	AGTTGCCTAC	CAATGGGCCA	AAGACTTAAA	AATGCCATTG	GTGATGATTA	950
20	TATGTCCTTA	GGTATTACTT	CTTATAGTGG	GCATACTGCA	GCCCTCTATC	1000
	CGGAAGTTGA	TACAAAATAT	GGTTTTTCGAG	TTGATAACTT	CCAAGTGCAG	1050
	GAACCAAATG	AAGGTTCTGT	CGAGAAAGCT	ATTTCTGGTT	GTGGAGTTAC	1100
	TAATTCCTTT	GTCTTTTTTA	GAAATATTCC	TGAAGATTTA	CAATCCATCC	1150
	CGAACATGAT	TCGATTTGAN	TCTATTTACA	TGAAAGCAGA	ACTCGAGAAA	1200
25	GCTTTCGATG	GAATATTTCA	AATTGAAAAG	TCATCTGTAT	CTGAGGTCGT	1250
	TTATGAATAA					1260

30 2) INFORMATION FOR SEQ ID NO: 1536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536

AGATGTATTA ACTGGAAAAC AACAA

25

45

2) INFORMATION FOR SEQ ID NO: 1537

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537

5 CTTTGTAATT AGTTTCTGAA AACCA

25

2) INFORMATION FOR SEQ ID NO: 1538

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538

20

TTAGAAGATA TAGGATACAA AATAGAAG

28

25 2) INFORMATION FOR SEQ ID NO: 1539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539

GAATGAAAAA GAAGTTGAGC TT

22

40

2) INFORMATION FOR SEQ ID NO: 1540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus haemolyticus*

(C) ACCESSION NUMBER: M14039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540

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5  ATGAAAAATA ATAATGTAAC AGAAAAAGAA TTATTTTATA TTTTAGATTT      50
   ATTTGAACAC ATGAAAGTAA CTTATTGGTT AGATGGTGGC TGGGGGGTAG      100
   ATGTATTAAAC TGGAAAACAA CAAAGAGAAC ACAGAGATAT AGATATAGAT      150
   TTTGACGCTC AACACACTCA AAAAGTTATA CAAAAATTAG AAGATATAGG      200
   ATACAAAATA GAAGTTCATT GGATGCCTTC ACGTATGGAA CTTAAGCATG      250
   AAGAATATGG GTATTTAGAT ATTCATCCTA TAAATCTAAA TGATGATGGA      300
10 TCAATTACCC AAGCAAACCC AGAAGGTGGT AATTATGTTT TCCAAAATGA      350
   CTGGTTTTCA GAAACTAATT ACAAAGATCG AAAAATACCA TGTATTTCAA      400
   AAGAAGCTCA ACTTCTTTT CATTCTGGTT ATGATTTAAC AGAAACAGAC      450
   CATTTTGATA TAAAAAATT AAAATCAATA ACATAA      486

```

15

2) INFORMATION FOR SEQ ID NO: 1541

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20  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 25 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541

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30  TGATAATCTT ATACGTGGGG AATTT      25

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2) INFORMATION FOR SEQ ID NO: 1542

```

35  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 26 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Single
      (D) TOPOLOGY: Linear

```

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542

```

45  ATAATTTTCT AATTGCCCTG TTTCAT      26

```

2) INFORMATION FOR SEQ ID NO: 1543

50

```

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 26 bases
  (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543

GGGCAATTAG AAAATTATTT ATCAGA

26

10

2) INFORMATION FOR SEQ ID NO: 1544

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544

TTTTACTCAT GTTTAGCCAA TTATCA

26

25

2) INFORMATION FOR SEQ ID NO: 1545

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 804 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Enterococcus faecium*
(C) ACCESSION NUMBER: AF110130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545

	ATGTTAAAAC	AAAAAGAATT	AATTGCAAAC	GTTAAGAATC	TTACTGAGTC	50
45	AGATGAACGA	ATTACAGCTT	GTATGATGTA	TGGATCGTTT	ACCAAAGGAG	100
	AAGGTGACCA	ATACTCTGAT	ATAGAGTTCT	ATATATTTTT	GAAACATAGT	150
	ATAACCTCGA	ACTTTGATTC	ATCCAACCTGG	TTGTTTGACG	TAGCTCCGTA	200
	CTTGATGCTT	TATAAAAATG	AGTACGGAAC	AGAGGTAGTT	ATTTTTGATA	250
	ATCTTATACG	TGGGGAATTT	CATTTCCTTT	CTGAAAAAGA	TATGAACATA	300
50	ATCCCTCTCGT	TTAAAGATTC	AGGTTATATT	CCTGATACGA	AGGCTATGCT	350
	TATTTACGAT	GAAACAGGGC	AATTAGAAAA	TTATTTATCA	GAGATAAGTG	400
	GTGCAAGACC	AAATAGACTT	ACTGAAGAAA	ATGCTAATTT	TTGTTGTGT	450
	AATTTCTCTA	ATCTATGGTT	GATGGGAATC	AACGTTCTAA	AAAGAGGAGA	500

ATATGCTCGT TCATTAGAAC TCTTATCACA ACTTCAAAAA AATACACTAC 550
 AACTTATACG TATGGCAGAA AAAAATGCTG ATAATTGGCT AAACATGAGT 600
 AAAAACCTTG AAAAAGAAAT TAGCCTTGAA AATTATAAAA AATTGCAAA 650
 GACCACTGCT CGATTAGATA AGGTAGAATT ATTTGAAGCC TATAAAAATT 700
 5 CTTTGCTATT AGTTATGGAT TTGCAAAGTC ACCTTATTGA ACAATACAAC 750
 TTAAAAGTTA CACATGACAT TTTAGAAAGA TTGTTGAATT ACATTAGTGA 800
 ATAG 804

10

2) INFORMATION FOR SEQ ID NO: 1546

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546

CAAGAAGGAA TGGCTGTACT AC

22

25

2) INFORMATION FOR SEQ ID NO: 1547

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 27 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

- 35 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1547

TAATTCCCAA ATAACCCTAA TAATAGA

27

40

2) INFORMATION FOR SEQ ID NO: 1548

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1218 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

50

- (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(C) ACCESSION NUMBER: U70055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548

```

5  ATGGAAAAAT ACAACAATTG GAAACTTAAG TTTTATACAA TATGGGCAGG      50
   GCAAGCAGTA TCATTAATCA CTAGTGCCAT CTTGCAAATG GCGATTATTT      100
   TTTACCTTAC AGAAAAAACT GGATCCGCGA TGGTCTTGTC TATGGCTTCA      150
   CTATTAGGTT TTTTACCCTA TGCGGTCTTT GGACCTGCAA TTGGTGTGCT      200
10  AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCT GATTTAATTA      250
   TCGCAGCAGC TGGTTCGGTG CTTACTATTG TTGCATTCTA TATGGAGCTA      300
   CCTGTCTGGA TGGTTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC      350
   TTTTCACACC CCGGCTCTCA ATGCGGTTAC GCCACTTTTA GTACCAGAAG      400
   AACAGCTTAC GAAATGTGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC      450
15  TATATTGTTA GTCCGGCGGT TGCAGCACTC TTATACTCCG TTTGGGAAC      500
   AAATGCTATT ATTGCCATCG ATGTATTGGG TGCTGTGATT GCATCTATTA      550
   CGGTAGCAAT TGTACGTATT CCTAAGCTGG GTGATCGCGT GCAAAGTTTG      600
   GACCCAAATT TCATAAGAGA AATGCAAGAA GGAATGGCTG TACTACGGCA      650
   AAATAAAGGA TTATTTGCTT TATTACTCGT TGGAACATTA TATATGTTTG      700
20  TTTATATGCC AATTAATGCA CTATTCCTT TAATTAGCAT GGATTACTTT      750
   AATGGAACAC CTGTGCATAT TTCTATTACG GAAATTTCCCT TTGCATCTGG      800
   AATGTTGATA GGGGGTCTAT TATTAGGGTT ATTTGGGAAT TACCAAAAGC      850
   GAATCTTATT AATAACGGCA TCCATTTTTA TGATGGGGAT AAGCTTAACC      900
   ATTTCAGGAT TACTTCCCCA AAGTGGATTT TTCATTTTGT TAGTCTGCTG      950
25  TGCAATAATG GGGCTTTCTG TTCCGTTTTA CAGCGGTGTG CAAACAGCTC     1000
   TTTTTCAGGA GAAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTA     1050
   ACTGGAAGTA TCATGTCTCT TGCTATGCCA ATTGGAATTAA TTCTTCTGCTC     1100
   ACTCTTTGCT GATAGAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA     1150
   CTTTAATTAT TTGCATTGCA ATAGTTTGCC CAATGATAAA TGAGATTAGA     1200
30  AAATTAGATT TAAATAAA                                     1218

```

2) INFORMATION FOR SEQ ID NO: 1549

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549

45

GCTTATTATT AGGAAGATTA GGGGGC

26

50 2) INFORMATION FOR SEQ ID NO: 1550

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

800

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550

TAGCAAGTGA CATGATACTT CCGA

24

10

2) INFORMATION FOR SEQ ID NO: 1551

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (C) ACCESSION NUMBER: U83667

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551

	ATGGAAAAAT ACAACAATTG GAAACGAAAA TTTTATGCAA TATGGGCAGG	50
30	GCAAGCAGTA TCATTAATCA CTAGTGCCAT CCTGCAAATG GCGATTATTT	100
	TTTACCTTAC AGAAAAAACA GGATCTGCGA TGGTCTTGTC TATGGCTTCA	150
	TTAGTAGGTT TTTTACCCTA TGCGATTTTG GGACCTGCCA TTGGTGTGCT	200
	AGTGGATCGT CATGATAGGA AGAAGATAAT GATTGGTGCC GATTTAATTA	250
	TCGCAGCAGC TGGTGCAGTG CTTGCTATTG TTGCATTCTG TATGGAGCTA	300
35	CCTGTCTGGA TGATTATGAT AGTATTGTTT ATCCGTAGCA TTGGAACAGC	350
	TTTTTCATACC CCAGCACTCA ATGCGGTTAC ACCACTTTTA GTACCAGAAG	400
	AACAGCTAAC GAAATGCGCA GGCTATAGTC AGTCTTTGCA GTCTATAAGC	450
	TATATTGTTA GTCCGGCAGT TGCAGCACTC TTATACTCCG TTTGGGATTT	500
	AAATGCTATT ATTGCCATCG ACGTATTGGG TGCTGTGATT GCATCTATTA	550
40	CGGTAGCAAT TGTACGTATA CCTAAGCTGG GTAATCAAGT GCAAAGTTTA	600
	GAACCAAATT TCATAAGGGA GATGAAAGAA GGAGTTGTGG TTCTGAGACA	650
	AAACAAAGGA TTGTTTGCCT TATTACTCTT AGGAACACTA TATACTTTTG	700
	TTTATATGCC AATCAATGCA CTATTTTCCTT TAATAAGCAT GGAACACTTT	750
	AATGGAACGC CTGTGCATAT TTCTATTACG GAAATTTCTT TTGCATTTGG	800
45	GATGCTAGCA GGAGGCTTAT TATTAGGAAG ATTAGGGGGC TTCGAAAAGC	850
	ATGTATTACT AATAACAAGT TCATTTTTTA TAATGGGGAC CAGTTTAGCC	900
	GTTTCGGGAA TACTTCCTCC AAATGGATTT GTAATATTCG TAGTTTGCTG	950
	TGCAATAATG GGGCTTTCGG TGCCATTTTA TAGCGGTGTG CAAACAGCTC	1000
	TTTTTCAGGA GAAAATTAAG CCTGAATATT TAGGACGTGT ATTTTCTTTG	1050
50	ATCGGAAGTA TCATGTCACT TGCTATGCCA ATTGGGTTAA TTCTTTCTGG	1100
	ATTCTTTGCT GATAAAATCG GTGTAAATCA TTGGTTTTTA CTATCAGGTA	1150
	TTTTAATTAT TGGCATTGCT ATAGTTTGCC AAATGATAAC TGAGGTTAGA	1200
	AAATTAGATT TAAAATAA	1218

2) INFORMATION FOR SEQ ID NO: 1552

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552

GGCAAGCAGT ATCATTAATC ACTA 24

15

2) INFORMATION FOR SEQ ID NO: 1553

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553

CAATGCTACG GATAACAAT ACTATC 26

30

2) INFORMATION FOR SEQ ID NO: 1554

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554

AGAAAATTAA GCCTGAATAT TTAGGAC 27

45

2) INFORMATION FOR SEQ ID NO: 1555

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid

50

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555

TAGTAAAAAC CAATGATTTA CACCG

25

10

2) INFORMATION FOR SEQ ID NO: 1556

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556

ACTGTACGCA CTTGCAGCCC GACAT

25

25

2) INFORMATION FOR SEQ ID NO: 1557

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557

GAACGGCAGG CGATTCTTGA GCAT

24

40

2) INFORMATION FOR SEQ ID NO: 1558

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558

GTGGTGGTGC ATGGCGATCT CT

22

5

2) INFORMATION FOR SEQ ID NO: 1559

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559

GCCGCAGCGA GGTACTCTTC GTTA

24

20

2) INFORMATION FOR SEQ ID NO: 1560

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 35 (C) ACCESSION NUMBER: D16251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560

	ATGACCGTAG	TCACGACCGC	CGATACCTCC	CAACTGTACG	CACTTGCAGC	50
40	CCGACATGGG	CTCAAGCTCC	ATGGCCCCGCT	GACTGTCAAT	GAGCTTGGGC	100
	TCGACTATAG	GATCGTGATC	GCCACCGTCG	ACGATGGACG	TCGGTGGGTG	150
	CTGCGCATCC	CGCGCCGAGC	CGAGGTAAGC	GCGAAGGTCG	AACCAGAGGC	200
	GCGGGTGCTG	GCAATGCTCA	AGAATCGCCT	GCCGTTTCGCG	GTGCCGGACT	250
	GGCGCGTGGC	CAACGCCGAG	CTCGTTGCCT	ATCCCATGCT	CGAAGACTCG	300
45	ACTGCGATGG	TCATCCAGCC	TGGTTCGTCC	ACGCCCCGACT	GGGTCGTGCC	350
	GCAGGACTCG	GAGGTCTTCG	CGGAGAGCTT	CGCGACCGCG	CTCGCCGCCC	400
	TGCATGCCGT	CCCCATTTCC	GCCGCCGTGG	ATGCGGGGAT	GCTCATCCGT	450
	ACACCGACGC	AGGCCCGTCA	GAAGGTGGCC	GACGACGTTG	ACCGCGTCCG	500
	ACGCGAGTTC	GTGGTGAACG	ACAAGCGCCT	CCACCGGTGG	CAGCGCTGGC	550
50	TCGACGACGA	TTCGTCTGTG	CCAGATTTCT	CCGTGGTGGT	GCATGGCGAT	600
	CTCTACGTGG	GCCATGTGCT	CATCGACAAC	ACGGAGCGCG	TCAGCGGGAT	650
	GATCGACTGG	AGCGAGGCCC	GCGTTGATGA	CCCTGCCATC	GACATGGCCG	700
	CGCACCTTAT	GGTCTTTGGT	GAAGAGGGGC	TCGCGAAGCT	CCTCCTCACG	750

TATGAAGCGG	CCGGTGGCCG	GGTGTGGCCG	CGGCTCGCCC	ACCACATCGC	800
GGAGCGCCTT	GCGTTCGGGG	CGGTACACCTA	CGCACTCTTC	GCCCTCGACT	850
CGGGTAACGA	AGAGTACCTC	GCTGCGGCGA	AGGCGCAGCT	CGCCGCAGCG	900
GAATGA					906

5

2) INFORMATION FOR SEQ ID NO: 1561

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: ATCC 18804

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1561

GATCATGGTA	AAACTACATT	GA CTGCTGCT	ATCACCAAAG	TTT TAGCCGA	50
25	ACAAGGTGGT	GCCAACTTCT	TGGATTAYGG	TTCTATTGAT	100
	AAGAAAGAGC	TAGAGGTATC	ACTATTTCCA	CTGCCCACGT	150
	ACCAAGAACA	GACACTATGC	CCACGTTGAT	TGTCCAGGAC	200
	TATCAAAAAT	ATGATTACTG	GTGCCGCTCA	AATGGATGGT	250
	TTGTTGCTGC	CACTGATGGT	CAAATGCCTC	AAACCAGAGA	300
30	TTGGCCAGAC	AAGTTGGTGT	TCAAGACTTG	GTTGTGTTTG	350
	CGATACTATT	GATGACCCTG	AAATGTTGGA	ATTAGTCGAA	400
	GAGAATTGTT	ATCCACCTAC	GGTTTTGATG	GTGACAACAC	450
	ATGGGATCTG	CTTTAATGGC	TTTGGAAGAC	AAGAAACCAG	500
	GGAAGCTATC	TTGAAATTGT	TAGATGCTGT	CGATGAACAC	550
35	CATCAAGAGA	CTTGGAACAA	CCATTTTTGT	TACCAGTTGA	600
	TCCATCTCCG	G TAGAGGAAC	TGTTGTCACT	GGTAGAGTTG	650
	TTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTT	700
	ACAAGACTAC	TGTTACCGGT	ATTGAAATGT	TCAAAAAGAG	750
	GCTATGGCTG	GTGACAACCTG	TGGTGTTTTG	TTAAGAGGTG	800
40	TGAAATCAAG	AGAGGTATGG	TTTTGGCCAA	ACCAGGTACT	850
	ACAAGAAGTT	CTTGGCTTCC	TTGTATATTT	TGACTTCCGA	900
	CGTTCCACTC	CATTTGGTGA	AGGTTACAAG	CCTCAATGCT	950
	TAACGATGTC	ACTACCACAT	TTTCATTCCC	AGAAGGAGAA	1000
45	ATTCTCAAAAT	GATCATGCCA	GGTGACAACA	TTGAAATGGT	1048

2) INFORMATION FOR SEQ ID NO: 1562

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida dubliniensis*

(B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562

```

10 TGATCACGGT AAAACCACAT TAACTGCTGC CATTACCAAA GTATTAGCTG      50
   AACAAAGGTGG TGCCAACTTT TTGGATTACG GTTCCATTGA TAGAGCTCCA      100
   GAAGAAAGAG CCAGAGGTAT CACTATTTCC ACTGCCCACG TTGAATACGA      150
   AACCAAGAAC AGACACTATG CCCACGTTGA TTGTCCAGGA CACGCTGATT      200
15 ATATCAAAAA CATGATTACT GGTGCTGCTC AAATGGATGG TGCTATCATT      250
   GTTGTGCTG CTACTGACGG TCAAATGCCA CAAACCAGAG AACATTTATT      300
   GTTGGCAAGA CAAGTTGGTG TTCAAGACTT GGTTGTCTTT GTCAACAAAG      350
   TTGATACTAT TGATGACCCT GAGATGTTGG AATTAGTCGA AATGGAAATG      400
   AGAGAATTGT TGTCCACCTA CGGTTTTGAT GGTGACAACA CTCCTGTTAT      450
20 TATGGGATCT GCTTTAATGG CTTTGAAGG CAAAAACCA GAAATTGGTA      500
   AGGAAGCTAT TTTGAGATTG TTAGATGCTG TCGATGAACA CATTCCAAC      550
   CCATCAAGAG ACTTGAACA ACCATTTTGT TTGCCAGTTG AAGACGTGTT      600
   CTCCATCTCT GGTAGAGGAA CTGTTGTCAC CGGTAGAGTT GAAAGAGGTG      650
   TCTTGAAGAA GGGTGAAGAA ATCGAAATTG TTGGTGGTTT TGACAAACCA      700
25 TACAAGACCA CTGTTACTGG TATTGAAATG TTCAAAAAGG AATTAGATTC      750
   TGCTATAGCT GGTGACAAC      GTGGTGT      GTTGAGAGGT GTTAAAAGAG      800
   ATGAAATCAA GAGAGGTATG GTTTTGGCCA AGCCAGGTAC TGCTACTTCT      850
   CACAAGAAAT TTTTAGCATC TTTGTATATT TTGACTTCAG AAGAAGGTGG      900
   TCGTTCCACT CCATTTGGAG AAGGTTACAA GCCTCAATGT TTCTTCAGAA      950
30 CTAATGACGT CACTACCACA TTTTCATTCC CAGAAGGAGA AGGTGTTGAC      1000
   CACTCCCAA      TGGTCATGCC AGGTGATAAC ATTGAAATGG TTGGTGAATT      1050
   GATCAAATCA TGTCCATTGG AAGT      1074

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35

2) INFORMATION FOR SEQ ID NO: 1563

(i) SEQUENCE CHARACTERISTICS:

```

40 (A) LENGTH: 1033 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida famata*

(B) STRAIN: ATCC 62894

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563

```

GATCACGGGA AGACTACTTT GACCGCTGCC ATCACCAAAG TTTTAGCCGA      50
AAAAGGTGGT GCTAACTTCT TGGACTACGG TTCTATCGAT AAAGCTCCAG      100

```

	AAGAAAGAGC	CAGAGGTATT	ACTATTTCTG	CTGCCCATGT	TGAATACGAA	150
	ACTGACAAGA	GACACTATGC	CCATGTTGAT	TGTCCAGGTC	ACGCAGATTA	200
	TATCAAGAAT	ATGATTACTG	GTGCTGCTCA	AATGGATGGT	GCCATTATTG	250
	TTGTTGCTGC	TTCCGATGGT	CAAATGCCTC	AAACCAGAGA	ACATTTGTTA	300
5	TTGGCCAGAC	AAGTTGGTGT	TCAACACTTG	GTTGTTTTTCG	TCAACAAGGT	350
	CGACACCATT	GACGATCCAG	AAATGTTGGA	ATTGGTTGAA	ATGGAAATGA	400
	GAGATTTGTT	AACTACTTAC	GGTTTTGATG	GTGATAACAC	CCCAGTTATC	450
	ATGGGATCTG	CTTTGTGTGC	TTTGGAAATCC	AGAGAACCAG	AAATTGGTCA	500
	AAAAGCCATT	GAAAAATTGT	TAGATGCCGT	CGATGAATAC	ATTCCAACCC	550
10	CAGTCAGAGA	CTTGGAACAA	CCATTCTTGA	TGCCAGTTGA	AGAAGTTTTTC	600
	TCCATTTCCG	GTAGAGGTAC	CGTTGTTGCT	GGTAGAGTCG	AAAGAGGTAC	650
	CTTGAAGAAG	GGTGAAGAAA	TCGAAATTGT	TGGTGGTTTC	GACAAGCCAT	700
	TCAAGGCCAC	TGTTACTGGT	ATTGAAATGT	TCAAGAAGGA	ATTGGACTCC	750
	GCTCTTGCTG	GTGACAACCTG	TGGTATCTTG	TTGAGAGGTG	TCAAGAGAGA	800
15	CGAAGTTAAG	AGAGGTATGG	TCTTGACCAA	GCCAAACACC	GTCATTCCC	850
	ACAAGAAGAT	CTTGGCCTCG	TTGTATATCT	TGACCAAGGA	AGAAGGTGGT	900
	AGACACTCTC	CATTTGGAGC	CAACTACAAG	CCCCAATTGT	TCATGAGAAC	950
	CACCGATGTT	ACCGGTACCA	TGACCTTCCC	AGAAGGTGCC	GACCAATCTG	1000
	CCATGGTCAT	GCCAGGTGAC	AACGTTGAAA	TGC		1033
20						

2) INFORMATION FOR SEQ ID NO: 1564

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564

	GATCACGGTA	AGACTACATT	GACAGCTGCT	ATCACCAAGA	CATTGGCCAA	50
40	GAACGGTGGT	GCTGATTTCT	TGGACTACTC	TTCCATTGAC	AAAGCTCCAG	100
	AGGAGAGAGC	CCGTGGTATC	ACTATCTCTA	CTGCCCATGT	CGAGTACGAG	150
	ACCGCCAAGA	GACATTACTC	CCACGTGAC	TGTCCAGGTC	ACGCCGACTA	200
	CATCAAGAAC	ATGATTACTG	GTGCTGCCCCA	AATGGACGGT	GCTATCATCG	250
	TTGTCGCCGC	CACCGATGGT	CAAATGCCAC	AACTAGAGA	GCATTTGCTG	300
45	TTGGCCAGAC	AAGTCGGTGT	TCAACGTATC	GTTGTCTTTG	TCAACAAGGT	350
	GGACACCATC	GATGACCCTG	AAATGTTGGA	ATTAGTGGAA	ATGGAAATGA	400
	GAGAATTGTT	GAACGAATAC	GGTTTTGACG	GTGACAATGC	CCCTATCATT	450
	ATGGGTTCCG	CTTTGTGTGC	CCTAGAAGGT	CGTCAACCTG	AAATTGGTGA	500
	GCAAGCTATC	ATGAAACTAT	TGGACGCTGT	TGATGAATAC	ATTCCAACCC	550
50	CAGAAAGAGA	CTTGAACAAG	CCATTCTTGA	TGCCTGTTGA	AGACATCTTC	600
	TCCATCTCTG	GTAGAGGTAC	CGTCGTCACT	GGACGTGTCG	AAAGAGGTAA	650
	CTTGAAGAAG	GGTGAAGAAG	TTGAAATTGT	TGGTCACAAC	ACTACCCCAT	700
	TGAAGACCAC	CGTTACTGGT	ATCGAAATGT	TCAGAAAGGA	ATTGGACCAA	750

GCTATGGCTG GTGACAACGC CGGTATCCTA TTGAGAGGTA TCAGAAGAGA 800
 CCAATTGAAG AGAGGTATGG TCATGGCCAA GCCAGGTACC GTCAAGGCTC 850
 ACACCAAGAT TTTGGCTTCT TTGTACATCT TGTCTAAGGA AGAAGGTGGT 900
 AGACATTCTG GTTTCGGTGA AAACCTACAGA CCTCAGATGT TTATCAGAAC 950
 5 CGCAGATGTC ACTGTTGTGA TGAAGTTCCC AGAATCTGTG GAAGACCACT 1000
 CTATGCAAGT TATGCCAGGT GACAACGTCG AAATGGTCTG TGAAGTAGTC 1050
 CACCCA 1056

10

2) INFORMATION FOR SEQ ID NO: 1565

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1061 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 20
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida guilliermondii*
 (B) STRAIN: ATCC 6260

 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565

GATCATGGTA AGACCACTTT GACCGCTGCT ATCACCAAGG TTTTGTCCGA 50
 AAAAGGAGGT GCTAATTTCT TGGATTACGG CTCCATCGAC AGAGCTCCAG 100
 AAGAGAGAGC CAGAGGTATC ACCATTTCCA CTGCCCATGT TGAGTACCAA 150
 30 ACTGATAAGA GACATTATGC CCACGTTGAC TGTCCAGGTC ACGCCGATTA 200
 CATTAGAAT ATGATTACTG GTGCCGCCCA GATGGACGGT GCCATTATTG 250
 TTGTTGCTGC CACTGACGGT CAAATGCCTC AGACCAGAGA GCACTTGTTG 300
 TTGGCCAGAC AAGTTGGTGT GCAACACTTG GTAGTTTTTG TGAACAAGGT 350
 GGACACCATT GACGATCCCG AGATGTTGGA ATTGGTCGAG ATGGAAATGA 400
 35 GAGAATTGTT GAGTCAGTAC GGTTCGATG GTGACAACAC CCCAGTTATC 450
 ATGGGATCTG CTTTGTGTGC TTTGGAAAGT AAGCAGCCAG AAATTGGTGT 500
 GCAAGCCATT GAAAAATTGT TGGACGCTGT CGATGAGCAC ATTCCTACTC 550
 CTACCCGTGA CTTGGAACAG CCATTCTTGT TGCCTGTTGA AGATGTGTTT 600
 TCCATTTCTG GTAGAGGAAC TGTGGTTACT GGTAGAGTCG AAAGAGGTTT 650
 40 GTTGAAGAAG GGTGAGGAAA TCGAGATTGT TGGTGACTTT GACAAGCCAT 700
 TCAAGACCAC TGTGACTGGA ATTGAAATGT TCAAGAAGGA ATTGGATGCT 750
 GCTATGGCTG GTGACAATGC TGGTATCTTG TTGAGAGGTG TCAAGAGAGA 800
 CGATGTCAAG AGAGGTATGG TTTTGGCCAA GCCTTCCACC GTCATTCTC 850
 ACAAGAAGGT GTTGGCTTCC TTGTACATCT TGAGTAAGGA AGAAGGTGGC 900
 45 CGTCACTCTC CTTTGGTGA GAACTACAAG CCTCAATTGT TCATCAGAAC 950
 TACTGACGTT ACCGGTACTT TAAGATTCCC AGCCGCGCAG GGTGTCGACC 1000
 ACTCGCAAT GGTATGCCA GGTGACAATG TTGAGATGGA AATTGAGCTT 1050
 GTGAGAAAGA C 1061

50

2) INFORMATION FOR SEQ ID NO: 1566

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida haemulonii*
 (B) STRAIN: ATCC 22991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566

```

15  GATCACGGTA AGACTACCTT GACTGCTGCT ATCACCAAGG TTTTGGCTTC      50
    TAAGGGTGGT GCTAGCTTCT TGGACTATGG TTCCATTGAC AGAGCCCCAG      100
    AGGAGAGAGC TAGAGGTATT ACTATTTCTA CTGCCCACGT TGAGTACCAA      150
    ACCGAAAAGA GACACTACGC CCACGTCGAC TGTCCAGGTC ACGCTGATTA      200
    CATTAAGAAAT ATGATTACTG GTGCCGCCCA GATGGACGGT GCTATCATTG      250
20  TTGTTGCTGC TTCTGATGGT CAGATGCCTC AGACCAGAGA GCACCTTTTG      300
    TTGGCCAGAC AGGTTGGTGT TCAGAACTTG GTTGTTTTCG TTAACAAGGT      350
    TGACACCATT GACGACCCTG AAATGTTGGA ATTGGTTGAG ATGGAAATGA      400
    GAGAATTGTT GACTACTTAC GGTTTTGACG GTGATGAGAC TCCTGTTATC      450
    ATGGGTTCTG CTTTGTGCGC TTTGGAAGAG AAGCAACCAG AGATTGGTGA      500
25  GCAGGCTATC ATGAAGTTGT TGGACGCTGT CGATGAGTAC ATTCCAACCC      550
    CACAGCGTGA CTTGGAGCAG CCATTCTTGA TGCCTGTTGA GGATGTTTTTC      600
    TCCATTTCTG GTAGAGGTAC TGTCGTTACT GGTAGAGTTG AGAGAGGTTT      650
    TTTGAAGAAG GGTGAGGAAA TCGAGATTGT CGGTGACTTC GCCAAGACTT      700
    TCAAGGCTAC CGTTACTGGT ATTGAGATGT TCAAGAAGGA ATTGGATGCT      750
30  GCTATGGCTG GTGACAACGC CGGTATCTTG TTGAGAGGTG TCAAGAGAGA      800
    TGAGATCTCC CGTGGTGATG TCTTGGCCAA GCCAGGTACT GTTACTCCAC      850
    ACAAGAAGAT CTTGGCTTCT TTGTACGTTT TGACCAAGGA AGAAGGTGGT      900
    CGTCACAACC CATTGCTGTA GAACTACAAG CCACAGTTGT TCCTCAGAAC      950
    CACCAACGTC ACTGGTACCA TGAGATTCCC AGAAGGTGAA GATGTTGACC     1000
35  ACTCTGCCAT GGTTAACCCA GGTGACAACG TTGAGATGGA AATCGAGTTG     1050
    GGTAGAAAGG CCCCACTTGA GTT                                     1073
  
```

40 2) INFORMATION FOR SEQ ID NO: 1567

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida kefyr*
 (B) STRAIN: ATCC 28838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567

	CATGGTAAGA	CCACTTTGAC	TGCTGCCATC	ACCAAGACTC	TAGCTGAACG	50
	TGGTGGTGCT	GACTTTTTTG	ACTACTCTTC	TATTGACAAG	GCTCCAGAAG	100
5	AAAGAGCYAG	AGGTATCACT	ATTTCTACTG	CTCATGTTGA	ATACGAGACT	150
	GAAAAGAGAC	ATTACTCCCA	CGTTGACTGT	CCAGGTCACG	CTGATTACAT	200
	CAAGAACATG	ATTACTGGTG	CTGCTCAAAT	GGACGGTGCT	ATTATTGTTG	250
	TTGCTGCTAC	TGATGGTCAA	ATGCCTCAAA	CCAGAGAGCA	TTTGTGTGTTG	300
	GCCAGACAAG	TTGGTGTCCA	ACACATTGTT	GTTTTCGTTA	ACAAGGTTGA	350
10	CACCATCGAT	GATCCAGAAA	TGTTGGAATT	GGTTGAAATG	GAAATGAGAG	400
	AATTRTTGAC	TCAATATGGC	TTTGACGGTG	ACAACACTCC	AGTGATCATG	450
	GGTTC TGCTT	TGTGTGCCTT	GGAAGGTAAG	CAACCAGAAA	TTGGTGAGCA	500
	AGCCATCATG	AAGTTGTTGG	ACGCTGTTGA	CGAATACATC	CCAACCCAG	550
	CCCGTGACTT	GGAAA VCCA	TTCTTGATGC	CTGTTGAAGA	TATCTTCTCC	600
15	ATTTCCGGTA	GAGGTACTGT	CGTCACTGGT	AGAGTTGAAC	GTGGTAACTT	650
	GAAGAAGGGT	GAAGAAATCG	AAATTGTTGG	TCACAACACC	ACTCCTTTCA	700
	AGACTACTGT	TACTGGTATT	GAAATGTTCA	GAAAGGAATT	GGACCAAGCC	750
	ATGGCTGGTG	ACAACGCTGG	TGTCCTTTTG	AGAGGTGTCA	GAAGAGACCA	800
	ATTGAAGAGA	GGTATGGTTT	TGGCTAAGCC	AGGTACTGTT	AAGGCCCACA	850
20	CCAAGTTCTT	GGCTTCCTTG	TACATTTTGA	CCAAGGAAGA	AGGTGGTAGA	900
	CACTCCGGTT	TCGGTGAAAA	CTACAGACCA	CAAATCTACG	TCAGAACTGC	950
	TGACGTTACC	GTDGTCTTGA	AGTTCCCAGA	ATCTGTTGAA	GACCATTTCCA	1000
	TGCAAGTCAT	GCCAGGTGAC	AATGTCGAAA	TGGAGTGTGA	ATTGGTTTAC	1050
	CCAACTCCAT	TG				1062

2) INFORMATION FOR SEQ ID NO: 1568

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
 (B) STRAIN: ATCC 66035

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568

	CGGAAAGACC	ACCTTGACCG	CCGCCATTAC	CAAGGTTTTG	GCTGACAAGG	50
45	GTGGCGCCAA	CTTCTTGAC	TACGGTGCCA	TTGACAAGGC	TCCTGAAGAA	100
	AGAGCACGTG	GTATCACCAT	TTCCACTGCC	CACGTTGAAT	ACGAGACCGA	150
	CAACAGACAC	TACGCCCACG	TTGACTGTCC	AGGTCACGCC	GATTACATCA	200
	AGAACATGAT	CACGGGTGCC	GCTCAAATGG	ACGGTGCCAT	TATTGTTGTT	250
	GCAGCCACCG	ACGGCCAAAT	GCCTCAAACC	AGAGAGCACT	TGTTGTTGGC	300
50	CAGACAAGTT	GGTGTGCAAC	ACTTGGTTGT	TTTCGTGAAC	AAGGTTGATA	350
	CCATCGACGA	CCCAGAAATG	TTGGAATTGG	TTGAAATGGA	AATGAGAGAA	400
	TTGTTGACTC	AATACGGATT	TGACGGCGAT	GAAACCCCTG	TTGTTATGGG	450
	CTCTGCTCTT	TGCGCTTTGG	AAGGTAGAGA	ACCAGAGATT	GGTGAGCAAG	500

	CCATCACCAA	GTTGTTGGAG	GCTGTTGACG	AGTACATCCC	AACCCACAAA	550
	CGTGACTTGG	AACAACCATT	CTTGATGCCT	GTTGAAGATG	TTTTCTCCAT	600
	TTCTGGTAGA	GGTACTGTTG	TCACTGGTAG	AGTGGAGAGA	GGTTCCTTGA	650
	AGAAGGGTGA	GGAGATCGAG	ATTGTTGGTG	ACTTTGACAA	GCCTTCAAG	700
5	ACTACTGTTA	CTGGTATTGA	GATGTTCAAG	AAGGAATTGG	ACGCTGCTAT	750
	GGCTGGTGAC	AATGCTGGTA	TCTTGTTGAG	AGGTGTCAAG	AGAGAACAAG	800
	TTTCCCGTGG	TATGGTTTTG	GCCAAGCCAG	GCACTGTGAC	CTCGCACAAG	850
	AAGGTTTTTG	CTTCTTTGTA	CATTTTGTCT	AAGGAAGAAG	GTGGTCGTCA	900
	CTCTCCATTT	GGCGAGAACT	ACAAGCCTCA	ATTGTTTCCTT	AGAACTACCG	950
10	ATGTCACTGG	TACTTTGAGA	TTCCCAGCAG	GTGAGGACGT	TGACCACTCC	1000
	GCTATGGTTT	CTCCAGGTGA	CAATGTCGAG	ATGGAAATCG	AGTTGGTCAG	1050
	AAAGACTCCT	CT				1062

15

2) INFORMATION FOR SEQ ID NO: 1569

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 990 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida sphaerica*
- (B) STRAIN: ATCC 2504
- (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569

	TCACCAAGAC	TTTGGCTGAA	CGTGGTGGTG	CTGATTTCTT	GGACTIONCT	50
35	TCCATTGACA	AGGCTCCAGA	AGAAAGAGCR	AGAGGTATCA	CTATTTCTAC	100
	TGCACATGTT	GAATATGAAA	CTGACAAGAG	ACATTACTCT	CACGTCGACT	150
	GTCCAGGTCA	TGCTGATTAC	ATCAAGAATA	TGATTACTGG	TGCTGCCCAA	200
	ATGGATGGTG	CTATCATTGT	TGTTGCTGCT	ACAGATGGTC	AAATGCCTCA	250
	AACCAGAGAA	CATTTGTTGT	TGGCTAGACA	AGTTGGTGTT	CAACAYATCG	300
40	TTGTTTTCGT	TAACAAGGTT	GACACTATCG	ATGACCCTGA	AATGTTAGAA	350
	TTGGTTGAAA	TGGAAATGAG	AGAATTATTG	ACCCAATACG	GTTTCGATGG	400
	TGACAACACT	CCAGTCATCA	TGGGTTCTGC	TTTGTGTGCT	TTAGAAGGTA	450
	AGCAACCAGA	AATTGGTGAA	CAAGCAATCA	TGAAGTTATT	GGACGCTGTT	500
	GACGAATACA	TCCCAACTCC	AGCTCGTGAT	TTGGAAAAGC	CTTTCTTGAT	550
45	GCCTGTTGAA	GATATCTTCT	CCATCTCCGG	TAGAGGTACC	GTCGTAACCTG	600
	GTAGAGTTGA	ACGTGGTAAC	TTGAACAAGG	GTRAAGAAAT	CGAAATCGTT	650
	GGTCACAACA	CCACTCCATT	CAAGACCACT	GTTACTGGTA	TTGAAATGTT	700
	CAGAAAGGAA	TTGGACCAAG	CTATGGCTGG	TGATAACGCT	GGTGTCTWTGT	750
	TGAGAGGTGT	CAGAAGAGAC	CAATTAAAGA	GAGGTATGGT	CTTGCCCAAG	800
50	CCAGGTACTG	TCAAGGCTCA	CACCRAATTC	TTGGCCTCTT	TGTATATCTT	850
	GACCAAGGAA	GAAGGTGGTA	GACATTCCGG	TTTCGGTGAA	AATTACAGAC	900
	CTCAAATCTA	CGTTAGAACT	GCTGATGTCA	CCGTTGTTTT	GAAGTTCCCA	950
	GAAGCTGTTG	AAGATCACTC	TATGCAAGTC	ATGCCAGGTG		990

2) INFORMATION FOR SEQ ID NO: 1570

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1184 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570

	GATCATGGTA	AAACCACTTT	GACTGCTGCC	ATTACTAAAG	TCTTGGCTGA	50
	TAAAGGTCAA	GCTAACTTCT	TAGATTACGG	TTCTATTGAT	AGAGCTCCAG	100
	AAGAAAGAGC	CAGAGGTATC	ACCATCTCTA	CTGCCCACGT	TGAATATGAA	150
20	ACCGAAAAAA	GACATTACGC	CCATGTTGAG	TATGTATACT	TTTTTTTGTT	200
	GTGTAATTGT	TTTAAAGATT	TTCTTTAAAG	CTGAAGAAGT	CAAATCAGTT	250
	CTTTGATAAC	TTCTATTAAA	AAAAGGGAAA	AATTAACAAG	ATATACTAAC	300
	ACTATAACAG	TTGTCCTGGA	CATCAAGATT	ATATCAAGAA	TATGATTACC	350
	GGTGCCGCTC	AAATGGATGG	TGCTATTATT	GTTGTTGCTG	CCACTGATGG	400
25	TCAAATGCCA	CAAACCAGAG	AACATTTGTT	GTTGGCTAGA	CAAGTCGGTG	450
	TTCAAGATTT	GGTTGTCTTT	GTTAACAAAG	TCGACACTAT	TGATGACCCA	500
	GAAATGTTGG	AATTGGTTGA	AATGGAAATG	AGAGAATTAT	TGACTACTTA	550
	CGGTTTTGAT	GGTGATAACA	CTCCTGTTAT	CATGGGTTCT	GCTTTGATGG	600
	CCTTGCAAGG	TAAACAACCA	GAAATTGGTG	AACAAGCTAT	CATGAAATTG	650
30	ATGGACGCTA	TTGATGAACA	CATTCCAACC	CCAACCAGAG	ACTTGGAACA	700
	ATCTTTCTTG	ATGCCAGTTG	AAGATGTTTT	CTCCATTCT	GGTAGAGGTA	750
	CTGTTGTTAC	TGGTAGAGTC	GAAAGAGGTG	TCTTAAAGAA	GGGTGAAGAA	800
	ATTGAAATTG	TTGGTGGTTT	CGAAAAACCA	TTCAAGACCA	CTGTTACTGG	850
	TATTGAAATG	TTCAAGAAAG	AATTAGATGC	TGCTATGGCT	GGTGACAAC	900
35	GTGGTGTCTT	GTTGAGAGGT	GTCAAGAGAG	ACGAAATCAA	GAGAGGTATG	950
	GTTTTGGCTA	AACCAGGTAC	TGCTACTTCC	CACAAGAAAT	TCTTGGCTTC	1000
	CATGTATATC	TTAACTGCTG	AAGAAGGTGG	TCGTTCCACT	CCATTCGGTG	1050
	AAGGTTACAA	GCCACAATGT	TTCTTCAGAA	CTAACGATGT	TACCACTTCC	1100
	TTCTCTTTCC	CAGAAGGTGA	AGGTGTTGAC	CACTCCCAAA	TGGTTATGCC	1150
40	AGGTGACAAC	ATTGAAATGG	TCGGTGAATT	GATT		1184

2) INFORMATION FOR SEQ ID NO: 1571

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida viswanathii*
 (B) STRAIN: ATCC 28269

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571

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CGATCACGGT AAGACCACCT TGACCGCCGC CATCACCAAG GTCTTGGCCG      50
ACAAGGGTCA GGCTAACTTC TTGGACTACG GATCCATTGA CAGAGCCCCT      100
GAAGAAAGAG CAAGAGGTAT CACTATCTCC ACTGCCCACG TTGAATACGA      150
10 GACTGATAAG AGACACTATG CCCACGTTGA TTGCCCCGGC CATCAAGATT      200
ATATCAAGAA TATGATCACT GGTGCTGCCA AAATGGACGG TGCTATCATT      250
GTTGTTGCTG CTA CTGACGG TCAGATGCCA CAAACCAGAG AACACTTGTT      300
GTTGGCTAGA CAAGTTGGTG TCCAAGACTT GGTTGTTTTC GTTAACAAGG      350
TTGACACTAT CGATGACCCA GAAATGTTGG AATTGGTTGA AATGGAAATG      400
15 AGAGAATTAT TATCTTCTTA YGGCTTTGAC GGTGACAACA CCCCAGTTGT      450
CATGGGTTCC GCTTTGATGG CTTTGCAAGG TAAGCAACCA GAAATTGGTG      500
AACAAGCTAT TATTAAGTTG ATGGACGCTA TTGATGAACA CATYCCAACC      550
CCAACCAGAG ACTTGAACA ACCATTCTTG TTGCCAGTTG AAGATGTCTT      600
TTCTATTTCC GGTAGAGGTA CCGTCGTCAC TGGTAGAGTC GAAAGAGGTG      650
20 TCTTGAAGAA GGGTGAAGAA ATTGAAATTG TCGGTAACCT TGAAAAGCCA      700
TTCAAGACCA CCGTTACTGG TATTGAAATG TTCAAGAAGG AATTGGATGC      750
TGCTATGGCT GGTGACAAC GTGGTGTCTT GTTGAGAGGT GTCAAGAGAG      800
ACGAAATCAG CAGAGGTATG GTTTTGGCCA AGCCAGGTAC CGTCACTTCC      850
CACAAGAAGT TCTTGGCCTC CATGTACATC TTGACTGGTG AAGAAGGTGG      900
25 TCGTCGTACC CCATTCGGTG AAGGTTACAA GCCACAATGT TTCTTCAGAA      950
CCAATGACAT CACCACCACT TTCCTTTCC CAGAAGGTGA AGGTGTCGAC      1000
CACTCCCAA TGGTTATGCC AGGTGACAAC ATCGAAATGG TTGGTGAATT      1050
GTACAAGGCT TGTCCTTGGA A                                1071

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30

2) INFORMATION FOR SEQ ID NO: 1572

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
 (B) STRAIN: ATCC 8750

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572

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TATCTTGGTT WGCTCGGCCG CTGACGGCCC AATGCCTCAG ACTCGCGAGC      50
ACATCCTGCT GAGCCGTCAG GTTGGCGTTC CTTACATCAT CGTGTTCTCTG      100
50 AACAAGGCCG ACATGGTTGA TGACGAAGAG CTGATCGAAC TGGTTGAAAT      150
GGAAGTTCGC GAGCTGTTGT CCAAGTACGA CTTCCCTGGC GACGACACCC      200
CGATCATCAA GGGTTCGGCC AAAGTGGCTC TGGAAGGCCA CGAAGGCCCA      250
CTGGGCAGCC AAGCCGTTCT GGCTCTGGCC GAAGCGCTGG ACAACTACAT      300

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	TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCCCTGATG	CCTGTTGAAG	350
	ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
	CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
	CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
5	ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
	CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
	GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
	GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
10	GGTTCTGCCA	GGCGACAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
	TCGCCATGGA	AGAAGGT				817

15 2) INFORMATION FOR SEQ ID NO: 1573

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella buccalis*
 (B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573

30	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTT	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAACTTCTTG	AGCAATACGA	ATTCGAAGAG	GATACTCCAA	200
35	TCGTTCTGTTG	TTCTGCACTG	GGTGCAATTGA	ATGGTGTTGA	CAAGTGGGTT	250
	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAACAG	GACGTATTGA	GAAGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450
40	GTCTGTTGTA	ACAGGCGTTG	AAATGTTCCG	TAAGATTCTT	TCTGAAGGTG	500
	AAGCAGGTGA	TAACGTAGGA	CTTTTGCTCC	GCGGTATCGA	TAAGGATGAA	550
	GTAAAGCGTG	GTATGGTTGT	TGTACACCCA	GGTGCCATCA	CTCCTCACGA	600
	TCACCTCAAG	GCTTCCATCT	ATGTATTGAA	GAAGGAAGAG	GGTGGACGTC	650
	ATACTCCATT	CGGAAACAAG	TATCGTCCTC	AGTTCTATCT	CCGTACAATG	700
45	GACTGTACAG	GTGAGATCAC	TTTGCCAGAA	GGCGTAGAGA	TGGTGATGCC	750
	TGGTGACAAC	GTAGAGATTG	AGGTTACCTT	GATTTACAAG	GTTGCC	796

50 2) INFORMATION FOR SEQ ID NO: 1574

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574

	GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
	GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
15	TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
	ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
	TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
	GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
	GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
20	CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
	GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
	ACCAAGACCA	CTGTAAC TGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
	AGGTCGTGCA	GGTGATAACG	TTGGTGTTCT	ACTACGTGGT	ACCAAGCGTG	550
	ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
25	CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
	TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
	CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
	ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
	TATGGCTGAA	GGCGAGAGAT				820

30

2) INFORMATION FOR SEQ ID NO: 1575

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
- (B) STRAIN: ATCC 33315

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575

	GGTAGTGTCT	GCAGCTGACG	GCCCAATGCC	ACAAACTCGT	GAACATATCC	50
50	TATTGTCACG	TAACGTTGGT	GTACCATACA	TCGTTGTATT	CTTAAACAAA	100
	ATGGATATGG	TTGACGATGA	AGAATTACTT	GAATTAGTTG	AAATGGAAGT	150
	ACGTGATCTA	TTAACTGAAT	ACGACTTCCC	AGGTGATGAT	ACTCCTGTTA	200
	TTTCTGGTTC	AGCTTTGAAA	GCTTTAGAAG	GCGACGAAGA	ATATGAACAA	250


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AAAGTCTTAG ACTTAATGGC AGCTGTAGAT GATTTTCATCC CAACTCCTGA 300
ACGTGACCAT GACAAACCGT TCATGATGCC GATTGAAGAT GTTTTCTCAA 350
TCACTGGTCG TGGAAGTGT GCTACAGGTC GTGTTGAACG TGGAACTATT 400
AAAGTCGGTG ATGAAGTTGA TATCATCGGT ATTCATGAAA ATGTTAAAAA 450
5 GACAACTGTT ACGGGTGTAG AAATGTTCCG TAAATTGTTG GATTACGCTG 500
AAGCTGGCGA TAACATCGGT ACATTATTGC GTGGTGTTC TCGTGATGAT 550
ATCGAACGTG GTCAAGTGT GGCTAAACCA GGCACAATCA CACCACATAC 600
AAAATTCTCA GCTGAAGTTT ATGTATTAAC AAAAGAAGAA GGCGGACGTC 650
ATACTCCATT CTTCTCAAAC TATCGCCAC AATTTTACTT CCGTACAACT 700
10 GACATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA TGGTTATGCC 750
AGGTGATAAC GTAGCAATGG AAGTTGAATT AATTCACCCT GTTGCTATTG 800
AAA 803

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2) INFORMATION FOR SEQ ID NO: 1576

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576

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TTAATGAAGC AATTGTTGTA AATTTTGAAA GCGAAGGAAA AAAACATAAA 50
CTTGTTTTAG AAGTAGCAGC TCATTTAGGA GATAATAGAG TTAGAAGTAT 100
TGCTATGGAT ATGACAGATG GTTTGGTAAG GGGCTTAAAA GCTGAGGCTT 150
35 TAGGTGCTCC TATTAGTGTT CCTGTTGGTG AGAAAGTTTT AGGAAGAATT 200
TTCAATGTTA CTGGAGATTT GATCGATGAA GGTGAAGAAA TTTCTTTTGA 250
TAAAAAATGG GCAATTCATA GAGATCCGCC AGCTTTTGAA GATCAAAGCA 300
CAAAAAGTGA GATTTTTGAA ACAGGGATTA AAGTTGTAGA TTTGCTTGCT 350
CCTTATGCAA AAGGTGGTAA AGTAGGTCTT TTTGGTGGTG CAGGTGTTGG 400
40 TAAACTGTT ATTATTATGG AGCTTATTCA CAATGTTGCA TTTAAGCATA 450
GCGGCTATTC TGTATTTGCA GGTGTGGGTG AGAGAACTCG TGAAGGAAAT 500
GACCTTTATA ATGAAATGAA AGAAAGTAAT GTTTTAGACA AAGTTGCTCT 550
ATGTTATGGA CAAATGAATG AACCACCAGG AGCAAGAAAT CGTATTGCTT 600
TAACAGGTTT AACAATGGCT GAGTATTTTA GAGATGAAAT GGGTCTTGAT 650
45 GTGCTTATGT TTATTGATAA TATCTTTAGA TTTTCACAAT CAGGTTCTGA 700
AATGTCAGCA CTTTTAGGAA GAATTCCATC AGCTGTGGGT TATCAACCAA 750
CCCTAGCAAG TGAAATGGGT AAATTCCAAG AAAGAATTAC TTCAACTAAA 800
AAAGG 805

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2) INFORMATION FOR SEQ ID NO: 1577

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*
 (B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577

```

15  ATTTACCCAA GATCAACGAA GCCGTCGAAG TAAATTTCTGA GGTTGAGGGC      50
    AAGCAAAACA GACTTGTGTT AGAGGTTGCC GCACACCTTG GCGATAACCG      100
    CGTAAGAACG ATCGCTATGG ATATGAGCGA AGGCTTAACC AGAGGCCTTG      150
    AGGCTACGGC TCTTGCGCGC CCTATTAGCG TTCCGGTCGG CGAAAAAGTT      200
    TTGGGAAGGA TTTTAAACGT CGTCGGCGAT CTGATCGACG AGGGTGAAGG      250
20  CATAGAATTT GATAAAAAAT GGTCTATCCA CCGCGATCCT CCGCCGTTTG      300
    AAGAGCAAAG CACGAAGAGT GAAATTTTGT AAACGGGTAT AAAAGTGGTC      350
    GATCTTCTAG CCCCTTATGC AAAAGGCGGT AAGGTCGGAT TATTCGGCGG      400
    TGCCGGCGTC GGTAAGACGG TTATTATCAT GGAGCTTATC CACAACGTTG      450
    CATTTAAGCA TAGCGGTTAT TCCGTGTTTG CCGGCGTGGG CGAGCGAACC      500
25  CGCGAAGGAA ACGACCTTTA TCACGAGATG AAAGAGAGTA ACGTTTGGGA      550
    CAAAGTCGCC TTGTGCTACG GCCAGATGAA CGAGCCGCCG GGAGCAAGAA      600
    ACCGCATCGC TCTAACAGGC CTAACGATGG CTGAATACTT CCGCGACGAG      650
    ATGGGACTTG ACGTTTTGAT GTTTATAGAC AACATCTTCC GTTTCTCTCA      700
    GTCTGGCGCT GAGATGTCGG CGCTTCTTGG ACGTATCCCG TCAGCCGTTG      750
30  GTTATCAGCC GACTTTGGCG AGCGAAATGG GCAAATTCCA AGAGAGAATT      800
    ACATCAACC                                     809
  
```

35 2) INFORMATION FOR SEQ ID NO: 1578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578

```

50  AATCGAAGTG CAACGTTTCT TGCCTGTACT TGATGGTGCT GTAAGTGTGT      50
    TGGACTCACA ATCAGGTGTA GAACCTCAAA CAGAAACAGT TTGGCGTCAA      100
    GCGACAGATT ACCGCGTACC GCGTGTGTGA TTCTGTAACA AAATGGACAA      150
  
```

	AATTGGTGCA	GACTTCTTAT	ACTCTGTATC	AACTTTACAT	GATCGTTTAC	200
	AAGCAAATGC	TCACCCAATC	CAATTACCAA	TTGGTGCGGA	AGATGACTTT	250
	ACTGGTATTA	TCGACTTAGT	AAAAATGAAA	GCTGAAATCT	ACACAAATGA	300
	CTTAGGAAC	GAAATCCAAG	AGACTGAAAT	TCCTGAAGAA	TACGTAGAAT	350
5	TAGCTGAAGA	ATGGCGCGAA	AAATTAATTG	AAGCTGTTGC	TGATACTGAT	400
	GAAGAACTAA	TGATGAAATT	CTTGGAAGGT	GAAGAAATCA	CTGAAGAAGA	450
	ATTGAAAGCT	GGTATTTCGTC	AAGCAACATT	GACTGTTGAC	TTTTTCCCTG	500
	TTCTTTGCGG	ATCTGCCTTT	AAAAACAAAG	GGGTTCAATT	GATGTTGGAT	550
	GCAGTCATCG	ACTACTTGCC	TTCACCACTT	GATGTTCCCTG	CGATTAAAGG	600
10	GATCAATCCT	AAAACAGACG	AAGAACTGA	TCGTCCGGCT	GACGATGAAG	650
	CACCATTTCG	TTCATTAGCA	TTTAAAGTAA	TGACTGACCC	ATTCGTARGET	700
	CGTTTGACAT	TCTTYCGTGT	GTATTTCARGT	ATCTTGAAC	CTGGATCATA	750
	CGTATTGAAT	GCTTCAAAAG	GCAAACGCGA	ACGTATCGGT	CGGATCCTAC	800
	AAATGCACGC	CAACACTCGT	GCTGAAATCC	AAACAGTATA	CTCAGGCGAT	850
15	ATCGCCGCTG	CTGTTGGTTT	GAAAGACACA	ACAACCTGGGG	ATCCACTATG	900
	TGATGAAAAA	TCCCCAGTAA	TCCTTGAATC	AATCGAATTC	CCAGAACCAG	950
	TTATCGAAGT	CGCTGTTGAG	CTTAAATCAA	AAGCTGACCA	AGATAAAATG	1000
	GGGGTTGCTT	TACAAAAACT	TGCTGAAGAA	GATCCATCAT	TCCGTGTGGA	1050
	AMCAAACGCT	GAAACAGGCG	AAACTGTTAT	CGCTGGTATG	GGAGAACTTC	1100
20	ACTTGACGT	CTTAGTTGAC	CGTATGCGTC	GCGAATTTAA	AGTTGAAGCA	1150
	AACGTAGGTG	CGCCTCAAGT	TTCTTATCGT	GAAACATTCC	GTGCAGCAAC	1200
	ACAAGCGGAA	GGTAAATTTG	TACGTCAGTC	TGGTGGTAAA	GGTCAATACG	1250
	GTCACGTATG	GGTCGAATTT	ACACCAAACG	AAGAAGGTAA	AGGCTTCGAA	1300
	TTCGAAAACG	CGATTGTCGG	TGGTGTGGTT	CCTCGTGAAT	ACATCCCAGC	1350
25	AGTTGAAAAA	GGACTTGAAG	AATCAATGGC	GAACGGTGTC	TTAGCCGGTT	1400
	ACCCATTAGT	AGACATCAAA	GCAAACTTT	ATGATGGTTC	ATACCATGAT	1450
	GTCGATTCAA	GTGAACTGC	CTTCCGTGTT	GCAGCTTCTA	TGGCTTTACG	1500
	TGCTGCAGCG	AAGAAAGCAA	ACCCAGTAAT	TCTTGAACCA	ATGATGAAAG	1550
	TAGTTATCAC	TGTACCAGAA	GATTACTTAG	GTGATGTTAT	GGGTCACGTA	1600
30	ACTGCTCGTC	GTGGACGCGT	AGAAGGAATG	GAAGCACWCG	GTAACTCACA	1650
	AATCGTGAAC	GCAATCGTGC	C			1671

35 2) INFORMATION FOR SEQ ID NO: 1579

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1662 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579

50	GAAGTACAAC	GTTCAC	TACG	GGTTCT	TGAC	GGWGCT	GTAA	CAGTATT	GGA	50
	CTCACAATCT	GGTGTAGAAC	CACAACTGA	AACAGTTTG	CGTCAAGCGA					100
	CAGATTACCG	CGTACCACGT	ATCGTATTCT	GTAACAAAAT	GGATAAAATC					150

	GGTGCAGACT	TCTTATACTC	TGTATCTACT	TTACATGATC	GCTTGCAAGC	200
	AAATGCTCAT	CCAATCCAAT	TACCAATTGG	TGCGGAAGAT	GACTTTACTG	250
	GTATCATCGA	TCTAGTAAAA	ATGAAAGCTG	AGATCTATAC	AAACGATTTA	300
	GGAACAGAGA	TTCAAGAAAC	TGAAATTCCT	GAAGAGTACA	AAGAATTAGC	350
5	TGAAGAATGG	CGCGAAAAAT	TAGTTGAAGC	TGTTGCAGAT	ACTGACGAAG	400
	AGCTAATGAT	GAAATTCTTG	GAAGGTGAAG	AAATCACTGA	AGAAGAATTG	450
	AAAGCTGGTA	TCCGTCAAGC	GACATTGACT	GTTGAATTTT	TCCCAGTTCT	500
	TTGTGGTTCA	GCCTTCAAAA	ACAAAGGGGT	TCAATTGATG	TTGGATGCAG	550
	TCATCGACTA	CCTTCCTTCA	CCACTTGATG	TTCCTGCAAT	CAAAGGGATC	600
10	AATCCTAAAA	CTGACGAAGA	AACTGATCGT	CCTGCTGACG	ATGAAGCGCC	650
	TTTTGCTTCA	CTAGCATTTA	AAGTAATGAC	TGACCCATTC	GTAGGTCGTT	700
	TGACATTCTT	CCGTGTGTAT	TCAGGTGTCT	TGAACCTCTG	ATCATATGTC	750
	TTGAATGCTT	CAAAAGACAA	ACGCGAACGT	ATCGGTCGTA	TTCTGCAAA	800
	GCACGCGAAC	ACTTGTGCAG	AAATCCAAAC	AGTTTATTCA	GGCGATATCG	850
15	CTGCAGCTGT	TGGTTTGAAA	GATTCCACAA	CAGGGGATAC	ATTGTGTGCG	900
	AAAAATCACC	CAGTAATCCT	TGAATCAATC	GAATTCCCAG	AMCCAGTTAT	950
	CGAAGTAGCT	GTTGAACYTA	AATCAAAAGC	TGACCAAGAT	AAAATGGGTG	1000
	TGGCTTTACA	AAAACCTTGCT	GAAGAAGATC	CTTCATTCCG	TGTAGAAMCA	1050
	AACGCTGAAA	CTGGCGAAAC	TGTTATCGCA	GGGATGGGTG	AACTTCACTT	1100
20	GGACGTCCTT	GTTGACCGTA	TGCGTCGCGA	ATTTAAAGTT	GAAGCAAACG	1150
	TTGGTGCGCC	TCAAGTTTCT	TACCGCGAAA	CATTCCGTGC	TTCTACGCAA	1200
	GCCGAAGGTA	AATTTGTACG	TCAGTCTGGT	GGTAAAGGTC	AATACGGTCA	1250
	CGTATGGATC	GAATTTACAC	CAAACGAAGA	AGGTAAAGGC	TTCGAATTCG	1300
	AAAACGCAAT	TGTCGGTGGT	GTGGTTCCAC	GTGAATACAT	CCCAGCAGTT	1350
25	GAAAAAGGAC	TTGAAGACTC	AATGGCTAAC	GGTGTTCTAG	CTGGTTATCC	1400
	ATTGGTTGAC	ATCAAAGCCA	AGCTTTACGA	TGGTTCATAC	CATGATGTCG	1450
	ATTCAGTGTA	AACAGCCTTC	CGTGTGGCAG	CTTCAATGGC	TTTACGTGCT	1500
	GCAGCGAAGA	AAGCTAATCC	AGTGATTCTT	GAACCAATGA	TGAAAGTTGT	1550
	TATCACTGTT	CCTGAAGATT	ACTTAGGTGA	TATTATGGGA	CACGTAACGT	1600
30	CTCGTCGTGG	ACGTGTTGAA	GGTATGGAAG	CGCATGGTAA	CTCACAAATC	1650
	GTTAACGCGA	TT				1662

35 2) INFORMATION FOR SEQ ID NO: 1580

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1669 bases
- (B) TYPE: Nucleic acid
- 40 (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580

50	CAATCGAAGT	ACAACGTTCT	CTTCGTGTAT	TGGATGGTGC	TGTTACCGTT	50
	CTTGACTCAC	AATCAGGTGT	TGAGCCTCAA	ACTGAAACAG	TTTGGCGTCA	100
	AGCAACTGAG	TATGGAGTTC	CACGTATCGT	ATTTGCCAAC	AAAATGGACA	150

	AAATCGGTGC	TGACTTCCTT	TACTCTGTAA	GCACACTTCA	CGATCGTCTT	200
	CAAGCAAATG	CACACCCAAT	CCAATTGCCA	ATCGGTTCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGACA	TCCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGATC	GAAGCAGTTG	CTGAAACTGA	400
	CGAAGAATTG	ATGATGAAAT	ACCTCGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGGTATCCGT	AAAGCGACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GCTCTGCCTT	CAAGAACAAA	GGTGTTCAAT	TGATGCTTGA	550
	TGCGGTTATT	GACTACCTTC	CAAGCCCACT	TGACATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGATGAA	650
	GAGCCATTTG	CAGCTCTTGC	CTTCAAGATC	ATGACAGACC	CATTTCGTAAG	700
	TCGTTTGACA	TTCTTCCGTG	TTTACTCARG	TGKTCTTCAA	TCAGGTTTCA	750
	ACGTATTGAA	CACTTCTAAA	GGKAAACGTG	AGCGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CCAACAGCCG	TCAAGAAATT	GACACTGGTT	ACTCAAGAGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TCCAACGGT	GACTCATTGC	900
	CAGATGAAAA	AGCTAAAATC	ATTCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGCCAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCTGGTAT	GGGTGAGCTT	1100
20	CACCTTGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTTGAAGC	1150
	AAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTTCGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	ACTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	TGCGGCTTCA	CTTGCTCTTA	1500
	AAGAAGCTGC	TAAATCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACAATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTTCG	TGCTTACGT				1669

35 2) INFORMATION FOR SEQ ID NO: 1581

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581

AATTGGGGAC TACACCTATT ATGATG

26

50

2) INFORMATION FOR SEQ ID NO: 1582

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582

10 GGCAAATCAG TCAGTTCAGG AGT

23

2) INFORMATION FOR SEQ ID NO: 1583

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583

25

CGATTGGCAA CAATACACTC CTG

23

30 2) INFORMATION FOR SEQ ID NO: 1584

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584

40

TCACCTATTT TTACGCCTGG TAGGAC

26

45

2) INFORMATION FOR SEQ ID NO: 1585

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*
 5 (C) ACCESSION NUMBER: AF139725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585

```

10 ATGACTATAC CTGACGCAAA TGCAATCTAT CCTAACTCAG CCATCAAAGA      50
   GGTGTCTTT ATCAAGAACG TGATCAAAAG TCCCAATATT GAAATTGGGG      100
   ACTACACCTA TTATGATGAC CCAGTAAATC CCACCGATTT TGAGAAACAC      150
   GTTACCCATC ACTATGAATT TCTAGGCGAC AAATTAATCA TCGGTAAATT      200
   TTGTTCTATC GCCAGTGGCA TTGAATTTAT CATGAACGGT GCCAACCACG      250
   TAATGAAAGG TATTTGACT TATCCATTTA ATATTTTAGG TGGCGATTGG      300
15 CAACAATACA CTCCTGAAC TACTGATTG CCGTTGAAAG GTGATACTGT      350
   AGTCGGAAAT GACGTGTGGT TTGGGCAAAA TGTGACCGTC CTACCAGGCG      400
   TAAAAATAGG TGACGGTGCC ATTATCGGAG CAAATAGTGT TGTAACAAAA      450
   GACGTCGCTC CATATACAAT TGTCGGTGGC AATCCAATTC AACTCATCGG      500
   ACCAAGATTT GAACCGGAAG TTATTCAAGC ATTAGAAAAT CTGGCATGGT      550
20 GGAATAAAGA TATTGAATGG ATAAGTCTA ATGTTCTTAA ACTAATGCAA      600
   ACAACACCCA CACTTGAATT GATAAACAGT TTAATGGAAA AATAA          645

```

25 2) INFORMATION FOR SEQ ID NO: 1586

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586

ATCCCCACAA TCTTTTTTAT CAATAA 26

40

2) INFORMATION FOR SEQ ID NO: 1587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587

CATTGTTTCA ATTCGGTAAA GTTC 24

2) INFORMATION FOR SEQ ID NO: 1588

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588

GTTTTTGAAG TTAAATAGTG TTCTT

25

15

2) INFORMATION FOR SEQ ID NO: 1589

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589

CTTCCATTTG TACTTTCCT A

21

30

2) INFORMATION FOR SEQ ID NO: 1590

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1920 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Cloning vector pFW16
- (C) ACCESSION NUMBER: U50983

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1590

ATGAAAATTA TTAATATTGG AGTTTTAGCT CATGTTGATG CAGGAAAAAC 50
TACCTTAACA GAAAGCTTAT TATATAACAG TGGAGCGATT ACAGAATTAG 100
GAAGCGTGGA CAAAGGTACA ACGAGGACGG ATAATACGCT TTTAGAACGT 150
CAGAGAGGAA TTACAATTCA GACAGGAATA ACCTCTTTTC AGTGGGAAAA 200
TACGAAGGTG AACATCATAG ACACGCCAGG ACATATGGAT TTCTTAGCAG 250

	AAGTATATCG	TTCATTATCA	GTTTTAGATG	GGGCAATTCT	ACTGATTTCT	300
	GCAAAAGATG	GCGTACAAGC	ACAAACTCGT	ATATTATTTT	ATGCACTTAG	350
	GAAAATGGGG	ATTCCCACAA	TCTTTTTTAT	CAATAAGATT	GACCAAAATG	400
	GAATTGATTT	ATCAACGGTT	TATCAGGATA	TAAAGAGAA	ACTTTCTGCC	450
5	GAAATTGTAA	TCAAACAGAA	GGTAGAACTG	TATCCTAATG	TGTGTGTGAC	500
	GAACTTTACC	GAATCTGAAC	AATGGGATAC	GGTAATAGAG	GGAAACGATG	550
	ACCTTTTAGA	GAAATATATG	TCCGGTAAAT	CATTAGAAGC	ATTGGAACCTC	600
	GAACAAGAGG	AAAGCATAAG	ATTTTCAGAA	TGTTCTCTGT	TCCCTCTTTA	650
	TCATGGAAGT	GCAAAAAGTA	ATATAGGGAT	TGATAACCTT	ATAGAAGTTA	700
10	TTACTAATAA	ATTTTATTCA	TCAACACATC	GAGGTCCGTC	TGAACCTTGC	750
	GGAAATGTTT	TCAAAATTGA	ATATACAAAA	AAAAGACAAC	GTCTTGCATA	800
	TATACGCCTT	TATAGTGGAG	TACTACATTT	ACGAGATTCT	GTTAGAGTAT	850
	CAGAAAAGGA	AAAAATAAAA	GTTACAGAAA	TGTATACTTC	AATAAATGGT	900
	GAATTATGTA	AGATTGATAG	AGCTTATTCT	GGAGAAATTG	TTATTTTGCA	950
15	AAATGAGTTT	TTGAAGTTAA	ATAGTGTTCT	TGGAGATACA	AACTATTGTC	1000
	CACAGAGAAA	AAAGATTGAA	AATCCGCACC	CTCTACTACA	AACAACCTGT	1050
	GAACCGAGTA	AACCTGAACA	GAGAGAAATG	TTGCTTGATG	CCCTTTTGGA	1100
	AATCTCAGAT	AGTGATCCGC	TTCTACGATA	TTACGTGGAT	TCTACGACAC	1150
	ATGAAATTAT	ACTTCTTTTC	TTAGGGAAAG	TACAAATGGA	AGTGATTAGT	1200
20	GCACTGTTGC	AAGAAAAGTA	TCATGTGGAG	ATAGAAATAA	CAGAGCCTAC	1250
	AGTCATTTAT	ATGGAGAGAC	CGTTAAAAAA	TGCAGAATAT	ACCATTCACA	1300
	TCGAAGTGCC	GCCAAATCCT	TTCTGGGCTT	CCATTGGTCT	ATCTGTATCA	1350
	CCGCTTCCGT	TGGGAAGTGG	AATGCAGTAT	GAGAGCTCGG	TTTCTCTTGG	1400
	ATACTTAAAT	CAATCATTTC	AAAATGCAGT	TATGGAAGGG	ATACGCTATG	1450
25	GTTGTGAACA	AGGATTGTAT	GGTTGGAATG	TGACGGACTG	TAAAATCTGT	1500
	TTTAAGTATG	GCTTATACTA	TAGCCCTGTT	AGTACCCAG	CAGATTTTCG	1550
	GATGCTTGCT	CCTATTGTAT	TGGAACAAGT	CTTAAAAAAA	GCTGGAACAG	1600
	AATTGTTAGA	GCCATATCTT	AGTTTTTAAA	TTTATGCGCC	ACAGGAATAT	1650
	CTTTCACGAG	CATACAACGA	TGCTCCTAAA	TATTGTGCGA	ACATCGTAGA	1700
30	CACTCAATTG	AAAAATAATG	AGGTCATTCT	TAGTGGAGAA	ATCCCTGCTC	1750
	GGTGTATTCA	AGAATATCGT	AGTGATTTAA	CTTTCTTTAC	AAATGGACGT	1800
	AGTGTTTGTT	TAACAGAGTT	AAAAGGGTAC	CATGTTACTA	CCGGTGAACC	1850
	TGTTTGCCAG	CCCCGTCGTC	CAAATAGTCG	GATAGATAAA	GTACGATATA	1900
	TGTTCAATAA	AATAACTTAG				1920

2) INFORMATION FOR SEQ ID NO: 1591

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591

50 ATGAGGTAAT AGAACGGATT

20

2) INFORMATION FOR SEQ ID NO: 1592

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592

CAGTATTTCA GTAAGCGTAA A

21

15

2) INFORMATION FOR SEQ ID NO: 1593

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593

CCGAGCGATT TACCGGATAC TTGGCTGCIC GCTCGG

36

30

2) INFORMATION FOR SEQ ID NO: 1594

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1032 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
(B) STRAIN: N97-330
45 (C) ACCESSION NUMBER: AF175293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594

ATGTTTAGAA TTAAAGTTGC AGTTCTGTTT GGGGGCTGTT CAGAGGAACA 50
50 TAATGTTTCG ATAAAATCTG CGATGGAGAT TGCCGCAAAC ATAGATACAA 100
AAAAGTATCA GCCTTATTAT ATTGGAATCA CAAAATCCGG CGTTTGGAAC 150
ATGTGTGAAA AACCTTGTTT GGAGTGGGAA CAATATGCGG GGGATCCGGT 200
TGTTTTTTTCA CCGGACAGAA GTACGCATGG TCTGCTGATA CAAAAGACA 250

	CTGGGTATGA	AATCCAGCCT	GTGGATGTGG	GATTACCGAT	GATTCATGGC	300
	AAGTTTGGCG	AGGATGGCTC	CATACAAGGC	TTGCTTGAAT	TGTCAGGCAT	350
	TCCGTATGTG	GGATGCGATA	TTCAAAGCTC	CGTGACCTGC	ATGGATAAGG	400
	CGCTTGCATA	TACCGTTGTG	AAAAATGCGG	GTATCGCTGT	GCCTGGGTTC	450
5	CGGATCCTTC	AGGAGGGGGA	TCGCCTGGAA	ACAGAGGATT	TCGTATATCC	500
	CGTTTTTGTA	AAGCCTGCCC	GTTCCGGCTC	ATCCTTTGGC	GTAAACAAGG	550
	TATGCAAGGC	AGAAGAACTG	CAGGCAGCAA	TCGAAGATGC	AAGAAAAATAT	600
	GACAGCAAGA	TTTTGATTGA	AGAGGCCGTT	ACCGGGAGTG	AGGTAGGCTG	650
	CGCCATACTG	GGAAACGGAA	ATGATCTCAT	GGCTGGCGAG	GTGGATCAGA	700
10	TTGAGCTGAG	ACACGGCTTT	TTTAAGATTC	ATCAGGAAGC	ACAGCCGGAG	750
	AAAGGATCTG	AAAATGCAGT	CATCCGAGTT	CCAGCCGCCCT	TACCGGATGA	800
	GGTAATAGAA	CGGATTGAGA	AAACAGCAAT	GAAGATTAC	CGGATACTTG	850
	GCTGCAGAGG	ATTGGCCCCG	ATTGACCTGT	TTTTGCGGGA	GGACGGCTGC	900
	ATTGTGTTGA	ATGAAGTGAA	TACCATGCCG	GGTTTTACTT	CCTACAGCCG	950
15	TTATCCCCGC	ATGATGACAG	CAGCCGGTTT	TACGCTTACT	GAAATACTGG	1000
	ATCGCTTGAT	TGAACTTTCA	CTTAGGAGGT	AA		1032

20 2) INFORMATION FOR SEQ ID NO: 1595

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595

AAATAATGCT CCATCAATTT GCTGA

25

35

2) INFORMATION FOR SEQ ID NO: 1596

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 40 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596

ATAGTCGAAA AAGCCATCCA CAAG

24

50

2) INFORMATION FOR SEQ ID NO: 1597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597

GATGAATTTG CGAAAATACA TGGA

24

2) INFORMATION FOR SEQ ID NO: 1598

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598

CAGCCAATTT CTACCCCTTT CAC

23

2) INFORMATION FOR SEQ ID NO: 1599

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: BM4405
(C) ACCESSION NUMBER: AF136925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599

CAGGGAGTAT TTGAGTTATT AGATATTCCA TATGTAGGTT GTGGTATCGG 50
AGCTGCAGCA ATTTCCATGA ATAAAATAAT GCTCCATCAA TTTGCTGAAA 100
TAGTTGGTGT AAAAAGCACT CCTAGTATGA TTATAGAAAA GGGACAAGAC 150
CTACAAAAAG TCGATGAATT TGCGAAAATA CATGGATTTC CTTTATATAT 200
CAAACCGAAT GAGGCAGGCT CATCAAAAGG AATTAGCAAG GTAGAACAAA 250
AAAGTGATTT ATATAAGCA ATAGACGAAG CTTCAAAATA TGATAGCCGT 300

ATTTTAATTC AAAAGGAAGT GAAAGGGGTA GAAATTGGCT GTGGGATTTT 350
 AGGGAATGAA CAATTGGTCG TTGGAGAATG TGATCAAATT AGTCTTGTGG 400
 ATGGCTTTTT CGACTATGAA GAGAAATACA ATTTAGTAAC AGCAGAAATT 450
 TTGTTACCAG CTAAACTATC AATAGACAAA AAAGAAGACA TCCAGATAAA 500
 5 AGCAAAAAAA CTATACAGAC TATTAGGGTG CAAAGGATTA GCGAGAATCG 550
 ACTTTTCTT AACGGATGAC GGAGAAATTT TATTAAATGA GATCAACACC 600
 CTCC 604

10

2) INFORMATION FOR SEQ ID NO: 1600

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 805 bases
- 15 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*
- (B) STRAIN: ATCC 49349

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600

ACCTCAAATT AATGAAGCAA TTGTTGTAAA TTTTGAAAGC GAAGGAAAAA 50
 AACATAAACT TGTTTTAGAA GTAGCAGCTC ATTTAGGAGA TAATAGAGTT 100
 AGAACTATTG CTATGGATAT GACAGATGGT TTGGTAAGGG GCTTAAAAGC 150
 30 TGAGGCTTTA GGTGCTCCTA TTAGTGTTC TGTGGTGAG AAAGTTTTAG 200
 GAAGAATTTT CAATGTTACT GGAGATTTGA TCGATGAAGG TGAAGAAATT 250
 CCTTTTGATA AAAAATGGGC AATTCATAGA GATCCGCCAG CTTTTGAAGA 300
 TCAAAGCACA AAAAGTGAGA TTTTGTAAAC AGGGATTAAA GTTGTAGATT 350
 TACTTGCTCC TTATGCAAAA GGTGGTAAAG TAGGTCTTTT TGGTGGTGCA 400
 35 GGTGTTGGTA AAAGTGTAT TATTATGGAG CTTATTCACA ATGTTGCATT 450
 TAAGCATAGC GGCTATTCTG TATTTGCAGG TGTGGGTGAG AGAACTCGTG 500
 AAGGAAATGA CCTTTATAAT GAAATGAAAG AAAGTAATGT TTTAGACAAA 550
 GTTGCTCTAT GTTATGGACA AATGAATGAA CCACCAGGAG CAAGAAATCG 600
 TATTGCTTTA ACAGGTTTAA CAATGGCTGA GTATTTTAGA GATGAAATGG 650
 40 GTCTTGATGT GCTTATGTTT ATTGATAATA TCTTTAGATT TTCACAATCA 700
 GGTTCTGAAA TGTCAGCACT TTTAGGAAGA ATTCCATCAG CTGTGGGTTA 750
 TCAACCAACC CTAGCAAGTG AAATGGGTAA ATTCCAAGAA AGAATTACTT 800
 CAACT 805

45

2) INFORMATION FOR SEQ ID NO: 1601

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus sulfureus*
(B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601

```

10 CTCCTTACCA GATATCAACA ATGCGCTGGT TGTATATAAA AATGATGCCA      50
   ATAAAACAAA AGTTGTTTAA GAAGCAGCGT TAGAATTAGG TGACGGAATC      100
   ATTCGTGCGA TTGCAATGGA ATCGACTGAT GGATTGCAAC GTGGGATGGA      150
   AGTTGTTCGAT ATGGGAGAAT CTATTTCTGT ACCAGTTGGA ACAGAACTT      200
   TAGGACGTGT GTTTAATGTA TTAGGAGATA CGATTGACTT AGAAGCTCCT      250
15 TTTCTTAAAG ATGCACCGCG TAGTGGAATC CATAAAAAAG CCCCTAATTT      300
   TGATGAATTA AGTACAAGCA CAGAAATTCT AGAAACAGGG ATCAAAGTCA      350
   TCGATCTATT AGCCCCTTAT TTAAAAGGTG GTAAAGTTGG ATTGTTTGGG      400
   GGAGCCGGTG TAGGAAAAAC GGTATTGATT CAAGAGTTGA TTCACAATAT      450
   CGCACAAGAA CACGGTGGA TTTCCGGTCTT TACTGGTGTT GGTGAGCGTA      500
20 CACGTGAAGG AAACGATTG TATTATGAAA TGAAAGATTC AGGAGTCATT      550
   GAAAAACAG CGATGGTGTT TGGACAAATG AATGAGCCAC CTGGTGCACG      600
   GATGCGTGTA GCCTTGACTG GATTAAACGAT TGCTGAATAT TTCCGTGATG      650
   TTGAAGGACA GGATGTACTG TTGTTTATCG ACAATATCTT CCGTTTTACA      700
   CAAGCTGGTT CTGAAGTGTC TGCCTTGTTA GGTCGTATGC CATCAGCTGT      750
25 GGGATATCAA CCAACATTAG CTACCGAAAT GGGGCAATTG CAAGAGCGGA      800
   TCACGTCAAC GAAAAAAGGA TCGATC      826

```

30 2) INFORMATION FOR SEQ ID NO: 1602

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Enterococcus solitarius*
(B) STRAIN: ATCC 49428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602

```

45 TGATACTTTA CCAGATATTA ATAATGCATT AGTAGTATAT AAAAAGGACG      50
   AGGACAAGAC ACGCGTTGTC TTAGAAGCCA CTTTGGAAC TGGAGATGGC      100
   ATGATTTCGTG CAATCTCTAT GGGATCGACT GATGGCTTGC AACGGGGAAT      150
   GGAAGTTGTG GACACACAAG CACCTATTTT TGTTCCAGTA GGAAATGAAA      200
50 CCTTAGGACG TGTTTTTAAT GTCTTAGGAG AAACGATTGA TAAACAGGCA      250
   CCGTTTCCTG AAGATGCCAA AAAAAGTGGT ATTCATAAAA AAGCACCCGC      300
   TTTTGATGAA TTAAGTACCA GTTCTGAAAT ATTGGAAACC GGGATTAAAG      350
   TAATCGATTT GCTAGCTCCT TATTTACGAG GTGGTAAAGT TGGATTATTT      400

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GGCGGTGCTG GCGTGGGTAA AACGGTATTA ATTCAAGAAT TAATTCATAA 450
CGTTGCCCAA GAACATGGGG GAATTTCTGT TTTTACGGGT GTCGGAGAGC 500
GTACTCGTGA AGGAAATGAC CTATATTATG AAATGCAGGA TTCAGGCGTT 550
ATTGAAAAAA CCGCTATGGT ATTTGGACAA ATGAACGAAC CCCCTGGTGC 600
5  ACGTATGCGT GTAGCGTTAA CTGGTTTGAC ACTTGCTGAG TACTTCCGTG 650
  ATGTACAAGG TCAAGACGTA TTATTATTTA TAGATAATAT TTTCCGCTTT 700
  ACTCAAGCAG GAACAGAAGT ATCTGCTTTA TTAGGACGGA TGCCGTCTGC 750
  CGTTGGTTAC CAACCAACTC TAGCAACGGA AATGGGACAG TTGCAAGAAC 800
  GAATCACATC GACAGATAAA GGATCAATTA CCT 833
10

```

2) INFORMATION FOR SEQ ID NO: 1603

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15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 806 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
20
      (ii) MOLECULE TYPE: Genomic DNA
      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Campylobacter sputorum subsp. sputorum
25  (B) STRAIN: ATCC 35980

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603

```

ATCAGCCTAA AATTAACGAA GCAATAGAAG TTAATTATGA ATTAGATGGT 50
30  AAAAAAATAA GACTTATTCT TGAAGTAGCT GGACATCTTG GCGATAATAG 100
  AGCAAGAACC ATTGCTATGG ATATGAGTGA TGGTTTACAA AGAGGATTAG 150
  AAGTTACGGC TCTTGGTGCT CCTATAACAG TTCCTGTTGG AGATAAAGTT 200
  TTAGGTAGAA TGTTTAATGT TGTAGGTGAC TTAATAGATG AAGGTGAAGT 250
  AACAGATTTT GATAAAAGAT GGGCTATCCA TAGAGATCCT CCTTCGTTTG 300
35  AAGATCAAAG TACAAAAAGT GAAATTTTGG AAACAGGTAT AAAAGTAGTT 350
  GATCTTCTTG CACCTTATGC AAAAGGTGGT AAAGTTGGCT TATTTGGTGG 400
  TGCTGGCGTT GGAAAAACAG TTATCATAAT GGAGCTTATA CATAATGTTG 450
  CATTAAACA CAGCGGTTAT TCAATTTTGG CCGGTGTTGG AGAGAGAACA 500
  AGAGAGGGAA ATGATCTTTA TAATGAGATG AAAGAGTCTG GTGTTTGGGA 550
40  TAAAGTTGCC TTATGTTATG GACAAATGAA TGAACCAACA GGAGCAAGAA 600
  ACCGTATAGC ATTAACAGGT CTTACAATGG CTGAATATTT CCGTGATGAA 650
  ATGGGGCTTG ATGTGTTGAT GTTTATAGAT AATATTTTAA GATTTTCTCA 700
  ATCAGGTTCT GAAATGTCAG CGCTGCTTGG TAGAATTCCA TCTGCTGTTG 750
  GTTATCAACC AACATTAGCA AGTGAGATGG GAAAACTTCA AGAAAGAATT 800
45  ACTTCC 806

```

2) INFORMATION FOR SEQ ID NO: 1604

```

50  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 738 bases
      (B) TYPE: Nucleic acid

```

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
(B) STRAIN: ATCC 49372

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604

	GGTGTATCC	GCACAATCGC	TATGGAATCT	ACAGATGGAT	TGCAACGGGG	50
	GATGGAAGTT	GTCGATACCG	GCAAACCAAT	CTCTGTTCCCT	GTAGGTAAAG	100
	AAACATTAGG	TCGTGTGTTT	AACGTATTAG	GTGAAACGAT	CGACAAAGAA	150
15	GCACCTTTTC	CAGAAGATGT	AGAAAAGAGC	GGTATTCACA	AAAAGGCCCC	200
	CGCTTTTGAA	GACCTTAGCA	CCAGTAATGA	GATTTTAGAA	ACTGGGATCA	250
	AGGTTATCGA	CTTATTAGCC	CCTTACTTAA	AAGGTGGTAA	AGTTGGACTA	300
	TTCCGTGGTG	CCGGTGTTGG	TAAAACCGTC	TTAATTCAAG	AACTGATTCA	350
	TAATATCGCC	CAAGAACACG	GTGGGATTTC	TGTCTTTACC	GGGGTTGGGG	400
20	AACGGACTCG	TGAAGGGAAC	GACCTTTATT	ATGAAATGAA	AGAATCCGGC	450
	GTTATTGAAA	AAACAGCGAT	GGTCTTCGGA	CAAATGAATG	AGCCACCAGG	500
	TGCGCGGATG	CGCGTTGCCT	TGACTGGTTT	GACATTAGCT	GAATATTTC	550
	GTGATGAAGA	AGGTCAAGAT	GTGTTGCTAT	TTATCGATAA	CATTTCCGC	600
	TTACACAAG	CCGGATCAGA	AGTTTCGGCG	CTATTAGGTC	GGATGCCATC	650
25	TGCCGTTGGT	TATCAACCAA	CCTTGCAAC	AGAAATGGGT	CAATTACAAG	700
	AACGAATCAC	TTCAACGAAA	AAAGGCTCAA	TTACATCG		738

30 2) INFORMATION FOR SEQ ID NO: 1605

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605

ATYATYGAAR TITAYGCICC

20

45

2) INFORMATION FOR SEQ ID NO: 1606

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606

5 CCRAACATIA YICCIAC TTT TTC

23

2) INFORMATION FOR SEQ ID NO: 1607

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20

- (A) ORGANISM: *Klebsiella ornithinolytica*
- (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607

25	CTGGATTATG CGATGTCGGT CATTGTTGGC CGTGCGCTGC CGGATGTCCG	50
	AGATGGCCTG AAACCGGTAC ACCGTCGCGT ACTTTACGCC ATGAACGTAT	100
	TGGGCAATGA CTGGAACAAA GCCTATAAAA AATCCGCCCCG TGTCGTTGGT	150
	GACGTAATCG GTAAATACCA CCCTCATGGT GATACCGCCG TTTATGACAC	200
	CATTGTACGT ATGGCACAGC CATTCTCCTT GCGTTATATG CTGGTCGATG	250
30	GCCAGGGTAA CTTCGGTTCT GTCGATGGCG ACTCCGCCGC AGCGATGCGT	300
	TATACGGAAA TCCGTATGTC GAAATCGCC CACGAG	336

35 2) INFORMATION FOR SEQ ID NO: 1608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608

50

CTATCTGGAT TATGCGATGT CGGTCATTGT TGGCCGTGCG CTGCCGGATG	50
TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTATA CGCCATGAAC	100
GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCTG CCCGTGTCGT	150

GGGTGACGTC ATCGGTAAAT ACCACCCCTCA TGGTGATACT GCCGTATACG 200
 ACACCATTTGT ACGTATGGCG CAGCCATTCT CCCTGCGTTA CATGCTGGTA 250
 GATGGCCAGG GTAACCTTTGG TTCGGTCGAC GGCGACTCCG CCGCAGCGAT 300
 GCGTTATACG GAAATCCGTA TGTCGAAGAT CGCCCATGAA C 341

5

2) INFORMATION FOR SEQ ID NO: 1609

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609

20 GCCCTGATCC AAATAGCATA TA

22

2) INFORMATION FOR SEQ ID NO: 1610

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 30 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610

35

CCTGGCATAA CAGTAACATT CTG

23

40 2) INFORMATION FOR SEQ ID NO: 1611

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 45 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611

TGGGAAAAAG CAACTCCATC TC

22

2) INFORMATION FOR SEQ ID NO: 1612

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612

ACAACTGAAT TCGCAGCAAC AAT

23

15

2) INFORMATION FOR SEQ ID NO: 1613

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (C) ACCESSION NUMBER: U19459

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613

	ATGAAATATG	GCCCTGATCC	AAATAGCATA	TATCCACATG	AAGAAATAAA	50
	AAGTGTGTTGT	TTTATTAAAA	ATACAATTAC	CAATCCAAAT	ATTATAGTTG	100
35	GAGATTATAC	TTACTATTCC	GATGTTAACG	GAGCTGAAAA	ATTTGAAGAA	150
	CATGTGACAC	ATCATTATGA	ATTTAGGGGT	GATAAACTTG	TAATTGGCAA	200
	GTTTTGTGCA	ATAGCTGAAG	GTATAGAATT	TATTATGAAT	GGAGCAAACC	250
	ATAGAATGAA	TTCAATAACA	ACTTATCCTT	TTAATATAAT	GGGAAATGGT	300
	TGGGAAAAAG	CAACTCCATC	TCTTGAAGAT	TTACCATTTA	AGGGAGATAC	350
40	TGTTGTTGGA	AATGATGTGT	GGATTGGTCA	GAATGTTACT	GTTATGCCAG	400
	GAATTCAAAT	AGGAGATGGA	GCAATTGTTG	CTGCGAATTC	AGTTGTTACA	450
	AAAGATGTAC	CACCATATCG	TATTATTGGT	GGAAATCCGA	GTAGAATTAT	500
	AAAGAAAAGG	TTTGAAGATG	AATTGATAGA	TTATTTATTG	CAAATAAAAT	550
	GGTGGGATTG	GTCAGCACAA	AAAATATTTT	CTAATCTTGA	AACACTTTGT	600
45	AGCTCTGATT	TAGAGAAAAT	AAAATCTATT	CGAGATTAG		639

2) INFORMATION FOR SEQ ID NO: 1614

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614

CCAATCCAGA AGAAATATAC CC

22

10

2) INFORMATION FOR SEQ ID NO: 1615

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615

ATTAGTTTAT CCCCAATCAA TTCA

24

25

2) INFORMATION FOR SEQ ID NO: 1616

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616

40 ATAATGAATG GGGCTAATCA TCGTAT

26

2) INFORMATION FOR SEQ ID NO: 1617

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617

GCCAACAACT GAATAAGGAT CAAC

24

5

2) INFORMATION FOR SEQ ID NO: 1618

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (C) ACCESSION NUMBER: AF015628

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618

	ATGAAATGGC	AAAATCAGCA	AGGCCCCAAT	CCAGAAGAAA	TATACCCTAT	50
	AGAAGGTAAT	AAACATGTTC	AATTTATTAA	ACCATCTATA	ACAAAGCCCA	100
25	ATATTTTAGT	TGGGGAATAT	TCATATTACG	ATAGTAAAGA	TGGTGAATCT	150
	TTTGAAAGCC	AAGTTCTTTA	TCACTATGAA	TTGATTGGGG	ATAAACTAAT	200
	ATTAGGGAAG	TTTTGTTCTA	TTGGACCCGG	AACGACATTT	ATAATGAATG	250
	GGGCTAATCA	TCGTATGGAT	GGTTCAACAT	TTCCATTCAA	TCTTTTCGGA	300
	AATGGTTGGG	AGAAGCATAC	CCCTACATTG	GAAGACCTTC	CTTATAAGGG	350
30	TAACACGGAA	ATTGGGAACG	ATGTTTGGAT	TGGACGAGAT	GTGACAATTA	400
	TGCCCCGTGT	AAAAATAGGA	AACGGGGCTA	TTATTGCAGC	AAAATCGGTT	450
	GTGACAAAGA	ACGTTGATCC	TTATTCAGTT	GTTGGCGGTA	ATCCTTCACG	500
	ATTAATTAAG	ATAAGGTTTT	CCAAGGAAAA	AATCGCAGCA	TTACTAAAAG	550
	TAAGGTGGTG	GGACCTAGAG	ATAGAGACGA	TAAATGAAAA	TATTGATTGC	600
35	ATCCTGAATG	GTGATATAAA	AAAGGTTAAA	AGAAGTTAG		639

2) INFORMATION FOR SEQ ID NO: 1619

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619

50

AAGGCAAAAT AAAAGGAGCA AAGC

24

2) INFORMATION FOR SEQ ID NO: 1620

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620

TGTACCCGAG ACATCTTCAC CAC

23

15

2) INFORMATION FOR SEQ ID NO: 1621

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621

AATTGAAGGA CGGGTATTGT GGAAAG

26

30

2) INFORMATION FOR SEQ ID NO: 1622

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622

45 CGATTTTGAC AGATGGCGAT AATGAA

26

2) INFORMATION FOR SEQ ID NO: 1623

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M90056

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623

ATGAAAATAA	TGTTAGAGGG	ACTTAATATA	AAACATTATG	TTCAAGATCG	50
TTTATTGTTG	AACATAAATC	GCCTAAAGAT	TTATCAGAAT	GATCGTATTG	100
GTTTAATTGG	TAAAAATGGA	AGTGGAAAAA	CAACGTTACT	TCACATATTA	150
15 TATAAAAAAA	TTGTGCCTGA	AGAAGGTATT	GTAAAACAAT	TTTCACATTG	200
TGAACTTATT	CCTCAATTGA	AGCTCATAGA	ATCAACTAAA	AGTGGTGGTG	250
AAGTAACACG	AACTATATTT	CGGCAAGCGC	TTGATAAAAA	TCCAGAACTG	300
CTATTAGCAG	ATGAACCAAC	AACTAACTTA	GATAATAACT	ATATAGAAAA	350
ATTAGAACAG	GATTTAAAAA	ATTGGCATGG	AGCATTATTT	ATAGTTTCAC	400
20 ATGATCGCGC	TTTTTTAGAT	AACTTGTGTA	CTACTATATG	GGAAATTGAC	450
GAGGGAAGAA	TAAGTGAATA	TAAGGGGAAT	TATAGTAACT	ATGTTGAACA	500
AAAAGAATTA	GAAAGACATC	GAGAAGAATT	AGAATATGAA	AAATATGAAA	550
AAGAAAAGAA	ACGATTGGAA	AAAGCTATAA	ATATAAAAGA	ACAGAAAGCT	600
CAACGAGCAA	CTAAAAAACC	GAAAAACTTA	AGTTTATCTG	AAGGCAAAAT	650
25 AAAAGGAGCA	AAGCCATACT	TTGCAGGTAA	GCAAAAAGAA	TTACGAAAAA	700
CTGTAAAATC	TCTAGAAAAC	AGACTAGAAA	AACTTGAAAG	CGTCGAAAAG	750
AGAAACGAAC	TTCCTCCACT	TAAAATGGAT	TTAGTGAACT	TAGAAAGTGT	800
AAAAAATAGA	ACTATAATAC	GTGGTGAAGA	TGTCTCGGGT	ACAATTGAAG	850
GACGGGTATT	GTGGAAAGCA	AAAAGTTTTA	GTATTCGCGG	AGGAGACAAG	900
30 ATGGCAATTA	TCGGATCTAA	TGGTACAGGA	AAGACAACGT	TTATTAAAAA	950
AATTGTGCAT	GGGAATCCTG	GTATTTTCATT	ATCGCCATCT	GTCAAAATCG	1000
GTTATTTTAG	CCAAAAAATA	GATACATTAG	AATTAGATAA	GAGCATTTTA	1050
GAAAATGTTT	AATCTTCTTC	ACAACAAAAT	GAAACTCTTA	TTCGAACTAT	1100
TCTAGCTAGA	ATGCATTTTT	TTAGAGATGA	TGTTTATAAA	CCAATAAGTG	1150
35 TCTTAAGTGG	TGGAGAGCGA	GTTAAAGTAG	CACTAACTAA	AGTATTCTTA	1200
AGTGAAGTTA	ATACGTTGGT	ACTAGATGAA	CCAACAAACT	TTCTTGATAT	1250
GGAAGCTATA	GAGGCGTTTG	AATCTTTGTT	AAAGGAATAT	AATGGCAGTA	1300
TAATCTTTGT	ATCTCACGAT	CGTAAATTTA	TCGAAAAAGT	AGCCACTCGA	1350
ATAATGACAA	TTGATAATAA	AGAAATAAAA	ATATTTGATG	GCACATATGA	1400
40 ACAATTTAAA	CAAGCTGAAA	AGCCAACAAG	GAATATTAAA	GAAGATAAAA	1450
AACTTTTACT	TGAGACAAAA	ATTACAGAAG	TACTCAGTCG	ATTGAGTATT	1500
GAACCTTCGG	AAGAATTAGA	ACAAGAGTTT	CAAAACTTAA	TAAATGAAAA	1550
AAGAAATTTG	GATAAATAA				1569

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2) INFORMATION FOR SEQ ID NO: 1624

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624

5

TTCTTTAATG CTCGTAGATG AACCTA

26

10 2) INFORMATION FOR SEQ ID NO: 1625

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1625

TTTTCGTATT CTTCTTGTTG CTTTC

25

25

2) INFORMATION FOR SEQ ID NO: 1626

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626

AGGAATGATT AAGCCCCCTT CAAAAA

26

40

2) INFORMATION FOR SEQ ID NO: 1627

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627

TTACATTGCG ACCATGAAAT TGCTCT

26

2) INFORMATION FOR SEQ ID NO: 1628

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
10 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: U82085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628

20	ATGCTTAAAA	TCGACATGAA	GAATGTAAAA	AAATATTATG	CAGATAAATT	50
	AATTTTAAAT	ATAAAAGAAC	TAAAGATTTA	TAGTGGGGAT	AAAATAGGTA	100
	TTGTAGGTAA	GAATGGAGTT	GGCAAAACAA	CACTTTTAAA	AATAATAAAA	150
	GGACTAATAG	AGATTGACGA	AGGAAATATA	ATTATAAGTG	AAAAACAAC	200
	TATTAAATAT	ATCTCTCAAT	TAGAAGAACC	ACATAGTAAG	ATAATTGATG	250
25	GAAAATATGC	TTCAATATTT	CAAGTTGAAA	ATAAGTGGAA	TGACAATATG	300
	AGTGGTGGTG	AAAAAAGTAG	ATTTAAACTA	GCAGAGGGAT	TTCAAGATCA	350
	ATGTTCTTTA	ATGCTCGTAG	ATGAACCTAC	AAGTAATTTA	GATATCGAAG	400
	GAATAGAGTT	GATAACAAAT	ACTTTTAAAG	AGTACCGTGA	TACTTTTTTG	450
	GTAGTATCTC	ATGATAGAAT	TTTTTTAGAT	CAAGTTTGTA	CAAAAATTTT	500
30	TGAAATTGAA	AATGGATATA	TTAGAGAATT	CATCGGTAAT	TATACAAACT	550
	ATATAGAGCA	AAAAGAAATG	CTTCTACGAA	AGCAACAAGA	AGAATACGAA	600
	AAGTATAATT	CTAAAAGAAA	GCAATTGGAG	CAAGCTATAA	AGCTAAAAGA	650
	GAATAAGGCG	CAAGGAATGA	TTAAGCCCCC	TTCAAAAACA	ATGGGAACAT	700
	CTGAATCTAG	AATATGGAAA	ATGCAACATG	CTACTAAACA	AAAAAAGATG	750
35	CATAGAAATA	CGAAATCGTT	GGAAACACGA	ATAGATAAAT	TAAATCATGT	800
	AGAAAAAATA	AAAGAGCTTC	CTTCTATTAA	AATGGATTTA	CCTAATAGAG	850
	AGCAATTTCA	TGGTCGCAAT	GTAATTAGTT	TAAAAAACTT	ATCTATAAAA	900
	TTTAATAATC	AATTTCTTTG	GAGAGATGCT	TCATTTGTCA	TTAAAGGTGG	950
	AGAAAAGGTT	GCTATAATTG	GTAACAATGG	TGTAGGAAAA	ACAACATTGT	1000
40	TGAAGCTGAT	TCTAGAAAAA	GTAGAATCAG	TAATAATATC	ACCATCAGTT	1050
	AAAATTGGAT	ACGTCAGTCA	AAACTTAGAT	GTTCTACAAT	CTCATAAATC	1100
	TATCTTAGAA	AATGTTATGT	CTACCTCCAT	TCAAGATGAA	ACAATAGCAA	1150
	GAATTGTTCT	AGCAAGATTA	CATTTTTATC	GCAATGATGT	TCATAAAGAA	1200
	ATAAATGTTT	TGAGTGGTGG	AGAACAAATA	AAGGTTGCTT	TTGCCAAGCT	1250
45	ATTTGTTAGC	GATTGTAATA	CATTAATTCT	TGATGAACCA	ACAAACTATT	1300
	TGGATATCGA	TGCTGTTGAG	GCATTAGAAG	AATTGTTAAT	TACCTATGAA	1350
	GGTGTTGTGT	TATTTGCTTC	CCATGATAAA	AAATTTATAC	AAAACCTAGC	1400
	TGAACAATTG	TTAATAATAG	AAAATAATAA	AGTGAAAAAA	TTCGAAGGAA	1450
	CATATATAGA	ATATTTAAAA	ATTAAAGATA	AACCAAAATT	AAATACAAAT	1500
50	GAAAAAGAAC	TCAAAGAAAA	AAAGATGATA	CTAGAAATGC	AAATTTCATC	1550
	ATTATTAAGT	AAAATCTCAA	TGGAAGAAAA	TGAAGAAAAA	AACAAAGAAT	1600
	TAGATGAAAA	GTACAAATTG	AAATTAAAAG	AATTGAAAAG	CCTAAATAAA	1650
	AATATTTA					1658

2) INFORMATION FOR SEQ ID NO: 1629

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629

AAGGGGAAAG TTTGGATTAC ACAACA

26

2) INFORMATION FOR SEQ ID NO: 1630

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630

GAACCACAGG GCATTATCAG AACC

24

2) INFORMATION FOR SEQ ID NO: 1631

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631

CGACGATGCT TTATGGTTTG T

21

2) INFORMATION FOR SEQ ID NO: 1632

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632

GTAAATTGTC CTATCTTGTC AACTC

26

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2) INFORMATION FOR SEQ ID NO: 1633

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 900 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(C) ACCESSION NUMBER: M36022

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633

ATGGAATTTA AATTACAAGA ATTAAATCTT ACTAACCAAG ATACAGGACC 50
ATATGGTATA ACCGTTTCAG ATAAGGGGAA AGTTTGGATT ACACAACATA 100
AAGCAAATAT GATAAGTTGC ATCAATTTAG ATGGAAAAAT TACAGAGTAC 150
30 CCACTACCGA CACCAGATGC AAAAGTCATG TGTTTAACTA TATCCTCAGA 200
TGGGGAAGTT TGGTTTACTG AGAATGCAGC AAACAAAATA GGGAGGATTA 250
CAAAAAAAGG GATTATTAAG GAATATACAT TGCCTAACCC AGATTCAGCA 300
CCCTACGGTA TTACAGAAGG ACCAAATGGA GATATATGGT TTACAGAAAT 350
GAATGGCAAC CGTATTGGAC GTATTACGGA CGACGGTAAA ATTCGTGAAT 400
35 ACGAGCTGCC TAATAAAGGA TCTTACCCTT CTTTATCAC TTTGGGTTCT 450
GATAATGCCC TGTGGTTCAC AGAAAATCAA AATAATGCTA TTGGTAGAAT 500
TACAGAAAGT GGGGATATTA CAGAGTTTAA AATTCCTACA CCTGCATCAG 550
GACCAGTTGG TATTACAAAG GGGAACGACG ATGCTTTATG GTTTGTGGAA 600
ATTATCGGTA ATAAGATAGG GCGAATAACT CCTCTGGGGG AAATTACCGA 650
40 ATTCAAAATT CCAACGCCAA ACGCTCGACC TCATGCAATT ACTGCTGGAG 700
CAGGAATTGA TTTATGGTTT ACTGAATGGG GGGCTAATAA AATAGGAAGG 750
CTGACAAGCA ATAATATAAT TGAGGAATAC CCAATTCAAA TCAAAAAGTGG 800
TGAACCACAT GGCATTTGTT TCGATGGTGA AACAATTTGG TTTGCAATGG 850
AGTGTGACAA GATAGGCAAA TTAACCTCTA TTAAGGATAA TATGGAGTGA 900
45

2) INFORMATION FOR SEQ ID NO: 1634

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634

TTAACTTGTC TATTCCCGAT TCAGG

25

10

2) INFORMATION FOR SEQ ID NO: 1635

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635

GCTGTGGCAA TGGATATTCT GTA

23

25

2) INFORMATION FOR SEQ ID NO: 1636

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636

TTCCTACCCC TGATGCTAAA GTGA

24

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2) INFORMATION FOR SEQ ID NO: 1637

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637

CAAAGTGCGT TATCCGAACC TAA

23

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2) INFORMATION FOR SEQ ID NO: 1638

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638

	GGTGGGGAAG	ACTGTCTTCA	TCCAGGAATT	GATTGTGAGT	CGTTCCACAT	50
	GCTCACCTAG	TTTTCGCTCG	ATCTTTTCAC	TAACGCAAAC	CATGTAGAAC	100
	AACATTGCCA	AGGCCACGG	TGGTTACTCC	GTCTTCACTG	GTGTTGGTGA	150
25	GCGTACTCGT	GAGGGTAACG	ATCTGTACCA	CGAAATGCAG	GAGACTGGTG	200
	TCATTAGCT	CGAGGGTGAA	TCCAAGGTCG	CACTGGTGTT	CGGACAGATG	250
	AACGAGCCCC	CCGGTGCCCG	TGCCCGTGTC	GCCCTTACCG	GTCTGACCAT	300
	TGCCGAGTAC	TTCCGTGACG	AGGAGGGTCA	GGACGTGCTG	CTCTTCATTG	350
	ACAACATTTT	CCGTTTCACC	CAGGCCGGTT	CTGAGGTGTC	TGCCCTTCTC	400
30	GGTCGTATCC	CCTCTGCCGT	CGGTTACCAG	CCCACCCTGG	CCGTCGACAT	450
	GGGTGGTATG	CAGGAGCGTA	TCACCACCAC	CAAGAAGGGT	TCTATTACCT	500
	CCGTCCARGC	CGTCTACGTC	CCCGCGA			527

35

2) INFORMATION FOR SEQ ID NO: 1639

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639

	ACTGTCTTGA	TTCAAGAACT	TATTAACAAC	ATTGCTAAAG	CCCATGGTGG	50
	TTACTCTATT	TTCTGTGGTG	TTGGTGAACG	TACTCGTGAA	GGTAACGATT	100

TATACCACGA AATGATGGAA ACTGGTGTCA TTAAACTTGA AGGTGACTCC 150
 AAGTGTGCTC TTGTATTCGG TCAAATGAAC GAACCTCCTG GTGCTCGTGC 200
 CCGTGTGCT TTAACCTGGT TAACCATTGC TGAATACTTC CGTGATGAAG 250
 AAGGTCAAGA TGTGTTACTT TTCATTGATA ACATTTTCCG TTCACTCAA 300
 5 GCTGGTCTG AAGTATCTGC CCTTTTAGGT CGTATTCCAT CTGCTGTAGG 350
 TTACCAACCC ACTTTATCTA CTGATATGGG TGGTATGCAA GAACGTATTA 400
 CTACTACCAA GAATGGTTCC ATTACCTCTG TACARGCCGT CTACGTCCCC 450
 GC 452

10

2) INFORMATION FOR SEQ ID NO: 1640

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 783 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462
 25 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640

ACGCCCTTAC GGTAACAA AGCAACGAAA ACGGAAGCAT GAACTTAACA 50
 30 TTTGAAGTTG CACTTCATTT AGGTGATGAT ACAGTTCGTA CAGTTGCGAT 100
 GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA GATACTGGTA 150
 AAGCAATCTC TGTAACAGTT GGTGATGCAA CACTTGGTCG TGTATTCAAC 200
 GTATTAGGTG ATGCAATTGA CTTAGATGGT GAACTTCCTG CGGATGTACA 250
 CCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA TTATCTACTA 300
 35 AAGTAGAAAT TCTTGAACT GGTATTAAAG TAGTAGACTT ACTTGCTCCT 350
 TACATTAAGG GTGGTAAGAT CGGCCTATTC GGTGGTGCCG GCGTAGGTAA 400
 AACAGTATTA ATCAAGAAT TAATTAACAA CATCGCACAA GAGCACGGTG 450
 GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTAGTTCGTA GGGTAATGAC 500
 TTATACCATG AAATGAGCGA TTCTGGCGTA ATCAAGAAAA CTGCGATGGT 550
 40 ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT GTTGCAATTAA 600
 CAGGTTTAAAC AATGGCTGAG CATTTCCTGT ATGAGCAAGG ACAAGACGTA 650
 CTTCTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCGG GTTCTGAAGT 700
 ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC CAACCAACAC 750
 45 TTGCAACAGA AATGGGTCAA TTACAAGAGC GTA 783

2) INFORMATION FOR SEQ ID NO: 1641

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL NRS-319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641

10 ATCTACAACG CCCTTACGGT AAAACAAAGC AACGAAAACG GAGCAAGCAT 50
 TAACTTAACA TTTGAAGTTG CACTTCATTT AGGTGATGAC ACAGTTCGTA 100
 CAGTTGCAAT GTCTTCCACA GATGGACTTG TTCGTGGCAC AGAAGTAGAA 150
 GATACTGGTA AAGCAATCTC TGTACCAGTT GGTGATGCAA CACTTGGTCG 200
 15 TGTATTCAAC GTATTAGGTG ATGCAATTGA CTTAGATGGT GATGTTCCCTG 250
 CGGATGTACG TCGTGATCCA ATTCACCGTC AAGCACCTGC ATTCGAAGAA 300
 CTATCTACTA AAGTAGAAAT TCTTGAACT GGTATTAAAG TAGTAGACTT 350
 ACTTGCTCCT TACATTAAGG GTGGTAAGAT CGGTCTATTC GGTGGTGCCG 400
 GTGTAGGTAA AACAGTATTA ATTCAGGAAT TAATTAACAA CATCGCACAA 450
 20 GAACACGGTG GTATCTCTGT ATTCGCTGGT GTAGGTGAGC GTACTCGTGA 500
 GGGTAACGAC TTATACCATG AAATGAGCGA TTCTGGCGTA ATTAAGAAAA 550
 CTGCGATGGT ATTCGGACAA ATGAATGAGC CACCTGGAGC ACGTCAACGT 600
 GTTGCAATTA CAGGTTTAAAC AATGGCTGAA CATTTCCGTG ATGAGCAAGG 650
 ACAAGACGTA CTATTGTTCA TCGATAACAT CTTCCGTTTC ACGCAAGCAG 700
 25 GTTCTGAAGT ATCTGCCCTT CTTGGTCGTA TGCCATCTGC GGTAGGTTAC 750
 CAACCAACAC TTGCAACAGA AATGGGTCAA TTACAAGAGC GTATTACATC 800
 TACAAATAAA GGATCTATCA CGT 823

30

2) INFORMATION FOR SEQ ID NO: 1642

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus mycoides*

(B) STRAIN: NRRL BD-15

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642

50 GATGGCGGAA AGCTACCAGA AATCTACAAC GCCCTTACGG TAAAACAAAG 50
 CAACGAAAAC GGAGCAAACA TTAAGTTAAC ATTTGAAGTT GCACTTCATT 100
 TAGGTGATGA TACAGTTCGT ACAGTTGCGA TGTCTTCCAC AGATGGACTT 150
 GTTCGTGGCA CAGAAGTAGA AGATACTGGT AAAGCAATCT CTGTACCAGT 200
 TGGTGATGTA ACACTTGGTC GTGTATTCAA CGTATTAGGT GATGCAATTG 250
 ACTTAGATGG TGAAGTTCCT GCGGATGTAC GTCGTGATCC AATTCACCGT 300
 CAAGCACCTG CATTGGAAGA ATTATCTACT AAAGTAGAAA TTCTTGAAAC 350

	TGGTATTAAA	G TAGTAGACT	T ACTTGCTCC	TTACATTAAAG	GGTGGTAAGA	400
	TTGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACAGTATT	AATTCAGGAA	450
	TTAATTAACA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCCGG	500
	TGTAGGTGAG	CGTACTCGTG	AAGGTAACGA	CTTATAACCAC	GAAATGAGCG	550
5	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCATTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGACGT	ACTACTGTTC	ATCGATAACA	700
	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	750
	ATGCCATCTG	CGGTAGGTTA	CCAGCCAACA	CTTGCAACAG	AAATGGGTCA	800
10	ATTACAAGAG	CGTATTACAT	CTACAAATA			829

2) INFORMATION FOR SEQ ID NO: 1643

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Bacillus pseudomyoides*
- (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643

30	AATCTACAAT	GCCCTTACGG	TAAAACAAAG	CAACGAAAAC	GGAGCAAGCA	50
	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	TAGGTGATGA	CACAGTTCGT	100
	ACAGTTGCGA	TGTCTTCCAC	AGATGGACTT	GTTCGTGGCA	CAGAAGTAGA	150
	AGATACTGGT	AAACCAATCT	CTGTACCGGT	TGGTGATGCA	ACACTTGGTC	200
	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	ACTTAGATGG	TGAAGTTCCT	250
35	GCGGATGTAC	GCCGTGATCC	AATTCACCGT	CAAGCACCTG	CGTTCGAAGA	300
	GTTATCTACG	AAAGTAGAAA	TTCTTGAAAC	TGGTATTAAA	G TAGTAGACT	350
	TACTTGCTCC	TTACATTAAA	GGTGGTAAAA	TCGGTCTATT	CGGTGGTGCC	400
	GGTGTAGGTA	AAACAGTATT	AATCCAGGAA	TTAATTAACA	ACATCGCACA	450
	AGAGCACGGT	GGTATTTCTG	TATTCGCTGG	TGTAGGTGAG	CGTACTCGTG	500
40	AAGGTAATGA	CTTATAACCAC	GAAATGAGCG	ATTCTGGCGT	AATCAAGAAA	550
	ACAGCGATGG	TATTCGGACA	AATGAACGAG	CCACCTGGTG	CACGTCAACG	600
	TGTTGCATTA	ACAGGATTAA	CAATGGCTGA	ACATTTCCGT	GATGAGCAAG	650
	GACAAGACGT	ACTATTGTTC	ATCGATAACA	TCTTCCGTTT	CACGCAAGCG	700
	GGTTCTGAAG	TATCTGCCCT	TCTTGGTCGT	ATGCCATCTG	CGGTAGGTTA	750
45	CCAACCAACT	CTTGCAACAG	AAATGGGTCA	ATTACAAGAG	CGTATTACAT	800
	CTACAAATAA	AGGATCTATC	ACG			823

50 2) INFORMATION FOR SEQ ID NO: 1644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomyoides*
- (B) STRAIN: NRRL B-617

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644

	GGAAAGCTAC	CTGAAATCTA	CAATGCCCTT	AGAATTAAAC	AAGACGCAGT	50
	TAACTTAACT	TTAGAAGTTG	CACTTCACTT	AGGTGATGAT	ACAGTTCGTA	100
15	CAGTTGCGAT	GTCTTCCACA	GACGGACTTG	TTCGTGGTAC	TGCAGTAGAA	150
	GATACTGGCA	AAGCGATTTT	TGTTCCAGTT	GGTGATGCAA	CACTTGGTCG	200
	TGTATTTAAC	GTATTAGGTG	ATGCAATTGA	CTTAGATGGT	GAGGTTCAG	250
	CAGATGTACG	CCGTGATCCA	ATTCACCGTC	AAGCACCTGC	ATTCGAAGAG	300
	TTATCTACAA	AAGTAGAAAT	TCTTGAAACT	GGTATTAAAG	TAGTAGACTT	350
20	ACTTGCTCCT	TACATTAAAG	GTGGTAAAT	CGGTCTATTC	GGTGGTGCCG	400
	GTGTAGGTAA	AACAGTATTA	ATTCAGGAAT	TAATTAAACAA	CATCGCACAA	450
	GAGCACGGTG	GTATCTCTGT	ATTCGCTGGT	GTAGGTGAGC	GTACTCGTGA	500
	AGGTAACGAC	TTATACCATG	AAATGAGCGA	TTCTGGCGTA	ATCAAGAAAA	550
	CTGCGATGGT	ATTCGGACAA	ATGAACGAGC	CACCTGGTGC	ACGTCAACGT	600
25	GTTGCATTAA	CAGGTTTAAAC	AATGGCTGAA	CATTTCCGTG	ATGAGCAAGG	650
	ACAAGACGTA	CTATTGTTCA	TCGATAACAT	CTTCCGTTTC	ACGCAAGCGG	700
	GTTCTGAA					708

30

2) INFORMATION FOR SEQ ID NO: 1645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- 35 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
- (B) STRAIN: ATCC 35567

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645

	GTACGATGCG	CTTGAAGTTC	AAAACGATGT	CAAAC TAGTG	CTGGAAGTTC	50
	AACAGCAGCT	CGGTGGTGGT	GTCGTTTCGTT	GTATCGCTAT	GGGTACCTCA	100
	GATGGCCTAA	GCCGCGGTCT	GAAAGTACTT	GATTTAGAAC	ACCCTATCGA	150
50	AGTTCCTGTC	GGTGTGGCAA	CTCTGGGCCG	TATTATGAAC	GTGCTTGGTG	200
	AGCCTATCGA	TATGAAGGGT	GACATTGGTG	AAGAAGAGCG	TTGGGCTATC	250
	CATCGCGCTG	CACCAAGCTA	CGAAGATTTA	TCCAGTGCTA	ACGAACTGCT	300
	GGAAACGGGC	ATCAAGGTTA	TCGACCTGAT	TTGTCCGTTT	GCCAAAGGCG	350

GTAAAGTTGG TCTGTTTGGT GGTGCCGGCG TAGGTAAAAC GGTAACATG 400
 ATGGAGCTGA TTCGTAATAT TGCGACTGAG CACTCAGGTT ACTCTGTATT 450
 TGCCGGCGTT GGTGAGCGTA CTCGTGAGGG TAATGACTTC TACCACGAAA 500
 TGACAGAATC TAACGTATTA GACAAAGTAT CTCTGGTTTA TGGCCAAATG 550
 5 AATGAGCCAC CGGGAAACCG TCTGCGCGTT GCGTTAACCG GCCTGACCAT 600
 GGCGGAAAAA TTCCGTGATG AAGGCCGTGA CGTTCTGCTG TTTATCGATA 650
 ACATTTATCG TTATACCTTA GCCGGTACAG AAGTATCAGC ACTGTTAGGT 700
 CGTATGCCAT CAGCGGTAGG TTACCAACCA ACGCTGGCGG AAGAGATGGG 750
 TACACTGCAA GAACGTATCA CYTCAACC 778
 10

2) INFORMATION FOR SEQ ID NO: 1646

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Buttiauxella agrestis*
 25 (B) STRAIN: ATCC 33320
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646

GATGCCGTAC CAAAAGTGTA CGACGCTCTT GAGGTTACAA ATGGTAAAGA 50
 30 CCGTCTGGTG CTGGAAGTTC AGCAACAGTT AGGTGGTGGC GTAGTGCGTA 100
 CTATCGCCAT GGGTACTTCT GATGGTTTGC GTCGTGGTCT GGAAGTTTCT 150
 AACCTCGATC ACCCAATTGA AGTGCCAGTA GGTAAGCAA CTCTGGGCCG 200
 TATCATGAAC GTCCTGGGCG AGCCTATCGA CATGAAAGGC GATATCGGCG 250
 AAGAAGAGCG TTGGGCGATT CACCGTGCTG CTCCTAGCTA CGAAGAACTG 300
 35 TCTAGCTCCC AGGATCTGCT GGAAACCGGC ATCAAAGTAA TGGACCTGAT 350
 TTGCCCCTTC GCTAAGGGTG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG 400
 TGGGTAAAAC TGTAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG 450
 CACTCCGGTT ACTCAGTGTT TGCAGGCGTG GGGGAACGTA CTCGTGAGGG 500
 TAACGACTTC TACCATGAAA TGACCGATTC CAACGTTCTG GACAAAGTAT 550
 40 CACTGGTTTA TGGCCAGATG AACGAGCCAC CAGGTAACCG TCTGCGCGTT 600
 GCGTTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA 650
 CGTTCTGCTG TTCGTTGATA ACATTTACCG TTATACCCTG GCCGGTACAG 700
 AAGTATCTGC GCTGCTGGGT CGTATGCCAT CTGCGGTAGG TTACCAGCCA 750
 ACTCTGGCAG AAGAGATGGG TGTTTTGCAG GAGCGTATTA CCTCCACCAA 800
 45 AACTGG 806

2) INFORMATION FOR SEQ ID NO: 1647

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1122 bases
 (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
(B) STRAIN: ATCC 36586

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647

	GAAACCGTTG	TTGACACTGG	TTCCCCAATC	ACCGTCCCAG	TTGGTCGTGA	50
	AACCTTGGGT	CGTATCATT	ACGTTATCGG	TGAACCAATC	GATGAACGTG	100
	GTCCAATCAA	CACCAAGCAA	AGAAACCCAA	TCCATGCTGA	TCCTCCTTCA	150
15	TTTGCTGAAC	AATCCACTTC	TGCTGAAGTT	TTAGAAACCG	GTATTAAAGT	200
	TGTCGATTTA	TTGGCTCCTT	ATGCCAGAGG	TGGTAAAATT	GGTTTATTCG	250
	GTGGTGCCGG	TGTCGGTAAA	ACCGTCTTTA	TCCAAGAATT	GATTAACAAC	300
	ATTGCTAAAG	CTCATGGTGG	TTTCTCAGTC	TTCACCGGTG	TCGGTGAAAG	350
	AACCAGAGAA	GGTAACGATT	TATACCGTGA	AATGAAAGAA	ACCGGTGTCA	400
20	TTAACTTGGA	AGGTGACTCT	AAAGTCGCTT	TAGTCTTCGG	TCAAATGAAC	450
	GAACCTCCAG	GTGCTAGAGC	CCGTGTTGCC	TTAACCGGTC	TAACCATTCG	500
	TGAATACTTC	AGAGATGAAG	AAGGTCAAGA	TGTCTTGTTA	TTCGTTGATA	550
	ACATTTTCAG	ATTCACCCAA	GCTGGTTCAG	AAGTCTCTGC	CTTATTAGGT	600
	CGTATTCCAT	CTGCTGTCGG	TTATCAACCA	ACCTTGGCCA	CTGATATGGG	650
25	TTTGTTGCAA	GAACGTATCA	CCACCACCAG	AAAAGGTTCC	GTCACCTCTG	700
	TCCAAGCTGT	TTATGTCCCA	GCTGATGATT	TGACTGATCC	TGCCCCAGCC	750
	ACCACTTTTCG	CGCATTTGGA	TGCTACTACT	GTCTTGCTCTC	GTGGTATCTC	800
	AGAATTGGGT	ATCTACCCAG	CTGTCGATCC	ATTGGATTCC	AAATCAAGAT	850
	TATTAGATGC	CGCTGTTGTT	GGTCAAGAAC	ATTACGATGT	TGCTACTCAA	900
30	GTTCAACAAA	CTTTACAAGC	CTACAAATCT	TTACAAGATA	TTATCGCTAT	950
	TTTAGGTATG	GATGAATTAT	CAGAACAAGA	TAAATTGACC	GTTGAAAGAG	1000
	CTAGAAAGAT	CCAACGTTTC	TTATCTCAAC	CATTTGCTGT	CGCTGAAGTT	1050
	TTCACTGGTA	TTCCAGGTAG	ATTAGTTAGA	TTGAAAGAAA	CCGTTGCTTC	1100
	ATTCAGAGAC	GTTTTAGCTG	GT			1122

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2) INFORMATION FOR SEQ ID NO: 1648

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: ATCC 700677

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648

	TACGTCTCTT	ACCCTGACGA	TGATTTGCAA	GTCGCATCTA	CGGTCGTAGA	50
	TGTTTTCAAAT	GGTAAAGTCA	TCGCCCCAACT	TGGAGCTCGT	CACCAAGCAA	100
	GTAACGTTTC	ATTTGGTACC	AACCAAGCTG	TGGAAACCAA	TCGTGACTGG	150
	GGATCAACTA	TGAAACCAAT	CACAGACTAT	GCTCCTGCCT	TGGAGTACGG	200
5	TGTCTACGAT	TCAACTGCTA	CTATCGTTCA	CGATGAGCCC	TATAACTACC	250
	CTGGGACAGA	TATCCCTCTC	TATAACTGGG	ATCGAGCATA	TTTCGGTAAT	300
	ATTACTCTGC	AATATGCCCT	TCAACAATCT	CGTAACGTAC	CTGCCGTTGA	350
	AACACTAAAC	AAGGTCGGTC	TAGATAAGGC	TAAAACCTTC	CTTAATGGTC	400
	TTGGTATCGA	CTATCCAAGC	ATGCATTATG	CAAACGCCAT	TTCAAGTAAT	450
10	ACAACCTGAAT	CCAACAAAAA	ATATGGTGCA	AGTAGTGAAA	AAATAGCTAC	500
	CGCCTATGCC	GCATTCGCAA	ATGGTGGTAT	TTACCACAAA	CCAATGTACA	550
	TCAATAAAGT	TGTCTTTAGC	GATGGTAGCG	AAAAAGAATT	TTCTGACCCT	600
	GGCACAAGAG	CCATGAAAGA	AACGACTGCT	TACATGATGA	CAGAAATGAT	650
	GAAAACAGTC	TGGACGTACG	GAAGTGGTCG	TGGTGCCTAC	CTGCCTTGGC	700
15	TTCTCAAGC	TGGTAAAAACA	GGTACCTCTA	ACTATACTGA	CGAAGAAATT	750
	GAAAAGTATA	TCAAGAACAC	TGGTTACGTA	GCTCCAGATG	AAATGTTTGT	800
	GGGTTATACC	CGT				813

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2) INFORMATION FOR SEQ ID NO: 1649

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter lari*
 (B) STRAIN: ATCC 43675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649

	ATTAATGAAG	CTATTGTTGT	TAATTATGAA	TTAGAAGGAA	AAGAATGCAA	50
	GCTAGTTCTT	GAAGTAGCTG	CACATTTAGG	CGATAATAAA	GTAAGAACCA	100
	TCGCTATGGA	TATGACAGAT	GGTCTTGTTA	GAGGTTTAAC	AGCCGTCGCA	150
40	ACTGGAAATC	CAATTAGTGT	TCCAGTAGGC	GAAAAAGTTC	TTGGAAGAAT	200
	TTTTAATGTA	ACGGGTGATT	TGATTGATGA	GGGCGAAGAA	ATCAATTTTG	250
	ATAAGCACTG	GTCAATTCAT	AGAGATCCAC	CTCCATTTGA	AGAACAAAGT	300
	ACAAAAAGCG	AAATCTTTGA	AACAGGTATA	AAGGTTGTTG	ATTTGCTAGC	350
	TCCTTATGCT	AAAGGTGGAA	AAGTTGGTCT	TTTTGGTGGT	GCAGGTGTTG	400
45	GTAAAACCGT	TATTATTATG	GAATTAATTC	ACAATGTTGC	ATTTAAACAT	450
	AGCGGATATT	CTGTTTTTGC	AGGTGTTGGC	GAAAGAAGTC	GTGAGGGTAA	500
	TGACCTTTAC	AATGAAATGA	AAGAAAGTAA	TGTATTAGAT	AAAGTTGCAT	550
	TGTGTTATGG	TCAAATGAAT	GAACCACCAG	GGGCAAGAAA	TCGTATAGCT	600
	TTAACAGGTC	TTACTATGGC	TGAGTATTTT	AGAGATGAAA	TGGGACTTGA	650
50	TGTTTTAATG	ATTATTGATA	ATATTTTCAG	ATTTTCTCAA	TCAGGCTCAG	700
	AAATGTCAGC	ACTTTTAGGA	AGAATTCCTT	CAGCTGTTGG	TTATCAACCA	750
	ACCTTAGCTA	GTGAAATGGG	TAAGTCCCAA	GAAAGAATTA	CTTCAACCAA	800
	GAAAGGATCT	ATT				813

2) INFORMATION FOR SEQ ID NO: 1650

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650

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GGTGGGGAAG ACTGTGTTCA TTCAGGAATT GATTGTAAGT TCTGTTATCA      50
ACTAAAGCCG ACAGCGGTTG CTGATATGCT CTAGAACAAC ATTGCTAAGG      100
CTCACGGTGG TTA CTCCGTG TTA CTGGTG TCGGTGAGCG TACCCGTGAG      150
20 GGTAACGATT TGTACCATGA AATGCAAGAG ACCCGTGTC TCAACTCGA      200
CGGAGAGTCC AAGGTCGCTC TTGTCTTCGG TCAAATGAAC GAGCCCCCTG      250
GTGCCCCGTG CCGTGTTGCC CTTACCGGTT TGACCATTC TGAATACTTC      300
CGTGACGAGG AAGGCCAAGA CCGTAGGCTT CATGCTTCTA TCGCTAGGGG      350
CGTGTGATAC AGGAGGCTAA TCGCTTTTCT AGTGCTTCTC TTTATTGACA      400
25 ACATTTTCCG TTCACTCAA GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT      450
CGTATTCCTT CCGCTGTCGG TTACCAACCT ACTCTCGCCG TCGACATGGG      500
TGTTATGCAG GAACGTATCA CCACCACCAC CAAGGGATCC ATTACTTCAG      550
TGCARGCCGT CTACGTCCCC                                     570

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2) INFORMATION FOR SEQ ID NO: 1651

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651

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TGTCTTCATC CAGGAGTTAA TTGTACGTTT TTTGTCTGCC TACTATAATA      50
GACGAAGAAA TATTTTGTAT TATTTTCTTA ATAATTCAAA TAGAACAACA      100
50 TTGCCAAAGC CCACGGTGGT TACTCTGTCT TCACTGGTGT TGGCGAGCGG      150
ACCCGTGAAG GAAACGATCT GTACCACGAA ATGCAGGAGA CCCGTGTCAT      200
CCAGCTCGAT GGCGAGTCCA AGGTCGCCCT CGTCTTCGGT CAAATGAACG      250
AACCCCCCGG AGCCCGTGCC CGTGTTGCC TCACCTGGTCT GACCGTTGCT      300

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	GAATACTTCC	GTGACGAGGA	AGGTCAAGAT	GGTGCGTATA	TATATATTCG	350
	CCAGTAATTT	GACTCGAAGC	TCCACTCACA	CATATATTAG	TGCTCCTCTT	400
	CATCGACAAC	ATTTTCCGCT	TCACCCAGGC	AGGTTCCGAA	GTGTCCGCCC	450
	TGCTCGGCCG	TATCCCCTCC	GCCGTCGGTT	ACCAGCCCAC	CCTCGCTGTC	500
5	GACATGGGTA	TGATGCAGGA	ACGTATCACC	ACCACCACCA	AGGGCTCCAT	550
	CACCTCCGTG					560

10 2) INFORMATION FOR SEQ ID NO: 1652

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652

25	CCACAAGTGT	ACAGCGCCCT	TGAGGTAAAA	AATGGTGATG	CTCGTCTGGT	50
	GCTGGAAGTT	CAGCAGCAGC	TGGGCGGTGG	CGTGGTTCGT	ACCATCGCCA	100
	TGGGTCTTTC	AGACGGCCTT	AAGCGTGGTC	TGGAAGCCGT	TGACCTTCAG	150
	CACCCAATTG	AAGTACCGGT	AGGTACTGCC	ACACTTGGCC	GTATCATGAA	200
30	CGTGCTGGGT	GAGCCGATCG	ATATGAAAGG	CGACATTGGC	GAAGAAGAGC	250
	GCTGGGCGAT	TCACCGCTCT	GCACCTTCTT	ACGAAGATCA	GTCGAACCTCT	300
	CAGGATCTGC	TGGAAACCGG	CATCAAGGTG	ATTGACCTGA	TGTGTCCGTT	350
	CGCCAAGGGC	GGTAAAGTCG	GCTTGTTCCG	TGGTGCGGGC	GTAGGTAAAA	400
	CCGTCAACAT	GATGGAGCTT	ATTCGTAACA	TTGCGGCTGA	GCACTCAGGT	450
35	TTCTCGGTAT	TTGCCGGTGT	GGGTGAGCGT	ACCCGTGAAG	GTAACGACTT	500
	CTACCACGAA	ATGACCGACT	CCAACGTTAT	CGACAAAGTT	TCGCTGGTCT	550
	ATGGTCAGAT	GAACGAGCCA	CCGGGTAAAC	GTCTGCGCGT	TGCGCTGACC	600
	GGTCTGACCA	TGGCGGAGAA	GTTCCGTGAC	GAAGGTCGTG	ACGTACTGCT	650
	GTTTATCGAT	AACATCTATC	GTTACACCTT	GGCCGGTACT	GAAGTCTCCG	700
40	CTCTGCTGGG	TCGTATGCCT	TCTGCGGTAG	GTTACCAGCC	AACGCTGGCG	750
	GAAGAGATGG	GCGTTCTGCA	GGAACGTATC			780

45 2) INFORMATION FOR SEQ ID NO: 1653

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fonsecaea pedrosoi*

(B) STRAIN: ATCC 18831

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653

TGTGTTTCATT CAGGAGCTGA TTGTGAGTAC CCCGGAGATT TTCCTGCGAT 50
 TGCGCATGAA GCAAGCGCTG ACGTCCATCT AGAACAACAT CGCCAAGGCT 100
 10 CACGGTGGTT ACTCCGTGTT CTGCGGTGTC GGCGAGCGTA CTCGTGAGGG 150
 TAACGATTTG TACCACGAAA TGCAGGAGAC CGGTGTCATC AACCTCGAGG 200
 GCGAGTCCAA GGTGCGCCCT GTCTTCGGTC AGATGAACGA GCGCCCGGGA 250
 GCGCGTGCCC GTGTCGCCCT TACTGGTCTT ACCGTCGCTG AGTAAGTTTT 300
 GACAACCAGA AGCGAGTATT GCCACAATTA CTGACTAAAA ATCAAGATAT 350
 15 TTCCGTGACG AGGAGGGCCA GGATGTGCTT CTCTTCATTG ACAACATTTT 400
 CCGTTTCACC CAGGCCGGTT CTGAGGTGTC CGCTCTTCTC GGCCGTATTC 450
 CCTCTGCCGT CGGTTACCAG CCCACTCTCG CCGTCGACAT GGGTATGATG 500
 CAGGAGCGTA TCACCACCAC CCAGAAGGGT TCCATCACTT CCGTC 545

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2) INFORMATION FOR SEQ ID NO: 1654

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 564 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium moniliforme*

(B) STRAIN: WSA-213

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654

TGTGTTTATT CAGGAGCTCA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCTGTCTT CACTGGTGTC GGTGAGCGAA CCCGTGAGGG TAACGATCTG 100
 40 TACCACGAAA TGCAGGAGAC TTCCGTTATT CAGCTTGATG GCGAGTCCAA 150
 GGTTGCCCTG GTTTTTCGGTC AGATGAACGA GCGCCCTGGA GCTCGTGCCC 200
 GTGTCGCTCT TACCGGGTAA GTTGATAGAT AGTGCCTTCC CTTCCTGTTT 250
 CAACACCTCA ACACCACCAC TCCCCAAGAC ATTGCTACTC ATACTGCACC 300
 ATGATATTAT ATTTACGCCT CTTGGACGCT AGCTAATGTT GTATCGACAG 350
 45 TTTGACTGTT GCTGAGTACT TCAGAGACGA GGAGGGTCAG GACGTGCTGC 400
 TTTTCATTGA CAACATTTTC CGATTCACTC AGGCCGGTTC CGAGGTGTCT 450
 GCCCTTCTCG GTCGTATCCC CTCTGCCGTC GGTACCAGC CCACTCTGGC 500
 CGTCGACATG GGTGGTATGC AGGAGCGTAT TACCACCACC ACCAAGGGTT 550
 CCATTACCTC AGTC 564

50

2) INFORMATION FOR SEQ ID NO: 1655

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 776 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655

15 CGTACCGCGC GTGTACGAGG CTCTTGAGGT ACAAATGGT AGTGAGAATC 50
 TGGTGCTGGA AGTTCAGCAG CAGCTCGGCG GCGGTATTGT TCGTACCATC 100
 GCCATGGGTT CTTCCGACGG TCTGCGTCGC GGTCTGGAAG TCAAAGACCT 150
 CGAGCATCCG ATCGAAGTCC CGGTAGGTAA AGCAACGCTG GGTCGTATCA 200
 20 TGAACGTACT GGGCCAACCG GTAGACATGA AAGGCGACAT CGGCGAAGAA 250
 GAGCGTTGGG CGATTACCG CGCAGCGCCT TCCTACGAAG AGTTGTCAAA 300
 CTCTCAGGAA CTGCTGGAAA CCGGCATCAA AGTTATCGAC CTGATGTGTC 350
 CGTTTGCGAA GGGCGGTAAA GTTGGTCTGT TCGGTGGTGC GGGTGTAGGT 400
 AAAACCGTAA ACATGATGGA GCTGATCCGT AACATCGCGA TCGAGCACTC 450
 25 CCGTTACTCC GTGTTTGCGG GCGTAGGTGA ACGTACTCGT GAGGGTAACG 500
 ACTTCTACCA CGAAATGACC GACTCCAACG TTATCGATAA AGTATCCCTG 550
 GTGTATGGCC AGATGAACGA GCCGCCGGGA AACCGTCTGC GCGTTGCGCT 600
 GACCGGCCTG ACCATGGCTG AGAAGTTCCG TGACGAAGGT CGTGACGTTT 650
 TGCTGTTCGT CGATAACATC TATCGTTACA CCCTGGCCGG TACTGAAGTA 700
 30 TCCGCACTGC TGGGTCGTAT GCCTTCAGCG GTAGGTTACC AGCCGACTCT 750
 GGC GGAAGAG ATGGGCGTTC TGCAGG 776

35 2) INFORMATION FOR SEQ ID NO: 1656

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 45 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Microsporium audouinii*
 (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656

50 GTGTTTCATCC AGGAGTTGAT TGTAAGTGAT TATATTCCCC TAGAAAGAAA 50
 TGTTTTGAAC AAAAGTCTCG AATTAGAAAA TTCTTTTCAG ATACTAATTT 100
 ACTATAGAAC AACATTGCCA AGGCTCACGG TGGTTACTCC GTCTTCACCG 150

GTGTCGGAGA GCGAACCCGT GAAGGAAACG ATCTGTACCA TGAAATGCAG 200
 GAAACTCGTG TCATCCAAC T GATGGCGAG TCCAAGGTCG CCCTGGTCTT 250
 CGGT CAGATG AACGAGCCCC CAGGTGCCCC TGCCCGTGTT GCTCTTACTG 300
 GTTTGACCAT TGCTGAGTAC TTCCGTGATG AGGAAGGTCA AGACGGTATG 350
 5 TTCTTTAAAT TAGATATCTT CTGGAGAAAC AGCGTCTAAC AAATTCTTCC 400
 AGTGCTTCTC TTCATCGACA ACATCTTCCG TTTCAC TCAG GCTGGTTCCG 450
 AAGTGTCTGC CCTGCTTGGT CGTATTCCAT CTGCCGTCGG TTACCAACCC 500
 ACTCTTGCCG TCGACATGGG TGGTATGCAG GAACGTATTA CCACCACCAA 550
 GAAGGGATCC ATTACCTCCG TC 572
 10

2) INFORMATION FOR SEQ ID NO: 1657

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 790 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Obesumbacterium proteus*
 25 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657

GCCTAAAGTG TATAACGCAC TTGAGGTGAA AGGCGGTGCC ACTAAACTGG 50
 30 TACTGGAAGT TCAGCAGCAG CTAGGCGGCG GCGTTGTACG CTGTATCGCT 100
 ATGGGTACTT CTGACGGTCT GCGTCGCGGA CTGGACGTTG TTGACCTGGA 150
 GCACCCGATT GAAGTCCCAG TAGGTAAAGC GACCTTAGGC CGCATTATGA 200
 ACGTACTGGG TGAGCCAATT GATATGAAGG GTGATATCGG CGAAGAAGAT 250
 CGCTGGGCTA TTCACCGTGA AGCTCCAAGC TACGAAGAAC TGTCTAACTC 300
 35 GCAAGAACTG CTGGAAACCG GTATCAAGGT AATGGACTTG ATTTGTCCGT 350
 TCGCTAAGGG CCGTAAAGTC GGTCTGTTCG GTGGTGCGGG TGTTGGTAAA 400
 ACAGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG AGCACTCAGG 450
 TTACTCTGTA TTTGCCGGCG TGGGTGAACG TACTCGTGAG GGTAACGACT 500
 TCTACCACGA AATGACCGAC TCCAACGTAT TGGACAAAGT ATCACTGGTT 550
 40 TATGGCCAGA TGAACGAGCC ACCAGGAAAC CGTCTGCGCG TTGCGCTGAC 600
 CGGTCTGACT ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT GACGTACTGC 650
 TGTTTCATCGA TAACATCTAC CGTTATACCT TGGCCGGTAC CGAAGTATCT 700
 GCACTGCTGG GTCGTATGCC TTCTGCGGTA GGTTATCAGC CAACGCTGGC 750
 45 GGAAGAGATG GGTGTTCTGC AAGAACGTAT CACCTCTACC 790

2) INFORMATION FOR SEQ ID NO: 1658

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paracoccidioides brasiliensis*

(B) STRAIN: ATCC 200443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658

10 TGTCTTCATT CAGGAGCTTA TCAACAACAT CGCCAAGGCC CACGGTGGTT 50
 ACTCCGTCTT CACTGGTGTG GGAGAGCGCA CTCGTGAGGG AAACGACTTG 100
 TATCACGAGA TGCAAGAGAC TTCCGTTATC CAGCTCGAAG GCGAATCCAA 150
 GGTGCCCCTC GTCTTCGGTC AAATGAACGA GCCTCCGGGT GCTCGTGCTC 200
 15 GTGTTGCTCT CACCGGTCGT AAGTGCTCCT TCCCAGATT CTCTTCCCCA 250
 GTTTCTGGAC CCACTTTTTC CTTCCACCAC CATTCTACTG GGTAGGACCA 300
 AGATAGCACT GCCTATTCTG GTGCCTTCCT ACCGCCTACT CTACTGCCTA 350
 TTCCACCACC TTTTCTACCG CCTCTTCTAC TTGCTATTGT ATACTAACTT 400
 ACTCAAACAG TTACTATTGC TGAGTACTTC CGTGACGCTG AGGGCCAGGA 450
 20 TGTGCTTCTC TTCATCGACA ACATTTTCCG TTTCACCCAG GCCGGTCCG 500
 AGGTGTCCGC TCTTCTCGGT CGTATCCCTT CCGCCGTCGG TTACCAGCCC 550
 ACCCTTGCCG TCGACATGGG TGGTATGCAG GAGCGTATCA CCACCACCAA 600
 GAAGGGATCC ATTACCTCCG TC 622

25

2) INFORMATION FOR SEQ ID NO: 1659

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Plesiomonas shigelloides*

(B) STRAIN: ATCC 14029

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659

GACGCTGTAC CTCAGGTGTA CGATGCACTG ACAGTTGAGG GTGCTGAGCT 50
 GGTACTGGAA GTGCAGCAGC AGCTGGGTGG TGGTGTGTT CGCTGTATCG 100
 45 CGATGGGTGC CTCTGATGGC CTCAAGCGCG GTCTGAAAGC GCACAATACT 150
 GGTGCTCCTA TCACTGTACC GGTGGGTGTG GAAACACTGG GCCGGATCAT 200
 GGATGTGTTG GGTAACCCGA TTGACCAGAA AGGTCCAATC GGTGAACAAG 250
 ATCGCTGGGT GATCCACCGT GAAGCACCAA GCTACGAAGA TCAGGCTAAC 300
 AGCACTGAAC TGCTGGAAAC CGGTATCAAG GTTATCGACC TGGTATGCCC 350
 50 GTTTGCGAAA GGCGGTAAAG TCGGTCTGTT CGGTGGTGCC GGTGTAGGTA 400
 AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC 450
 GGTTATTCCG TGTTTTCGGG CGTGGGTGAG CGTACCCGTG AAGGTAACGA 500
 CTTCTACCAC GAAATGACAG ACTCCAACGT ACTGGACAAA GTATCCCTGG 550

	TGTACGGTCA	GATGAACGAG	CCGCCAGGTA	ACCGTCTGCG	CGTAGCACTG	600
	ACCGGCCTGA	CCATTGCGGA	GAAATTCCGT	GATGAAGGTC	GTGACGTACT	650
	GCTGTTTCATC	GATAACATCT	ACCGTTATAC	CCTGGCGGGG	ACCGAAGTAT	700
	CGGCACTGCT	GGGCCGTATG	CCTTCTGCGG	TAGGTTATCA	GCCAACGCTG	750
5	CGGGAAGAGA	TGGGTGTACT	GCAAGAGCGT	ATTACCTCTA	CCCG	794

2) INFORMATION FOR SEQ ID NO: 1660

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660

25	AGGTATATGA	CGCTSTGAAG	ATCACAGGTG	AAGGCGCCTG	TAATGGTTTG	50
	GTGCTGGAAG	TTCAGCAACA	GCTAGGCGGT	GGTGTAGTTC	GTACTATCGC	100
	TATGGGTTCT	TCTGATGGTC	TGCGTCGTGG	TCTTGAGGTT	GTAACTCAG	150
	GTTCACCTAT	TTCTGTTCCCT	GTTGGTACCG	CCACGCTTGG	CCGTATCATG	200
	AACGTATTAG	GTGAGCCTAT	TGATGAAGCG	GGTCCAATCG	GTGAAGAAGA	250
30	GCGTTATGTT	ATTCACCGTG	CAGCACCTTC	ATATGAAGAT	CAATCGAACA	300
	CTACTGAACT	GTTAGAGACA	GGTATCAAGG	TTATTGACCT	TGTTTGTCCA	350
	TTCGCTAAGG	GTGGTAAAGT	AGGTCTGTTC	GGTGGTGCGG	GTGTTGGTAA	400
	AACAGTTAAC	ATGATGGAAC	TGATTAACAA	CATCGCTAAA	GCTCACTCGG	450
	GTCTTTCCGGT	GTTCGCCCGGT	GTGGGTGAAC	GTACTCGTGA	AGGTAACGAC	500
35	TTCTACTACG	AGATGAAAGA	TTCTGGCGTT	CTCGACAAAG	TGGCCATGGT	550
	TTATGGTCAG	ATGAACGAGC	CACCAGGAAA	CCGTTTACGC	GTAGCACTGT	600
	CAGGTCTGAC	AATGGCTGAG	AAGTTCCGTG	ACGAAGGTCG	TGACGTATTG	650
	TTGTTTCGTTG	ACAACATCTA	CCGTTATACC	TTAGCCGGTA	CTGAAGTATC	700
	TGCACTGTTA	GGCCGTATGC	CTTCTGCGGT	AGGTTATCAA	CCAACATTGG	750
40	CTGAAGAAAT	GGGCGTTCTG	CAAGAGCGTA	TTACTTCAAC	TAAGACGGG	799

2) INFORMATION FOR SEQ ID NO: 1661

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661

TGGGAAGCGA AAATCCTG

18

5.

2) INFORMATION FOR SEQ ID NO: 1662

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 774 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter curvus*
 (B) STRAIN: ATCC 35224

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662

CTATGCCTCA AACTAGAGAG CATATCTTGC TATCTCGCCA AGTAGGCGTT 50
 CCATATATCG TTGTATTTAT GAACAAAGCC GATATGGTCG ATGACGCTGA 100
 25 GCTTCTTGAG CTAGTCGAGA TGGAAATTCG CGAGCTTCTT AACGAGTACA 150
 ACTTCCCTGG CGATGATACT CCTATCATAT CAGGTTCTGC TCTTAAAGCC 200
 CTCGAAGAGG CTAAAGCAGG CGTTGATGGC GAGTGGTCAG CAAAAGTTCT 250
 TGAGCTTATG GATAAAGTCG ATGAGTATAT CCCAACTCCA GTTCGTGCTA 300
 CCGATAAAGA CTTCTTGATG CCTATCGAAG ACGTTTTCTC TATCTCAGGT 350
 30 CGTGGAACGG TCGTTACTGG TAGGATCGAA AAAGGTGTCG TAAAAGTTGG 400
 CGATACTATC GAGATCGTTG GTATCAAACC TACTCAAAC ACGACAGTTA 450
 CTGGCGTTGA GATGTTTAGG AAAGAGATGG AACAAGGCGA GGCCGGTGAT 500
 AACGTAGGTG TTCTTTTAAG AGGTACTAAA AAAGAAGACG TCGAGCGCGG 550
 CATGGTTCTT TGTAAGCCAA AATCAATCAC TCCTCATACA AAATTTGAGG 600
 35 GTGAGGTTTA TATCCTAACA AAAGAGGAAG GCGGACGCCA CACTCCATTC 650
 TTTAACAAC ATAGACCACA ATTTTATGTA AGAACAACAG ACGTTACAGG 700
 TTCTATCACA CTTCCAGAAG GAACTGAGAT GGTTATGCCT GGAGATAATG 750
 TCAGAAATTC CGTTGAACTC ATCG 774

10

2) INFORMATION FOR SEQ ID NO: 1663

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter rectus*

(B) STRAIN: ATCC 33238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663

```

5  TTCTGCGGCT GACGGCCCAA TGCCACAAAC TAGAGAGCAC ATCTTGCTAT      50
   CTCGCCAAGT AGGCGTTCCG TATATCGTTG TTTTATGAA CAAAGCCGAT      100
   ATGGTCGATG ATGCCGAGCT TCTTGAGCTG GTTGAGATGG AGATTCGCGA      150
   GCTTCTAAAC GAGTATGATT TCCCTGGTGA CGATACTCCA ATCGTAGCAG      200
   GCTCTGCTCT TCAAGCTCTT AATGAAGCCA AAGCCGGAAC AGAAGGCGAG      250
10  TGGTCTGCAA AAATTCCTGA GCTTATGGCT AAAGTTGACG AGTATATCCC      300
   GACTCCGGTT CGTGCAACGG ATAAAGACTT CTTGATGCCT ATTGAGGACG      350
   TTTTCTCTAT CTCCGGTCGC GGCACCGTCG TTACCGGCAG AATCGAAAAA      400
   GGTATCGTAA AAGTCGGTGA TACTATCGAG ATCGTAGGTA TCCGCGATAC      450
   TCAAACAACCT ACCGTTACCG GCGTTGAGAT GTTCAGAAAA GAGATGGATC      500
15  AAGGCGAAGC GGGCGATAAC GTAGGCGTTC TTCTAAGAGG CACTAAAAAA      550
   GAAGACGTTG AGCGCGGTAT GGTTCCTTGC AAACCTAAAT CAATCACTCC      600
   TCACACTAAA TTTGAGGGAG AGGTTTATAT CTTAACTAAA GAGGAAGGCG      650
   GACGCCATAC TCCATTCTTT AATAACTATA GACCGCAGTT TTATGTAAGA      700
   ACTACCGACG TTACCGGTTT TATCACTCTT CCGGAAGGAA CAGAGATGGT      750
20  TATGCCTGGC GATAACTTAA AGATAAGCGT TGAGCTTATC G              791

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2) INFORMATION FOR SEQ ID NO: 1664

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Fonsecaea pedrosoi*
- (B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664

```

40  CGACGGACAG ATGCCCCAGA CCAGGGAGCA CTTGCTCCTC GCCCGCCAGG      50
   TCGGTGTCAA GCGCATTGTC GTCTTCGTCA ACAAGGTCGA TGCCATTGAG      100
   GACAAGGAGA TGTTGGAGCT CGTCGAGATG GAGATGCGTG AGCTTCTCTC      150
   CAGCTACGGC TTCGAGGGTG ACGACACTCC CATCGTCATG GGTTCCGCCC      200
   TTTGCGCCAT TGAGGGCCGC GAGCCCGACA TTGGTGTCGA GAAGATTGAC      250
45  GAGCTCCTCG AGCACGTCGA CACCTGGATC CCCACCCCGG AGCGTGACAT      300
   CGCCAAGCCT TTCCTCATGT CCGTTGAGGA CGTCTTCTCC ATTCCCGGCC      350
   GTGGTACCGT CGCTTCTGGC CGTGTGAGC GTGGTGTCCT GAAGAAGGAT      400
   TCCGAAGTCG AGCTTGTCGG CAAGAACAAG AACCCCATCA AGACCAAGGT      450
   TACCGACATC GAGACCTTCA AGAAGTCTTG CGACGAGTCC CGCGCTGGTG      500
50  ACAACTCCGG TCTCCTTCTC CGTGGTGTC AAGCGTGACGA TGTCTCCGT      550
   GGCATGGTCG TTGTCCAGCC CGGCACCACC AAGGCCACA AGAAGTTCCT      600
   TGCCTCCATG TACGTCTCA CCAAGGAGGA GGGTGGCCGC CACACTGGTT      650
   TCGCCAACAA CTACAAGCCC CAGATGTTCA TCCGTACCGC CGATGAGGCC      700

```

GCCACTCTTA	CCTGGCCCGA	GGGTACCGAG	GAGGACAAGA	TGGTCATGCC	750
CGGTGACAAT	GTCGAGATGA	TCTGCGAGAT	CCACAAGCCC	ATTGCCGTCG	800
AGCAAGGCCA					810

5

2) INFORMATION FOR SEQ ID NO: 1665

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665

CAGTACAGGT AGACTTCTG 19

20

2) INFORMATION FOR SEQ ID NO: 1666

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 888 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
- (B) STRAIN: ATCC 11347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666

ATGATTGCGA	AACCTACTTG	CTGTGGAAGA	ATTTGGATAT	TCTAACATTT	50
CTCTAGGCCT	CAAACCAGAG	AGCATCTGCT	CCTTGCCCGC	CAGGTCGGTG	100
TTCAGAAGCT	CGTCGTTTTT	GTAAACAAGG	TCGACGCTGT	TGAGGACCCA	150
GAGATGTTGG	AACTTGTCGA	GCTAGAGATG	CGTGAGCTGC	TCAGCCACTA	200
TGGTTTCGAG	GGTGAGGAGA	CCCCAATCAT	TTTTGGCTCT	GCTCTCTGCG	250
CCCTTGAATC	TCGACGACCA	GAATTGGGTG	TTGAGAAGAT	CGATGAGCTA	300
TTGAACGCTG	TGGATACCTG	GATTCCCACC	CCAGAGCGTG	CCACTGATAA	350
GCCTTTCCTT	ATGTCCATTG	AGGAAGTTTT	CTCCATCTCT	GGTCGTGGTA	400
CCGTCGTTTC	CGGTCGTGTC	GAGCGTGGTA	TCCTCAAGAA	GGACTCTGAT	450
GTCGAAATTG	TGGGTGGATC	TGATACACCC	ATCAAGACGA	AGGTCACCGA	500
CATTGAAACC	TTCAAGAAGT	CTTGTGACGA	ATCCCAGAGCT	GGTGACAAC	550
CCGGTCTACT	TCTCCGAGGT	GTCAAGCGTG	AGGACTTGAG	ACGTGGAATG	600
GTTGTTGCTG	CTCCCGGATC	GACCAAGGCT	CATACCGACT	TCATGGTCTC	650
CCTTTATGTT	CTGACCGAGG	CTGAGGGTGG	CCGTTCCAAT	GGATTCACCC	700
ACAAGTACCG	CCCACAGATG	TTCATCCGTA	CTGCCGGTAT	GTAAACCCTT	750

```

TTTCTACCAT TCACCTTGTGTT TCACCACTGA CTTGTATACT TTACCGCAGA      800
CGAAGCCGCA TCTTTCAGCT GGCCTGGAGA GGATCAAGAC AAGAAGGCCA      850
TGCCTGGTGA CAATGTCGAG ATGATTTGCA AGACCCCTC      888

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5

2) INFORMATION FOR SEQ ID NO: 1667

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667

```

ATGCCGCAGA CCCGCGAGCA CTTGCTGCTC GCCCGTCAGG TCGGTGTCCA      50
GAAGATCGTT GTTTTCGTCA ACAAGGTTGA TGCTATCGAC GACCCGGAGA      100
25 TGCTGGAGCT TGTCGAGATG GAGATGCGTG AACTTCTCAG CACATACGGT      150
TTCGAGGGTG ACGAGACCCC TGTTATTATG GGCTCCGCGC TCATGGCTCT      200
CAACAACCAG CGCCCCGAGA TTGGTCAACA GAAGATTGAT GAACTCATGG      250
CCGCTGTCTGA CGAGTGGATC CCTACTCCCC AGCGTGACCT CGACAAGCCT      300
TTCCTGATGT CTGTTGAGGA TGTCTTCTCC ATTGCTGGCC GTGGTACCGT      350
30 TGTGTCCGGC CGTGTGGAGC GCGGTACCCCT CAAGCGTGAT GAGGAAGTCG      400
AGCTTGTCGG CAAGGGTGTC GACCCCATCA AGACCAAGGT CACCGATATC      450
GAGACTTTCA AGAAGTCCTG CGAGGAGGCT CAGGCTGGTG ACAACTCTGG      500
TCTTCTGATC CGTGGTGTCC GCCGCGAGGA TGTTTCGTCGC GGTATGGTTG      550
TCTCCAAGCC CGGCACCGTC AAGTCTCACA CTCAGTTCCT GGCCTCGCTT      600
35 TACGTTCTCA CCAAGGAGGA GGGTGGTCGC CACACTGGTT TCGGCGAGCA      650
CTACCGTCCC CAGCTCTACC TCCGTACCTC AGACGAGTCT GTCGATCTGA      700
CCTTCCCCGA GGGAACTGAG GATCAACCACT CCAAGATCGT CATGCCTGGT      750
GACAACATCG AGATGGTCGT CACGATGACT CACGCCAACG CTA      793

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40

2) INFORMATION FOR SEQ ID NO: 1668

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(B) STRAIN: K-12 KL1699
(C) ACCESSION NUMBER: J01717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668

```

5 AACATGATCA CCGGTGCTGC GCAGATGGAC GGCGCGATCC TGGTAGTTGC      50
  TGCGACTGAC GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC      100
  GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA ATGCGACATG      150
  GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG TTCGTGAACT      200
10 TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC GTTCGTGGTT      250
  CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC GAAAATCCTG      300
  GAACTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG AGCGTGCGAT      350
  TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC ATCTCCGGTC      400
  GTGGTACCGT TGTTACCGGT CGTGTAGAAG GCGGTATCAT CAAAGTTGGT      450
15 GAAGAAGTTG AAATCGTTGG TATCAAAGAG ACTCAGAAGT CTACCTGTAC      500
  TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT GCTGGTGAGA      550
  ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT CGAACGTGGT      600
  CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC      650
  TGAAGTGTAC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT      700
20 TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA CGTGACTGGT      750
  ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG GCGACAACAT      800
  CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC GACGGTCTGC      850
  GTTTCGCAAT CCGTGAAGGC GGCCGTACCG TTGGCGCGGG C              891

```

25

2) INFORMATION FOR SEQ ID NO: 1669

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30 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 805 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Saksenaea vasiformis
        (B) STRAIN: ATCC 60625

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40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669

```

  TCCTCGTGGT CGCCGCCACC GACGGCCCGA TGCCGCAGAC CAAGGAGCAC      50
  GTGCTCCTGG CCCGCCAGGT CGGCGTTCCG TACATCGTCG TCGCCCTCAA      100
45 CAAGGCCGAC ATGGTGGACG ACGAGGAGAT CCTGGAGCTC GTCGAGCTCG      150
  AGGTCCGTGA GCTCCTCTCC GAGTACGAGT TCCCGGGCGA CGACGTTCCC      200
  GTCGTCAAGG TCTCCGCTCT GAAGGCCCTC GAGGGCGACA AGGAGTGGGG      250
  CAACTCGGTT CTCGAGCTCA TGAACGCCGT CGACACGGCG ATCCCCGAGC      300
  CCGAGCGTGA CGTCGACAAG CCGTTCCTCA TGCCGATCGA GGACGTCTTC      350
50 ACGATCACCG GTCGCGGTAC GGTCGTCACC GGCCGTATCG AGCGTGGTGT      400
  CCTGAAGGTC AACGAGACCG TCGACATCAT CGGCATCAAG ACCGAGAAGA      450
  CCACCACCAC GGTCACCGGC ATCGAGATGT TCCGGAAGCT CCTCGACGAG      500
  GGCCAGGCCG GTGAGAACGT CGGTCTGCTC CTCCGTGGCA TCAAGCGCGA      550

```



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GGACGTCGAG CGCGGCCAGG TCATCATCAA GCCGGGCTCG GTCACGCCGC      600
ACACGGAGTT CGAGGCGCAG GCCTACATCC TGTCCAAGGA CGAGGGTGGC      650
CGCCACACGC CGTTCTTCAA CAACTACCGC CCGCAGTTCT ACTTCCGTAC      700
GACGGACGTG ACCGGCGTGG TGACCCTCCC CGAGGGCACC GAGATGGTCA      750
5  TGCCGGGTGA CAACACCGAG ATGAAGGTGG AGCTCATCCA GCCCGTCGCC      800
ATGGA                                                    805

```

10 2) INFORMATION FOR SEQ ID NO: 1670

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 935 bases
 - (B) TYPE: Nucleic acid
 - 15 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Trichophyton tonsurans*
 - (B) STRAIN: ATCC 56185

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670

```

GCTTCTGACG GTCAAATGTA ATTGAATGCC CGCCCAGACA GATGAAAGGA      50
TTTGACGTTT CTAACATCAG TCTAGGCCTC AGACCAGAGA ACATTTGCTC      100
CTTGCCCGCC AGGTCGGTGT CCAGAAGCTG GTCGTTTTCG TTAACAAGGT      150
CGATGCCGTT GAGGACCCAG AGATGTTGGA GCTTGTCGAA CTTGAAATGC      200
30 GTGAACTCCT CAGCCACTAC GGTTTCGAGG GTGAGGAGAC CCCCATCATT      250
TTTGGCTCTG CTCTCTGTGC CCTCGAGTCC CGTCGACCTG AGCTTGGTGT      300
CGAGAAGATT GACGAGCTAT TGAACGCCGT CGACACCTGG ATCCCCACCC      350
CAGAGCGCGC CACTGATAAG CTTTCTCTCA TGTCATTGA GGAAGTGTTT      400
TCTATCTCTG GTCGTGGTAC CGTCGTCTCC GGTCGTGTTG AGCGTGGTAT      450
35 CCTCAAGAAG GATTCCGACG TCGAAATTGT TGGTGGCTCT ACCACCCCTA      500
TCAAGACCAA GGTCACCGAT ATCGAAACCT TCAAGAAGTC CTGCGATGAA      550
TCTCGAGCTG GTGACAACTC TGGTCTCCTT CTCCGAGGTA TCAAGCGTGA      600
GGACTTGAAG CGTGGAATGG TTGTTGCTGC CCCC GGATCC ACCAAGGCTC      650
ACACCGACTT CATGGTCTCC CTCTACGTCC TGACTGAGGC TGAGGGTGGT      700
40 CGTTCCAACG GCTTCACCCA CAAGTACCGC CCCCAAATGT TCATCCGTAC      750
TGCTGGTATG TAACCCAAGT TTCCGCTATT TACTAAGTAG ATCATTGCTA      800
ACTTGTATTT CTTTCCGTAG ACGAAGCCGC ATCTTTCAGC TGGCCTGGAG      850
AAGACCAAGA CAAGAAGGCT ATGCCTGGTG ACAACGTCGA GATGATTTCG      900
AAGACCCTCC ACCCCATTGC TGCCGAGGCT GGCCA                    935
45

```

2) INFORMATION FOR SEQ ID NO: 1671

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter aerogenes*

(B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671

10 ACGATGCCCT TGAGGTACAG AATGGTAATG AGAGCCTGGT GCTGGAAGTT 50
CAGCAGCAGC TCGGCGGTGG CGTAGTCCGT GCTATCGCCA TGGGTTCTTC 100
CGACGGTCTG CGTCGTGGTC TGGAAGTTAA AGACCTTGAG CACCCGATCG 150
AAGTCCCAGT AGGTAAAGCG ACTCTGGGCC GTATCATGAA CGTCCTGGGT 200
15 CAGCCGATCG ACATGAAAGG CGACATCGGC GAAGAAGAAC GTTGGGCTAT 250
CCACCGCGCG GCGCCTTCCT ATGAAGAGCT GTCCAGCTCT CAGGAACTGC 300
TGGAACCGG CATCAAAGTT ATCGACTTGA TGTGTCCGTT CGCTAAGGGC 350
GGTAAAGTTG GTCTGTTCGG TGGTGCGGGT GTAGGTAAAA CCGTAAACAT 400
GATGGAGCTG ATCCGTAACA TCGCGATCGA GCACTCCGGT TACTCCGTGT 450
20 TTGCGGGCGT TGGTGAGCGT ACTCGTGAGG GTAACGACTT CTATCACGAA 500
ATGACCGACT CCAACGTTCT GGATAAGTA TCCCTGGTTT ACGGCCAGAT 550
GAACGAGCCG CCGGGAACCG GTCTGCGCGT TCGCTGACC GGCCTGACCA 600
TGGCTGAGAA ATTCCGTGAC GAAGGTCGTG ACGTTCTGCT GTTCGTGAT 650
AACATCTATC GTTACACCTT GGCCGGTACT GAAGTATCTG CACTGCTGGG 700
25 CCGTATGCCT TCAGCGGTAG GTTATCAGCC GACTCTGGCG GAAGAGATGG 750
GCGTTCTGCA GGAACGTATC AC 772

30 2) INFORMATION FOR SEQ ID NO: 1672

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1401 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(B) STRAIN: Tohama 1

(C) ACCESSION NUMBER: Genome project

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1672

ATGAGCAACG GAACCATCGT TCAGTGCATC GGCGCCGTGG TGGATATTCA 50
GTTCCCCCGC GATAACATGC CCAAGATCTA CGAAGCGCTC ACCCTGGTCG 100
ACGAGGGTTC CTCGTTTCGCC GAGAAGGGCT TGACGCTGGA AGTGCAACAA 150
50 CAGCTGGGCG ACGGCGTGGT GCGTACCATC GCGCTGGGTT CCAGCGACGG 200
GCTGCGCCGC GGCATGCAAG TGGCCGGCAC CGGCGCACCG ATCTCGGTGC 250
CCGTGGGCCA CGGCACCCTG GGCCGCATCA TGGACGTGCT GGGCCGTCCC 300
ATCGACGAAG CCGGTCCCAT CGCCTCCGAC GAGAAGCGCG CCATCCACCA 350

	CCCCGCGCCC	CGTTTCGACG	AGCTGTCGCC	GTCGGTCGAG	CTGCTGGAAA	400
	CCGGCATCAA	GGTTATCGAC	CTGGTGTGCC	CGTTCGCCAA	GGGCGGCAAG	450
	GTCGGCCTGT	TCGGCGGCGC	CGGCGTGGGC	AAGACCGTCA	ACATGATGGA	500
	ACTGATCAAC	AACATCGCCA	AGCAGCACAG	CGGCTTGTCG	GTGTTCGCCG	550
5	GCGTGGGCGA	GCGTACCCGC	GAAGGCAACG	ACTTCTACCA	CGAAATGGAA	600
	GAGTCGAACG	TTCTGGACAA	GGTGGCCATG	GTGTTGCGCC	AGATGAACGA	650
	GCCCCCGGGC	AACCGCCTGC	GCGTGGCGCT	GACCGGCCTG	ACCATGGCCG	700
	AGAAGTTCCG	CGACGAAGGC	CGTGACATCC	TGTTCTTCGT	CGACAACATC	750
	TACCGCTACA	CCCTGGCCGG	TACCGAAGTG	TCGGCGCTGC	TGGGCCGTAT	800
10	GCCGTCGGCG	GTGGGCTACC	AGCCTACGCT	GGCCGAGGAA	ATGGGCGTGC	850
	TGCAAGAGCG	CATCACCTCG	ACCAAGACCG	GTTCGATCAC	CTCGATCCAG	900
	GCCGTGTACG	TGCCTGCCGA	CGACTTGACC	GACCCGTCGC	CCGCCACGAC	950
	CTTCCAGCAC	TTGGACTCGA	CCGTCGTGCT	GTCGCGTGAC	ATCGCTGCGC	1000
	TGGGCATCTA	TCCCGCCGTG	GACCCGCTGG	ATTCCTCCAG	CCGCCAGCTC	1050
15	GACCCGCAAG	TCGTGGGCGA	AGAGCACTAC	CAGGTGGCCC	GTGGCGTGCA	1100
	GCAGACGCTG	CAGCGCTACA	AGGAACTGCG	CGACATCATC	GCGATTCTGG	1150
	GCATGGACGA	ACTGTCGCCG	GAAGACAAGC	AGGCCGTGGC	CCGCGCGCGC	1200
	AAGATCCAGC	GCTTCCTGTC	GCAGCCCTTC	TACGTGGCCG	AAGTGTTCAC	1250
	CGGCTCGCCG	GGCAAGTACG	TGTCGCTGGC	CGAAACGATC	CGTGGCTTCA	1300
20	AGATGATCGT	CGACGGCGAG	TGCGACGCGC	TGCCCGAGCA	GGCGTTCTAC	1350
	ATGGTCGGCA	CGATCGACGA	GGCCTTCGAG	AAGGCCAAGA	AACTCCAATA	1400
	A					1401

25

2) INFORMATION FOR SEQ ID NO: 1673

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 797 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Arcanobacterium haemolyticum*
- (B) STRAIN: ATCC 9345
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673

	CAGCTACCGA	CGGTCCAATG	GCTCAGACCC	GCGAGCACGT	TCTTCTTGCT	50
	CGCCAGGTTG	GCGTTCCACA	GATCATCGTT	GCTCTCAACA	AGGCTGACAT	100
	GGTTGACGAC	GAGGAAATCC	TCGAACTCGT	CGAAATGGAA	GTTCGTGAGC	150
45	TTCTCTCTTC	CCAGGAGTAC	CCAGGTGACG	ACCTCCCAGT	CGTCAAGATC	200
	TCGGCACTCA	AGGCTCTCGA	AGGCGATGCC	GAATGGAGCA	AGGCAATCGA	250
	AGATCTCATG	GAAGCTGTCG	ATACCTACTT	CGACGATCCA	GTGCGTGACC	300
	TCGATAAGCC	ATTCTTCATG	CCAATCGAAG	ACGTCTTCAC	CATCACCAGT	350
	CGTGGCACCG	TTGTTACCGG	CCGTGCAGAG	CGCGGTATGC	TCAACTTGAA	400
50	CGAAGAAGTT	GAAATCCTCG	GTATCCGTGC	ACCACAGAAG	ACAACCGTTA	450
	CCGGTATCGA	AATGTTCCAC	AAGTCGATGG	ATCACGCAGA	TGCAGGCGAA	500
	AACTGTGGTC	TTCTCCTCCG	TGGCACCAAG	CGCGAAGATG	TTGAACGTGG	550
	TCAGGTTGTT	GCCAAGCCAG	GCACCATCAC	CCCACACACC	AACTTCGAAG	600

CTCAGGTCTA	CGTGCTCGGT	AAGGAAGAAG	GTGGCCGTCA	CAACCCATTC	650
TTCTCCAAC	ACCGTCCACA	GTTCTACTTC	CGTACCACGG	ATGTTACCGG	700
CGTGATCACC	CTTCCAGAGG	GCACCGAAAT	GGTTATGCCA	GGCGACAACA	750
CCGACATGAC	AGTTGAGCTC	ATCCAGCCAA	TCGCTATGGA	AGAGGGC	797

5

2) INFORMATION FOR SEQ ID NO: 1674

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Butyrivibrio fibrisolvens*
- (B) STRAIN: ATCC 19171

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674

CTGATGGTCC	TATGCCACAG	ACCCGTGAGC	ACATCCTATT	AGCACGTCAG	50
25 GTAGGCGTAC	CATACATCAT	CGTATTCCTA	AACAAGTGCG	ATATGGTTGA	100
CGACGAGGAA	TTATTAGAGT	TAGTTGAGAT	GGACGTACGT	GATCTATTAA	150
ATCAGTACCA	GTTCCCAGGC	GACGACACTC	CAATCATCCG	TGGTTCAGCA	200
CTAGGTGCAT	TAAACGGCGA	AGAGAAGTGG	AAAGAGGCAA	TCTATCAGTT	250
AGCAGACACT	CTAGATTCAT	ACATTCCAGA	GCCAAAGCGT	GATATCGATG	300
30 ATCCATTCCCT	ATTACCAATC	GAAGATATCT	TCTCAATCTC	AGGTCGTGGT	350
ACTGTAGTAA	CCGGCCGTGT	AGAGCGTGGT	ATTGTACACG	TAGGTGACGA	400
AGTTGAAATC	GTTGGTATTC	GTCCAACCAC	CAAGACCACT	GTAAGTGGCG	450
TTGAAATGTT	CCGTAAGTTA	CTAGACGAAG	GTCGTGCAGG	TGATAACGTT	500
GGTGTTCTAC	TACGTGGTAC	CAAGCGTGAT	GAGGTTGAGC	GTGGTCAGGT	550
35 TCTAGCTGCT	CCAGGCACAA	TCACTCCACA	CACCAAGTTC	ACTGGTCAGG	600
TTTACGTACT	AAGCAAGGAT	GAAGGTGGTC	GTCACACTCC	ATTCTTCAAG	650
GGCTACCGTC	CACAGTTCTT	CTTCCGTACA	ACCGATATTA	CCGGTTCTAT	700
CGATCTGAAA	GAGGGCGTAG	AGATGGTAAT	GCCAGGTGAT	AACACCGACA	750
40 TGACCGTAAC	CCTAATCCAC	CCAGTAGCTA	TGGCT		785

40

2) INFORMATION FOR SEQ ID NO: 1675

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter jejuni* subsp. *doylei*

(B) STRAIN: ATCC 49349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675

5 TGGGGCGATC TTGTTTGTTC CTGCTGCAGA TGGTCCTATG CCACAAACTA 50
 GAGAGCACAT TCTTCTTTCT CGTCAAGTAG GCGTTCCATA TATTGTTGTT 100
 TTTATGAATA AAGCAGATAT GGTGATGAT GCTGAGCTTT TAGAGTTAGT 150
 TGAAATGGAA ATTAGAGAAT TATTAAGCTC TTATGATTTC CCAGGCGATG 200
 10 ATACACCTAT TATTTCTGGT TCTGCTTTAA AAGCTCTTGA AGAAGCTAAA 250
 GCTGGACAAG ATGGTGAATG GTCAGCAAAA ATTATGGATC TTATGGCTGC 300
 AGTTGATAGT TATATTCCAA CTCCAACCTG TGATACTGAA AAAGACTTCT 350
 TGATGCCAAT TGAAGACGTT TTCTCAATT CAGGTCGTGG TACTGTTGTT 400
 ACAGGTAGAA TTGAAAAAGG TGTTGTAAAA GTAGGTGATA CTATCGAAAT 450
 15 CGTTGGTATT AAAGACACTC AAACAACAAC TGTAACAGGT GTTGAAATGT 500
 TCAGAAAAGA AATGGATCAA GGCGAGGCAG GAGATAACGT AGGTGTTCTT 550
 CTTCGTGGTA CTAAAAAAGA AGAAGTTATT CGCGGTATGG TTCTTGCTAA 600
 ACCAAAATCA ATTACTCCAC AACTGACTT CGAAGCTGAA GTTTATATCT 650
 TAAATAAAGA TGAAGGTGGT AGACATACTC CATTCTTTAA CAACTATAGA 700
 20 CCACAGTTTT ATGTAAGAAC AACTGATGTT ACAGGTTCGA TTAAATTAGC 750
 TGATGGTGTG GAAATGGTTA TGCCAGGTGA AAATGTGAGA ATTACTGTAA 800
 GCTTGATCGC TCCAGTAGCA CTTGAAGAAG GAACT 835

25

2) INFORMATION FOR SEQ ID NO: 1676

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter lari*

(B) STRAIN: ATCC 43675

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676

TTCTGCAGCA GACGGCCCTA TGCCACAAAC TAGAGAGCAT ATCTTACTTT 50
 CTCGTCAAGT AGGTGTACCA TATATTGTTG TTTTCATGAA CAAAGCTGAT 100
 ATGGTTGATG ATGCAGAATT ATTAGAATTA GTTGAAATGG AAATTAGAGA 150
 45 ATTACTAAGC TCTTATGATT TCCCAGGAGA TGATACTCCA ATTATTTTCCAG 200
 GTTCAGCATT ACAAGCTCTT GAAGAAGCAA AAGCTGGTCA AGATGGTGAA 250
 TGGTCTAAAA AAATCTTAGA TCTTATGGCT GCAGTTGATG ATTATATTCC 300
 AACTCCGGCT CGTGATACAG ATAAAGATTT CTTGATGCCA ATCGAAGATG 350
 TTTTCTCAAT CTCAGGTCGT GGAAGTGTG TTACCGGTAG AATTGAAAAA 400
 50 GGTGTTGTAA AAGTTGGTGA TACTATAGAA ATCGTTGGTA TTAGAGACAC 450
 TCAAACAACC ACAGTTACTG GTGTTGAAAT GTTTAGAAAA GAAATGGATC 500
 AAGGTGAAGC TGGTGATAAT GTTGGTGTAT TACTTCGTGG AACTAAAAAA 550
 GAAGATGTTG AACGTGGTAT GGTTCTTGCT AAACCAAAAT CAATCACTCC 600

	ACATACTGAT	TTTGAAGCAG	AAGTTTATAT	CTTAAATAAA	GATGAAGGTG	650
	GTCGTCATAC	TCCATTCTTT	AATAATTATA	GACCGCAATT	TTATGTAAGA	700
	ACAACTGATG	TTACAGGTGC	TATTAAACTT	GCAGAAGGCG	TTGAGATGGT	750
	TATGCCAGGC	GATAATGATA	GAATTACTGT	AAGTCTTATT	GCTCCAGTTG	800
5	CACTTGAGGA	AG				812

2) INFORMATION FOR SEQ ID NO: 1677

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter sputorum* subsp. *sputorum*
- (B) STRAIN: ATCC 35980

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677

25	GCTATTCTTG	TATGTTTCAGC	TGCAGATGGT	CCAATGCCAC	AGACTAGAGA	50
	GCATATTCTA	CTATCAAGAC	AAGTTGGTGT	TCCATACATA	GTTGTTTTCT	100
	TAAATAAAGA	AGATATGGTT	GATGATGCTG	AGCTTATAGA	GTTGGTTGAA	150
	GTTGAGGTTA	GAGATTTATT	AAATGAATAT	GATTTCCCTG	GAGATGATAC	200
	TCCAATCGTA	ATAGGTTCTG	CTCTTAAAGC	TTTAGAAGAA	GCAAAAGCTG	250
30	GAACAGAGGG	TGAATGGTCT	GCTAAAATTA	TGAAACTTAT	GGATGCTGTT	300
	GATAGCTATA	TCCCAACTCC	AACAAGAGAT	ACAGATAAAG	ATTCCTTAT	350
	GCCAATCGAA	GATATCTTCT	CAATTTCTGG	TCGTGGTACA	GTTGTAACAG	400
	GTAGAATTGA	AAAAGGTGTA	GTAAAAGTTG	GCGAGACTAT	TGAGATAGTT	450
	GGTATTAGAC	CTACTCAAAC	AACAACAGTT	ACTGGTGTTG	AAATGTTTAG	500
35	AAAAGAGCTA	GATCAAGGTG	AAGCTGGAGA	TAATGTTGGT	ATCTTGTTAA	550
	GAGGTACAAA	AAAAGAAGAT	GTTGAAAGAG	GTATGGTTTT	ATGTAAACCA	600
	AAATCAATCA	CTCCTCACAA	GAAATTTGAA	GGCGAAGTTT	ATATTCTTAC	650
	AAAAGATGAA	GGTGGTAGAC	ATACTCCTTT	CTTTAGTAAC	TATAGACCAC	700
	AATTTTATGT	TAGAACAACA	GATGTAACAG	GTTCTATATC	TCTTCCTGAG	750
40	GGAACAGAGA	TGGATATGCC	TGGTGATAAT	GTAAAACCTA	CAGTTGAACT	800
	TATAAACCCA	ATTGCTCTTG	AGCAAGGA			828

45 2) INFORMATION FOR SEQ ID NO: 1678

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter upsaliensis*

(B) STRAIN: ATCC 49815

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678

CGATTTTGGT TGTTCCTGCT GCTGATGGTC CTATGCCACA AACTAGAGAG 50
 CACATTTTGC TTTCTCGTCA AGTGGGTGTT CCTTATATCG TAGTTTTTAT 100
 10 GAATAAGGCT GATATGGTTG ATGATGCAGA GCTTTTAGAA TTGGTTGAAA 150
 TGGAAATTAG AGAACTTTTA AGCTCTTATG ATTTCCCGGG CGATGACACT 200
 CCTATCATTT CAGGCTCTGC TCTTCAAGCC TTAGAAGAGG CTAAGGCGGG 250
 ACAAGATGGC GAGTGGTCAG CTAAGATTTT AGAGCTTATG AAGGCAGTTG 300
 ATGAGTATAT CCCAACTCCT GTTCGCGATA CTGAAAAAGA TTTCTTGATG 350
 15 CCTATTGAAG ATGTTTTTTC AATTTCTGGT CGTGGAAGT TGTAAACAGG 400
 TAGAATTGAA AAAGGTGTGG TTAAAGTCGG CGATACTATT GAGATAGTAG 450
 GTATCAAAGA TACTCAAAC ACAACAGTTA CAGGCGTTGA GATGTTTAGA 500
 AAAGAAATGG ATCAAGGTGA GGCTGGCGAT AATGTCGGTG TGCTTTTAAG 550
 AGGAACAAAA AAAGAAGATG TTCTTCGTGG TATGGTTCTT GCAAAGCCTA 600
 20 AATCTATCAC TCCTCATACT GATTTTGAAG CAGAAGTTTA TATTCTAAAT 650
 AAAGATGAGG GCGGTCGCCA TACTCCTTTC TTAAACAATT ATCGTCCGCA 700
 GTTTTATGTA AGAACGACTG ATGTAACTGG TTCTATTAAA TTAGCTGATG 750
 GTGTTGAGAT GGTATGCCG GGTGAAAATG TAAGAATTAC AGTTAGCCTT 800
 ATCGCTCCAG TTGCACTTGA 820

25

2) INFORMATION FOR SEQ ID NO: 1679

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Globicatella sanguis*

40

(B) STRAIN: ATCC 51173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679

CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACATAT CTTATTATCA 50
 45 CGTCAAGTAG GTGTTCTTA CATGGTTGTC TTCTTAAACA AAGTTGACAT 100
 GGTTGACGAT GAAGAATTAT TAGAATTAGT TGAAATGGAA GTTCGTGATT 150
 TATTATCTGA ATACGAATTC CCTGGAGACG ACGTTCCAGT AATCGCTGGT 200
 TCAGCTTTAA AAGCTTTAGA AGGCGAAGAA CAATATGAAG CAAAAGTATT 250
 AGAATTAATG GAAGCTGTAG ATACATACAT TCCAGAACCA GTTCGTGATA 300
 50 CTGAAAAACC ATTCATGATG CCAGTTGAAG ATGTGTTCTC AATCACAGGT 350
 CGTGGTACAG TTGCTACTGG ACGTGTTGAA CGTGGACAAG TTAAGTTGG 400
 TGACGAAGTT GAAATCGTTG GTATTGCTGA AGAAATTAGC AAAACAACCTG 450
 TAACTGGTGT TGAAATGTTC CGTAAATTAT TAGATTACGC TGAAGCTGGA 500

GATAACATTG GTGCGTTATT ACGTGGTGTG ACACGTGAAC AAATCCAACG 550
 TGGTCAAGTA TTAGCAAAAC CAGGAACAAT TACACCTCAT ACTAAATTCG 600
 AGGCGGAAGT TTACGTATTA TCAAAAGAAG AAGGTGGACG TCATACTCCA 650
 TTCTTCGCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CTGACGTTAC 700
 5 AGGTGTTGTA GAATTACCAG AAGGTACAGA AATGGTAATG CCTGGAGATA 750
 ACGTATCAAT GACAGTTGAA TTAATTCACC CAA 783

10 2) INFORMATION FOR SEQ ID NO: 1680

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 823 bases
 - (B) TYPE: Nucleic acid
 - 15 (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Lactobacillus acidophilus*
 - (B) STRAIN: ATCC 4356

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680

GCTATCTTAG TTGTTGCTGC AACTGATGGT CCTATGCCAC AAACCTCGTGA 50
 ACACATTTTG CTTGCTCGTC AAGTTGGTGT TAACTACATC GTAGTATTCT 100
 TGAACAAGTG CGATTTAGTT GACGACCCAG AATTGATCGA CTTGGTTGAA 150
 ATGGAAGTTC GTGACTTGTT GACTGAATAC GATTACCCTG GTGATGATAT 200
 30 TCCAGTTGTT CGTGGTTCAG CATTAAAGGC TTTACAAGGT GACAAGGAAG 250
 CTCAAGACCA AATCATGAAG TTGATGGACA TTGTTGATGA ATACATCCCA 300
 ACTCCAGAAC GTCAAACCTGA CAAGCCATTC TTGATGCCAG TTGAAGACGT 350
 ATTCACTATC ACTGGTCGTG GTACTGTTGC TTCAGGTCGT ATCGACCCGTG 400
 GTACTGTAA GGTCCGGTGAC GAAGTTGAAA TCGTTGGTTT GGTAGATAAA 450
 35 GTTCTTAAGT CAGTTGTTAC TGGTTTGAA ATGTTCCACA AGACTTTGGA 500
 CTTAGGTGAA GCCGGCGATA ACGTTGGTGT ATTGCTTCGT GGTGTTGACC 550
 GTGATCAAGT GTTTCGTGGT CAAGTATTGG CTGCACCCGG CTCAATCCAA 600
 ACTCATAAGA AGTTTAAGGC ACAAGTTTAT GTTTTGAAGA AGGACGAAGG 650
 TGGTCGTCAC ACTCCATTCT TCTCAGACTA CCGTCCACAA TTCTACTTCC 700
 40 ACACCACTGA TATTACTGGT GAAATTGAAT TGCCAGAAGG TACTGAAATG 750
 GTTATGCCTG GTGATAACAC TGAATTCAC TTTACTTTGA TCAAGCCAGC 800
 TGCCATCGAA AAGGGTACTA AGT 823

45 2) INFORMATION FOR SEQ ID NO: 1681

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 793 bases
 - 50 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leuconostoc mesenteroides* subsp.
5 *dextranicum*

(B) STRAIN: ATCC 19255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681

10	GCTGCAACTG	ATGGTCCTAT	GCCACAAACA	CGTGAACACA	TCTTGTTGGC	50
	ACGTCAAGTT	GGTGTGACT	ACTTGTTGT	CTTCTTGAAC	AAGACTGATT	100
	TGGTTGATGA	TGAAGAATTA	GTTGAATTGG	TTGAAATGGA	AGTTCGTGAA	150
	TTGTTGTCAG	AATATGACTT	CCCAGGTGAC	GATATTCCTG	TACTTAAGGG	200
	TTCAGCTTTG	AAGGCTTTGG	AAGGTGATCC	TGAACAAGTT	AAGGTTATCG	250
15	AAGAATTGAT	GGATACTGTT	GATTCATACA	TTCCAGAACC	AGCACGTGAA	300
	ACAGACAAGC	CATTCTTGAT	GCCTGTCGAA	GACGTCTTCA	CAATCACTGG	350
	TCGTGGTACA	GTTGCTTCTG	GTCGTGTTGA	CCGTGGTGTA	TTGACTACAG	400
	GAAGTGAAT	TGAAATCGTT	GGTTTGAAGG	ACGAAGTTCA	AAAGACTACT	450
	GTTACAGGTA	TCGAAATGTT	CCGTAAGACT	TTGGAAGAAG	CTCAAGCGGG	500
20	TGATAACATT	GGTGCATTGT	TGCGTGGTGT	TGATCGTAGC	AACATTGAAC	550
	GTGGTCAAGT	TTTGGCAAAG	CCAGGTTCAA	TTAAGACACA	CAAGAAGTTC	600
	AAGGCTGAAG	TTTATGTCTT	GACAAAGGAA	GAAGGTGGTC	GTCATACACC	650
	ATTCTTCACT	AACTACCGTC	CACAATTCTA	CTTCCACACA	ACTGATGTTA	700
	CAGGTGTTGT	TGAATTGCCA	GCCGGTGTTG	AAATGGTTAT	GCCTGGTGAC	750
25	CAAGTGACAT	TCGAAATCGA	ATTGATCTCA	CCAGTTGCCA	TCG	793

2) INFORMATION FOR SEQ ID NO: 1682

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 796 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

35

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Prevotella buccalis*

(B) STRAIN: ATCC 35310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682

45	TATCCTTGTA	GTTGCTGCTA	CTGATGGTCC	TATGCCACAG	ACACGTGAGC	50
	ACGTGCTTTT	GGCTCGTCAG	GTAAACGTTT	CTCGTTTGGT	TGTGTTTCATG	100
	AACAAGTGTG	ACTTGGTAGA	AGACGAAGAG	ATGCTTGAAC	TCGTTGAAAT	150
	GGAGTTGCGC	GAAGTTCTTG	AGCAATACGA	ATTCGAAGAG	GATACTCCAA	200
	TCGTTCTGTT	TTCTGCACTG	GGTGCATTGA	ATGGTGTTGA	CAAGTGGGTT	250
50	GACAGCGTGA	TGACGTTGAT	GGACACTGTT	GACGAGTGGA	TTCAAGAGCC	300
	AGAGCGTGAC	CTTGACAAAC	CTTTCTTGAT	GCCAGTAGAG	GACGTGTTCT	350
	CTATCACAGG	TCGTGGTACC	GTTGTAACAG	GACGTATTGA	GACTGGTAAG	400
	GTAAAGGTTG	GCGACGAGAT	TCAGTTGCTC	GGTCTTGGTG	AGGACAAGAA	450

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GTCTGTTGTA ACAGGCGTTG AAATGTTCCG TAAGATTCTT TCTGAAGGTG      500
AAGCAGGTGA TAACGTAGGA CTTTTGCTCC GCGGTATCGA TAAGGATGAA      550
GTAAAGCGTG GTATGGTTGT TGTACACCCA GGTGCCATCA CTCCTCACGA      600
TCAC TTCAAG GCTTCCATCT ATGTATTGAA GAAGGAAGAG GGTGGACGTC      650
5  ATACTCCATT CGGAAACAAG TATCGTCCTC AGTTCTATCT CCGTACAATG      700
   GACTGTACAG GTGAGATCAC TTTGCCAGAA GGCGTAGAGA TGGTGATGCC      750
   TGGTGACAAC GTAGAGATTG AGGTTACCTT GATTTACAAG GTTGCC        796

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10

2) INFORMATION FOR SEQ ID NO: 1683

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 800 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Ruminococcus bromii*
 - (B) STRAIN: ATCC 27255

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683

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GGTTGCTGCT ACTGACGGCC CGATGCCTCA GACTCGTGAG CACGTTCTGC      50
TCGCTCGTCA GGTGGGTGTG CCCGCCATCG TCGTCGCCCT CAACAAGTGC      100
GACATGGTTG ACGATGAGGA GCTCATTGAG CTTGTCGAGA TGGAGGTCCG      150
30  CGAGCTGCTG ACCTCGCAGG AGTTCGACGG CGACAACTGC CCTGTCGTTT      200
   GCATCTCCGC CTTCCAGGCC CTCCAGGGTG ACGAGAAGTG GACCCAGTCG      250
   ATCCTCGACC TCATGGACGC CGTGGACGAG TACATCCCGC AGCCTGAGCG      300
   CGATCTCGAC AAGCCCTTCC TTATGCCGAT CGAGGACGTC TTCACCATCA      350
   CCGGCCGTGG CACCGTTGTC ACCGGTCGTG TCGAGCGTGG TGTCGTCAAG      400
35  ACTGGCGAAG AGGTCGAGAT CGTCGGTATC CACGAGAAGA CCCAGAAGAC      450
   CACCGTTACC GGTGTCGAGA TGTTCCGTAA GATCCTCGAC GAGGGCCGCG      500
   CTGGTGAGAA CGTCGGCGTT CTGCTCCGTG GCACCAAGAA GGAGGACGTC      550
   GTTCGCGGCA TGGTCCTCTC CAAGCCTGGT TCCACCACCC CCCACACCGA      600
   CTTCGAGGGC CAGGTCTACG TCCTCAAGAA GGATGAGGGT GGCCGCCACA      650
40  AGCCGTTCTT CTCCCATTAC AGCCCCCAGT TCTACTTCCG TACCACGGAC      700
   GTGACTGGCA CTGTTGAGCT CCCCAGGGGC ACCGAGATGG TCATGCCTGG      750
   CGACAACACC GACATGACTG TGCACCTGAT TCACCCGGTT GCCATGGAGG      800

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45

2) INFORMATION FOR SEQ ID NO: 1684

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 545 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 5 (B) STRAIN: ATCC 32075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684

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10 TGTCTTTATT CAGGAAGTGA TTGTATGTTT CTTCTCGTTT ATATATAACA      50
   TACCTTCTAT ATTTTCATGTG TTTCTAACGA ACTCATAGAA CAACATTGCC      100
   AAGGCTCACG GTGGTTACTC CGTGTTTACC GGTGTCGGTG AGCGTACCCG      150
   TGAAGGAAAC GATCTGTACC ACGAAATGCA GGAAACCCGC GTCATCCAGC      200
   TGGACGGCGA GTCCAAAGTC GCCCTCGTCT TCGGCCAGAT GAACGAGCCC      250
   CCCGGAGCCC GTGCCCCTGT TGCCCTGACC GGTCTGACCA TCGCTGAATA      300
15 CTTCCGTGAC GAAGAAGGCC AAGATGGTAC GTTCCCCCAT TCCATATATG      350
   TTTCTTGTGC GCTTTGCCAA CTAAACACCA CCTAGTGCTC CTCTTCATCG      400
   ACAATATCTT CCGCTTCACC CAAGCCGGTT CCGAAGTGTC CGCCCTGCTA      450
   GGCCGCATCC CCTCCGCCGT CGGCTATCAA CCCACCCTCG CCGTCGACAT      500
   GGGTGGTATG CAGGAGCGCA TCACAACCTAC AACAAAAGGC TCCAT          545
20

```

2) INFORMATION FOR SEQ ID NO: 1685

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegica*
 35 (B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685

```

40 GATATCGCTT TATGGAAATT CGAAACTCCA AAATTCCACG TTACYGTTAT      50
   CGATGCTCCA GGTCACAGAG ATTTTCATCAA GAATATGATT ACYGGTACCT      100
   CCCAAGCTGA TTGTGCTATT TTAATCATTG CTGGTGGTGT TGGTGAATTC      150
   GAAGCTGGTA TCTCCAAAGA TGGTCAAACC AGAGAACACG CTTTGTTAGC      200
   TTTCACCTTA GGTGTYAAAC AATTGATTGT TGCCGTAAAC AAAATGGACT      250
   CTGTCAAATG GGATCAATCC CGTTTCGAAG AAATCGTCAA GGAAGCTTCC      300
45 GGTTTCATCA AGAAAGTTGG TTACAACCCA AAGACTGTTC CATTTCGTTCC      350
   AATCTCTGGT TGGAATGGTG ACAACATGAT TGAAGTYTCW GCTAACGCYC      400
   CATGGTACAA AGGTTGGGAA AAGGAAACCA AAGCYGGTGT CGTTAAAGGT      450
   AAAACTTTAT TAGAAGCCAT TGATGCTATT GAACCACCTT CAAGACCAAC      500
   TGAAAAACCA TTGAGATTGC CATTGCAAGA TGTCTACAAG ATTGGTGGTA      550
50 TCGGAACCGT ACCAGTCGGT ARAGTTGAAA CCGGTGTCAT TAAACCAGGT      600
   ATGATTGTTA CTTTCGCCCC AGCCGGTGTT ACTACTGAAG TCAAACTCTGT      650
   TGAAATGCAT CACGAACAAT TAGAAGCTGG TTACCCAGGT GACAATGTTG      700
   GTTTCACCGT CAAGAATGTT TCAGTTAAAG AAATCAGAAG AGGTAHGTG      750

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	GCTGGTGACT	CCAAGAACGA	TCCACCAAAA	GGTGCTGAAT	CTTTCAACGC	800
	TCAAGTTATT	GTCTTGAACC	ATCCAGGTCA	AATCTYTGCT	GGTTACTYTC	850
	CAGTTTTGGA	TTGTCACACT	GCCCACATTG	CTTGTAATTT	CGATGAAATC	900
	TTGGAAAAGA	TTGACAGAAG	ATCCGGTAAG	AAATTGGAAG	AAAATCCAAA	950
5	ATTCATCAA	TCTGGTGACG	CTGCTAWTGT	CAAATTTGTT	CCATWTAAAC	1000
	CATTRTGTGT	TGAAGCTTTC				1020

10 2) INFORMATION FOR SEQ ID NO: 1686

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686

25	TGCTGCTTCC	GATGGTCAAA	TGTACGATTG	ATATTCCTTC	CAGCCAGTCA	50
	GGATAACAGC	TGATACCAGT	TGCAAATAGG	CCCCAGACTC	GTGAGCACTT	100
	GTTGCTTGCC	CGTCAGGTTG	GTGTCCAGAA	GATCGTTGTC	TTCGTCAACA	150
	AGGTTGACGC	TGTCGATGAC	CCTGAGATGT	TGGAGCTTGT	TGAGCTCGAG	200
30	ATGCGTGAGC	TCCTCAACAC	TTACGGTTTC	GAGGGAGAGG	AGACCCCTAT	250
	CATCTTCGGT	TCCGCCCTGT	GCGCTCTCGA	AGGCCGCCGC	GAGGACATTG	300
	GTA CT CAGCG	TATTGACTCC	CTCCTCGAGG	CCGTTGACAC	TTGGATCCCT	350
	ACCCCCCAGC	GTGACTTGGA	CAAGCCCTTC	CTGATGTCCA	TTGAGGAAGT	400
	TTTCTCCATT	GGTGGTCGTG	GTACCGTCGC	CTCTGGTCGT	GTCGAGCGTG	450
35	GTCTCCTCAA	GAAGGATACC	GAAGTTGAAA	TTCACGGTGC	TGATGGTATT	500
	CTGAAGACCA	AGGTCACCGA	CATTGAGACC	TTCAAGAAGA	GCTGCGATGA	550
	GTCTCGTGCT	GGTGACAACT	CCGGTCTTCT	CCTCCGTGGT	ATCCGTCGTG	600
	AGGATGTTTCG	TCGTGGTATG	GTCATCGCTG	CCCCTGGCTC	CATCAAGGCC	650
	TCCAAGAAGT	TCATGGTCTC	CATGTACGTC	TTGACTGAGG	CTGAAGGTGG	700
40	CCGCAAGAAC	GGCTTCGGTG	CCAACTACCG	CCCCCAGGCT	TTCATCCGCA	750
	CTGCTGGTAA	GTTTCGAACT	ATTTGATTCA	TTGATCACGT	CCCTAACTGT	800
	TACTTTAGAC	GAGGCTTGCG	ACCTTCATTT	CCCTGATGAG	GCCGACAAGG	850
	ACCGCCACGT	CATGCCCGGT	GACAACGTCG	AAATGGTCCT	CAACCTCAAC	900
	AACCCCGTTG	CTGCTGAGGC	TGGACAGCG			929

45

2) INFORMATION FOR SEQ ID NO: 1687

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus terreus*

(B) STRAIN: WSA-174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687

10 TGCCGCTTCC GATGGTCAGA TGTACGCTCA AGCCCCAGTT TCCATATAAA 50
 CATAAACGAT CTATCATCAG CACAACGCTG ACTTCTTCGC TTCCAGGCCC 100
 CAGACCCGTG AGCACTTGCT GTTGGCCCGT CAGGTCGGTG TCCAGAAGAT 150
 CGTGGTCTTC GTCAACAAGG TCGATGCCGT TGATGACCCG GAGATGTTGG 200
 15 AGCTCGTTGA GCTGGAAATG CGCGAGCTCC TGACCAGCTA CGGATTCGAG 250
 GGTGAAGAGA CCCCCATCAT CTTCGGTTCT GCTCTCTGCG CTCTTGAGGG 300
 CCGCCGTCCT GAGATTGGTA CTGAGAAGAT TGACGAGCTG ATGCACGCCG 350
 TCGACACCTG GATCCCCACC CCCCAGCGTG ACCTCGACAA GCCCTTCCTG 400
 ATGTCCGTCG AGGAAGTCTT CTCCATTGCT GGTCGTGGTA CCGTCGCTTC 450
 20 CGGCCGTGTC GAGCGTGGTA TTCTGAAGAA GGATAGCGAA GTCGAGATCA 500
 TCGGTGGTGC TTTCGACGCC ACGAAGACCA AGGTCACTGA CATCGAGACC 550
 TTCAAGAAGT CTTGCGACGA GTCTCGCGCT GGTGACAACT CTGGTCTCCT 600
 CCTCCGTGGT ATCCGTCGTG AGGATGTTTCG GCGTGGTATG GTCATTGCTG 650
 CTCCTGGCAG CACCAAGGCC CACGACAAGT TCCTTGCTCTC TATGTACGTC 700
 25 CTCACTGAGG CTGAGGGTGG CCGTCGTACC GGATTCGGTA CCAACTACCG 750
 CCCCCAGGTC TTCATCCGTA CTGCCGGTAA GTGTTCTCTG AAGAGGCTTT 800
 GAGCCTATAT AGGATCTCGG ATAATTTACT AATCCACCAT ATAGATGAGG 850
 CCGCTGACCT CAGCTTCCCC GACAACGATG ACTCCCGCCG TGTCATGCCC 900
 GGTGACAACG TTGAGATGGT CTTGAAGACC CACCGCCCCG TGGCTGCTGA 950
 30 G 951

2) INFORMATION FOR SEQ ID NO: 1688

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 823 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Candida norvegica*

(B) STRAIN: ATCC 36586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688

50 CGTTGCCGCT ACCGATGGTC AAATGCCTCA AACTAGAGAA CATTGCTAT 50
 TGGCTAGACA GGTTGGTGTT CAACACATTG TCGTGTGTTGT TAACAAGGTT 100
 GACACTATTG ATGATCCAGA AATGTTGGAA TTGGTTGAAA TGGAAATGAG 150
 AGAGTTGATT GCCACTTATG GTTTCGATGG TGATAACACC CCAGTTATCA 200

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TGGGTTCTGC TCTATGTGCT TTGGAAGGTC GTGAACCTGA AATCGGTGCT 250
CAATCAATCG ACAGATTGTT GGAAGCCGTT GATGAATACA TTCCAACCTCC 300
AACTAGAGAT TTGGAAAAAC CATTCTTGAT GGGTGTGTA GATGTCTTCT 350
CCATTTCTGG TAGAGGTACC GTCTGTACCG GTCGTGTTGA AAGAGGTAAC 400
5 TTGAAGAAAG GTGATGAAAT CGAAATTGTC GGCTACAACA AGACTCCAAT 450
CAAAACCACC GTCACCGGTA TTGAGATGTT CAAAAGGAA TTAGACCAAG 500
CTATGGCTGG TGATAACTGT GGTATCTTAT TACGTGGTGT TAAGAGAGAT 550
GATATCAAGA GAGGTATGGT TATCTCTAAA GTCAACACCG TTTCCGCACA 600
CACCAAATTC TTGGCCTCTT TATACGTCTT GACTAAAGAA GAAGGTGGTC 650
10 GTCATTGAGG TTTTGCTGAA AACTACAGAC CTCAATTGTT CATCAGAACC 700
GGTGATGTCA CTGTTACTTT AACCTTCCCA GAAGATGCTG ATCACTCTCA 750
GCAAGTCTTA CCAGGTGACA ACGTTGAAAT GGAATGTACC TTGGTTCATC 800
CAACTGCTCT TGAAACCGGT CAA 823

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15

2) INFORMATION FOR SEQ ID NO: 1689

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 803 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Candida parapsilosis
        (B) STRAIN: ATCC 201076

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689

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GCTGCTACTG ACGGTCAAAT GCCTCAAACCT AGGGAACATA TGTTGTTGGC 50
GAGACAAGTT GGTATCCAAA ACTTGTTTGT TTTTGTTAAC AAAGTTGATA 100
35 CCATTGATGA CCCAGAAATG TTGGAATTGG TTGAAATGGA AATGAGGGAA 150
TTATTGAGCT CTTATGGGTT TGATGGTGAA AACACTCCAG TTATCATGGG 200
ATCAGCCTTG TGTGCTTTAG AAGGTAAACA ACCAGAAATC GGTGTTCAAG 250
CCATTCAAAA ATTATTGGAT GCTGTTGATG AATATATTCC AACTCCAGAA 300
AGAGATGCTG ACCAACCATT TTTGATGCCA GTGGAAGATG TGTTTTCTAT 350
40 TTCAGGTAGA GGAACCGTTG TCACCGGAAG AGTTGAAAGA GGTATGTTGA 400
AGAAAGGTGA AGAAGTAKAA GTCATTGGTG AAAACTCATT TAAGGCTACT 450
TCCACGGGTA TTGAGATGTT CAAAAGGAA TTGGATGCCG CTATGGCCGG 500
TGACAACTGT GGTATTTTGT TGAGAGGTGT CAAGAGAGAC GAAGTCAAGA 550
GGGGTATGGT TTTGGCCAAA CCAGGTACCA CCACCCACCA CCAAAAGTTT 600
45 TTGGCTTCCA TTTATATCTT GACTGCTGAA GAAGGTGGAC GTAGTACCCC 650
TTTCAGTGAA GGATACAAAC CACAATGTTT CTTTAGAACT AGTGATGTTA 700
CCACGACATT TACTTTCCCA GAAGGTGAAG GTGTTGACCA CTCACAAATG 750
GTTATGCCAG GAGRCAATGT TGAAATGGTG GGAACCTTAA TCAAGAAAGC 800
TCC 803
50

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2) INFORMATION FOR SEQ ID NO: 1690

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690

CAGGTCCTGT TGCGACTGAA GAA

23

15

2) INFORMATION FOR SEQ ID NO: 1691

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691

CACAGATAAA CCTGAGTGTG CTTTC

25

30

2) INFORMATION FOR SEQ ID NO: 1692

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692

GGTGAGAACT GTGGTATCTT ACTT

24

45

2) INFORMATION FOR SEQ ID NO: 1693

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693

CATTTCACG CCTTCTTTCA ACTG

24

10

2) INFORMATION FOR SEQ ID NO: 1694

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694

AAGGCAAGGA TGACAACGGC

20

25

2) INFORMATION FOR SEQ ID NO: 1695

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695

ACGATTTCCTTCTTCCTG G

21

40

2) INFORMATION FOR SEQ ID NO: 1696

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696

ATGTTCTGT AGTTGCTGGA

20

5

2) INFORMATION FOR SEQ ID NO: 1697

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697

TTTCTTCAGC AATACCAACA AC

22

20

2) INFORMATION FOR SEQ ID NO: 1698

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698

35 GGAATCAACA GATGGTTTAC AAA

23

2) INFORMATION FOR SEQ ID NO: 1699

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699

50

GCATCTTCTG GGAAAGGTGT

20

2) INFORMATION FOR SEQ ID NO: 1700

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700

AAGATGCGGA AAGAAGCGAA

20

2) INFORMATION FOR SEQ ID NO: 1701

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701

ATTATGGATC AGTTCTTGGA TCA

23

2) INFORMATION FOR SEQ ID NO: 1702

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: Challis V288
 (C) ACCESSION NUMBER: L20574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702

50

TTCATAGACG	CTGAGCACGC	TTTGGATCCA	TCTTACGCGG	CTGCTCTAGG	50
TGTAAATATT	GATGAGCTGT	TGCTATCTCA	ACCAGATTCT	GGTGAGCAAG	100
GTTTAGAAAT	TGCAGGAAAA	TTGATTGACT	CTGGGGCAGT	TGATTTAGTT	150

GTCATCGACT CTGTTGCAGC TCTTGTACCA CGTGCGGAAA TCGATGGAGA 200
 TATCGGTGAT AGC 213

5

2) INFORMATION FOR SEQ ID NO: 1703

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: strain GS-5
 (C) ACCESSION NUMBER: M61897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703

	GGGCCGGAAT	CTTCTGGTAA	GACAACTGTC	GCTCTTCATG	CTGCTGCTCA	50
	GGCGCAAAAA	GATGGCGGTA	TTGCCGCTTT	CATTGATGCA	GAACATGCCC	100
25	TTGATCCAGC	CTATGCTGCT	GCTCTTGGCG	TTAATATTGA	TGAGCTTTTG	150
	CTTTCACAAC	CAGATTCAGG	AGAACAGGGT	CTTGAAATTG	CAGGGAAATT	200
	GATTGATTCT	GGCGCTGTTG	ATTTAGTTGT	TGTTGACTCA	GTGGCAGCTT	250
	TAGTACCACG	TGCGGAGATT	GACGGAGATA	TTGGTAATAG	TCATGTTGGC	300
	TTACAAGCAC	GCATGATGAG	TCAAGCGATG	CGTAAATTAT	CAGCTTCAAT	350
30	CAATAAAACA	AAAACCATTG	CTATTTTTAT	TAATCAATTG	CGGGAAAAAG	400
	TTGGTATTAT	GTTTGGTAAT	CCAGAAACAA	CCCCTGGCGG	GCGTGCCTTG	450
	AAGTTTTATT	CTTCTGTGCG	TCTTGATGTC	CGCGGCAATA	CTCAAATTAA	500
	AGGAACCGGG	GAACAAAAAG	ACAGCAATAT	TGGTAAAGAG	ACCAAAATTA	550
	AAGTTGTTAA	AAATAAAGTT	GCTCCACCAT	TTAAGGAAGC	TTTTGTAGAA	600
35	ATTATATATG	GTGAAGGCAT	TTCTCGTACA	GGTGAATTAG	TTAAGATTGC	650
	CAGTGATTTG	GGAATTATCC	AAAAGCTGG	AGCTTGGTAC	TC	692

40 2) INFORMATION FOR SEQ ID NO: 1704

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (C) ACCESSION NUMBER: Z17307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704

	ATGGCGAAAA	AACCAAAAAA	ATTAGAAGAA	ATTTCAAAAA	AATTTGGGGC	50
	AGAACGTGAA	AAGGCCTTGA	ATGACGCTCT	TAAATTGATT	GAGAAAGACT	100
5	TTGGTAAAGG	ATCAATCATG	CGTTTGGGTG	AACGTGCGGA	GCAAAAGGTG	150
	CAAGTGATGA	GCTCAGGTTC	TTTAGCTCTT	GACATTGCCC	TTGGCTCAGG	200
	TGGTTATCCT	AAGGGACGTA	TCATCGAAAT	CTATGGCCCA	GAGTCATCTG	250
	GTAAGACAAC	GGTTGCCCTT	CATGCAGTTG	CACAAGCGCA	AAAAGAAGGT	300
	GGGATTGCTG	CCTTTATCGA	TGCGGAACAT	GCCCTTGATC	CAGCTTATGC	350
10	TGCGGCCCTT	GGTGTCAATA	TTGACGAATT	GCTCTTGTCT	CAACCAGACT	400
	CAGGAGAGCA	AGGTCTTGAG	ATTGCGGGAA	AATTGATTGA	CTCAGGTGCA	450
	GTTGATCTTG	TCGTAGTCGA	CTCAGTTGCT	GCCCTTGTTT	CTCGTGCGGA	500
	AATTGATGGA	GATATCGGAG	ATAGCCATGT	TGGTTTGCAG	GCTCGTATGA	550
	TGAGCCAGGC	CATGCGTAAA	CTTGGCGCCT	CTATCAATAA	AACCAAAAACA	600
15	ATTGCCATTT	TTATCAACCA	ATTGCGTGAA	AAAGTTGGAG	TGATGTTTGG	650
	AAATCCAGAA	ACAACACCGG	GCGGACGTGC	TTTGAAATTC	TATGCTTCAG	700
	TCCGCTTGGA	TGTTTCGTGGT	AATACACAAA	TTAAGGGAAC	TGGTGATCAA	750
	AAAGAAACCA	ATGTCGGTAA	AGAACTAAG	ATTAAGGTTG	TAAAAAATAA	800
	GGTAGCTCCA	CCGTTTAAGG	AAGCCGTAGT	TGAAATTATG	TACGGAGAAG	850
20	GAATTTCTAA	GACTGGTGAG	CTTTTGAAGA	TTGCAAGCGA	TTTGGATATT	900
	ATCAAAAAAG	CAGGGGCTTG	GTATTCTTAC	AAAGATGAAA	AAATTGGGCA	950
	AGGTTCTGAG	AATGCTAAGA	AATACTTGGC	AGAGCACCCA	GAAATCTTTG	1000
	ATGAAATTGA	TAAGCAAGTC	CGTTCTAAAT	TTGGCTTGAT	TGATGGAGAA	1050
	GAAGTTTCAG	AACAAGATAC	TGAAAACAAA	AAAGATGAGC	CAAAGAAAGA	1100
25	AGAAGCAGTG	AATGAAGAAG	TTCCGCTTGA	CTTAGGCGAT	GAACCTGAAA	1150
	TCGAAATTGA	AGAATAAGCT	GTAAAGCAG	TGGAGAAATC	CGCTACTTTT	1200
	TCGA					1204

30.

2) INFORMATION FOR SEQ ID NO: 1705

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 981 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*
(B) STRAIN: NZ131
(C) ACCESSION NUMBER: U21934

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705

	ATGCGTTCAG	GAAGTCTAGC	TCTTGATATT	GCTTGGATAG	CTGGTGGTTA	50
	TCCTAAAGGA	CGTATCATCG	AAATCTATGG	TCCAGAGTCT	TCCGGTAAAA	100
50	CGACTGTGGC	TTTACATGCT	GTAGCACAAG	CTCAAAAAGA	AGGTGGAATC	150
	GCAGCCTTTA	TCGATGCCGA	GCATGCGCTT	GATCCAGCTT	ATGCTGCTGC	200
	GCTTGGGGTT	AATATTGATG	AACTTCTCTT	GTCTCAACCA	GATTCTGGAG	250
	AACAAGGACT	TGAAATTGCA	GGTAAATTGA	TTGATTCTGG	TGCGGTTGAC	300

	CTGGTTGTTG	TCGATTCAGT	AGCAGCTTTA	GTGCCACGTG	CTGAAATTGA	350
	TGGTGATATT	GGCGATAGCC	ATGTCGGATT	GCAAGCACGT	ATGATGAGTC	400
	AGGCCATGCG	TAAATTATCA	GCTTCTATTA	ATAAAACAAA	AACTATCGCA	450
	ATCTTTATCA	ACCAATTGCG	TGAAAAAGTT	GGTGTGATGT	TTGGAAATCC	500
5	TGAAACAACA	CCAGGTGGTC	GAGCTTTGAA	ATTCTATGCT	TCTGTTCCGC	550
	TGGATGTGCG	TGGAAACAAC	CAAATTAAAG	GAAGTGGTGA	CCAAAAGATA	600
	GCCAGCATTG	GTAAGGAGAC	CAAAATCAAG	GTTGTTAAAA	ACAAGGTCGC	650
	TCCGCCATTT	AAGGTAGCAG	AAGTTGAAAT	CATGTATGGG	GAAGGTATTT	700
	CTCGTACAGG	GGAGCTTGTG	AAAATTGCTT	CTGATTTGGA	CATTATCCAA	750
10	AAAGCAGGTG	CTTGGTTCTC	TTATAATGGT	GAGAAGATTG	GCCAAGGTTC	800
	TGAAAATGCT	AAGCGTTATT	TGGCCGATCA	TCCACAATTG	TTTGATGAAA	850
	TCGACCGTAA	AGTACGTGTT	AAATTTGGTT	TGCTTGAAGA	AAGCGAAGAA	900
	GAATCTGCTA	TGGCAGTAGC	ATCAGAAGAA	ACCGATGATC	TTGCTTTAGA	950
	TTTAGATAAT	GGTATTGAAA	TTGAAGATTA	A		981

2) INFORMATION FOR SEQ ID NO: 1706

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius* subsp. *thermophilus*
 (C) ACCESSION NUMBER: M94062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706

35	GCGTATGCAC	GAGCTCTAGG	TGTTAATATC	GATGAGCTTC	TTTTGTCGCA	50
	GCCTGATTCT	GGTGAGCAAG	GTCTCGAAAT	TGCAGGTAAG	CTGATTGACT	100
	CTGGTGCAGT	GGATTTAGTT	GTTGTTGACT	CAGTTGCGGC	CTTCGTACCA	150
	CGTGCAGAAA	TTGATGGAGA	TAGTGGTGAC	AGTCATGTAG	GACTTCAAGC	200
	GCGTATGATG	AGTCAAGCCA	TGCGTAAACT	TTCTGCATCT	ATTAATAAAA	250
40	CAAAAACGAT	TGCTATCTTT	ATTAACCACT	TGCGTGAAAA	AGTTGGTATC	300
	ATGTTTGGTA	AC				312

2) INFORMATION FOR SEQ ID NO: 1707

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: J02967

5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707

	ATGAAAAACA	CAATACATAT	CAACTTCGCT	ATTTTTTTTAA	TAATTGCAAA	50
	TATTATCTAC	AGCAGCGCCA	GTGCATCAAC	AGATATCTCT	ACTGTTGCAT	100
10	CTCCATTATT	TGAAGGAACT	GAAGGTTGTT	TTTTACTTTA	CGATGCATCC	150
	ACAAACGCTG	AAATTGCTCA	ATTCAATAAA	GCAAAGTGTG	CAACGCAAAT	200
	GGCACCAGAT	TCAACTTTCA	AGATCGCATT	ATCACTTATG	GCATTTGATG	250
	CGGAAATAAT	AGATCAGAAA	ACCATATTCA	AATGGGATAA	AACCCCCAAA	300
	GGAATGGAGA	TCTGGAACAG	CAATCATACA	CCAAAGACGT	GGATGCAATT	350
15	TTCTGTTGTT	TGGGTTTCGC	AAGAAATAAC	CCAAAAAATT	AGATTAAATA	400
	AAATCAAGAA	TTATCTCAAA	GATTTTGATT	ATGGAAATCA	AGACTTCTCT	450
	GGAGATAAAG	AAAGAAACAA	CGGATTAACA	GAAGCATGGC	TCGAAAGTAG	500
	CTTAAAAATT	TCACCAGAAG	AACAAATTCA	ATTCCTGCGT	AAAATTATTA	550
	ATCACAAATCT	CCCAGTTAAA	AACTCAGCCA	TAGAAAACAC	CATAGAGAAC	600
20	ATGTATCTAC	AAGATCTGGA	TAATAGTACA	AAACTGTATG	GGAAAACCTGG	650
	TGCAGGATTC	ACAGCAAATA	GAACCTTACA	AAACGGATGG	TTTGAAGGGT	700
	TTATTATAAG	CAAATCAGGA	CATAAATATG	TTTTTGTGTC	CGCACTTACA	750
	GGAAACTTGG	GGTCGAATTT	AACATCAAGC	ATAAAAGCCA	AGAAAAATGC	800
	GATCACCATT	CTAAACACAC	TAAATTTATA	A		831
25						

2) INFORMATION FOR SEQ ID NO: 1708

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

40 (B) STRAIN: HH22

(C) ACCESSION NUMBER: M60253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708

45	TTGAAAAAGT	TAATATTTTT	AATTGTAATT	GCTTTAGTTT	TAAGTGCATG	50
	TAATTCAAAC	AGTTCACATG	CCAAAGAGTT	AAATGATTTA	GAAAAAAAAT	100
	ATAATGCTCA	TATTGGTGTT	TATGCTTTAG	ATACTAAAAG	TGGTAAGGAA	150
	GTAAAATTTA	ATTCAGATAA	GAGATTTGCC	TATGCTTCAA	CTTCAAAAGC	200
	GATAAATAGT	GCTATTTTGT	TAGAACAAGT	ACCTTATAAT	AAGTTAAATA	250
50	AAAAAGTACA	TATTAACAAA	GATGATATAG	TTGCTTATTC	TCCTATTTTA	300
	GAAAAATATG	TAGGAAAAGA	TATCACTTTA	AAAGCACTTA	TTGAGGCTTC	350
	AATGACATAT	AGTGATAATA	CAGCAAACAA	TAAAATTATA	AAAGAAATCG	400
	GTGGAATCAA	AAAAGTTAAA	CAACGTCTAA	AAGAACTAGG	AGATAAAGTA	450

ACAAATCCAG TTAGATATGA GATAGAATTA AATTACTATT CACCAAAGAG 500
 CAAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT TTAAATAAAC 550
 TTATCGCAAA TGGAAAATTA AGCAAAGAAA ACAAAAAATT CTTACTTGAT 600
 TTAATGTAA ATAATAAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC 650
 5 AAAAGACTAT AAGGTTGCTG ATAAAAGTGG TCAAGCAATA ACATATGCTT 700
 CTAGAAATGA TGTGCTTTT GTTTATCCTA AGGGCCAATC TGAACCTATT 750
 GTTTTAGTCA TTTTACGAA TAAAGACAAT AAAAGTGATA AGCCAAATGA 800
 TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA TTTTAA 846

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2) INFORMATION FOR SEQ ID NO: 1709

- (i) SEQUENCE CHARACTERISTICS:
- 15 (A) LENGTH: 555 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 20 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Pseudomonas aeruginosa*
 (C) ACCESSION NUMBER: M29695

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709

ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA 50
 CCTGCCGATG CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT 100
 30 GGGGTGGCGA CGAAGAGCGA CCGACTCTTG ATGAAGTGCT GGAACACTAC 150
 CTGCCCAGAG CGATGGCGGA AGAGTCCGTA ACACCGTACA TCGCAATGCT 200
 GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG CTCGGAAGCG 250
 GTGATGGCTG GTGGGAAGAT GAACTGATC CAGGAGTGCG AGGAATAGAC 300
 CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT 350
 35 TGTCGCGCT CTCGTTGAAC TACTGTTCTC GGACCCACC GTGACGAAGA 400
 TTCAGACCGA CCCGACTCCG AACAACCATC GAGCCATACG CTGCTATGAG 450
 AAGGCAGGAT TCGTGCGGGA GAAGATCATC ACCACGCCTG ACGGGCCGGC 500
 GGTTTACATG GTTCAAACAC GACAAGCCTT CGAGAGAAAG CGCGGTGTTG 550
 CCTAA

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2) INFORMATION FOR SEQ ID NO: 1710

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 732 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 50 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: K02987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710

5
 ATGAACCAGA AAAACCCTAA AGACACGCAA AATTTTATTA CTTCTAAAAA 50
 GCATGTAAAA GAAATATTGA ATCACACGAA TATCAGTAAA CAAGACAACG 100
 TAATAGAAAT CGGATCAGGA AAAGGACATT TTACCAAAGA GCTAGTCAAA 150
 ATGAGTCGAT CAGTTACTGC TATAGAAATT GATGGAGGCT TATGTCAAGT 200
 10 GACTAAAGAA GCGGTAAACC CCTCTGAGAA TATAAAAGTG ATTCAAACGG 250
 ATATTCTAAA ATTTTCCTTC CCAAAACATA TAAACTATAA GATATATGGT 300
 AATATTCCTT ATAACATCAG TACGGATATT GTCAAAAGAA TTACCTTTGA 350
 AAGTCAGGCT AAATATAGCT ATCTTATCGT TGAGAAGGGA TTTGCGAAAA 400
 GATTGCAAAA TCTGCAACGA GCTTTGGGTT TACTATTAAT GGTGGAGATG 450
 15 GATATAAAAA TGCTCAAAAA AGTACCACCA CTATATTTTC ATCCTAAGCC 500
 AAGTGTAGAC TCTGTATTGA TTGTTCTTGA ACGACATCAA CCATTGATTT 550
 CAAAGAAGGA CTACAAAAAG TATCGATCTT TTGTTTATAA GTGGGTAAAC 600
 CGTGAATATC GTGTTCTTTT CACTAAAAAC CAATTCCGAC AGGCTTTGAA 650
 GCATGCAAAAT GTCATAATA TTAATAAACT ATCGAAGGAA CAATTTCTTT 700
 20 CTATTTTCAA TAGTTACAAA TTGTTTCACT AA 732

2) INFORMATION FOR SEQ ID NO: 1711

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 738 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Escherichia coli*

(B) STRAIN: BM2570

(C) ACCESSION NUMBER: M19270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711

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ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTAAACGA GTGAAAAAGT 50
 ACTCAACCAA ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT 100
 ACGAAATTGG AACAGGTAAA GGGCATTTAA CGACGAAACT GGCTAAAATA 150
 AGTAAACAGG TAACGTCTAT TGAATTAGAC AGTCATCTAT TCAACTTATC 200
 45 GTCAGAAAAA TTAAATCGA ATACTCGTGT CACTTTAATT CACCAAGATA 250
 TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT 300
 ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGTGAAAG 350
 CCATGCGTCT GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA 400
 CCTTGGATAT TCACCGAACA CTAGGGTTGC TCTTGCACAC TCAAGTCTCG 450
 50 ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA TGCTTTCATC CTAAACCAAG 500
 AGTAAACAGT GTCTTAATAA AACTTACCCG CCATACCACA GATGTTCCAG 550
 ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA 600
 GAATATCGTC AACTGTTTAC TAAAAATCAG TTTTCATCAAG CAATGAAACA 650

CGCCAAAGTA	AACAATTTAA	GTACCGTTAC	TTATGAGCAA	GTATTGTCTA	700
TTTTTAATAG	TTATCTATTA	TTTAACGGGA	GGAAATAA		738

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2) INFORMATION FOR SEQ ID NO: 1712

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: RN451
 (C) ACCESSION NUMBER: M17990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712

ATGAACGAGA	AAAATATAAA	ACACAGTCAA	AACTTTATTA	CTTCAAAACA	50
TAATATAGAT	AAAATAATGA	CAAATATAAG	ATTAAATGAA	CATGATAATA	100
TCTTTGAAAT	CGGCTCAGGA	AAAGGGCATT	TTACCCTTGA	ATTAGTACAG	150
AGGTGTAATT	TCGTAAGTGC	CATTGAAATA	GACCATAAAT	TATGCAAAAC	200
TACAGAAAAT	AAACTTGTTG	ATCACGATAA	TTCCAAGTT	TTAAACAAGG	250
ATATATTGCA	GTTTAAATTT	CCTAAAACCC	AATCCTATAA	AATATTTGGT	300
AATATACCTT	ATAACATAAG	TACGGATATA	ATACGCAAAA	TTGTTTTTGA	350
TAGTATAGCT	GATGAGATTT	ATTTAATCGT	GGAATACGGG	TTTGCTAAAA	400
GATTATTAAA	TACAAAACGC	TCATTGGCAT	TATTTTTAAT	GGCAGAAGTT	450
GATATTTCTA	TATTAAGTAT	GGTTCCAAGA	GAATATTTTC	ATCCTAAACC	500
TAGAGTGAAT	AGCTCACTTA	TCAGATTAAA	TAGAAAAAAA	TCAAGAATAT	550
CACACAAAGA	TAAACAGAAG	TATAATTATT	TCGTTATGAA	ATGGGTTAAC	600
AAAGAATACA	AGAAAATATT	TACAAAAAAT	CAATTTAACA	ATTCCTTAAA	650
ACATGCAGGA	ATTGACGATT	TAAACAATAT	TAGCTTTGAA	CAATTCCTTAT	700
CTCTTTTCAA	TAGCTATAAA	TTATTTAATA	AGTAA		735

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2) INFORMATION FOR SEQ ID NO: 1713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: V583

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(C) ACCESSION NUMBER: U00456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713

5	ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
	TGATGTGTCTG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
	AAAAATTCGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
	CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
	ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
10	AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
	TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
	CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGCAATG	GACAAATCAC	400
	TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
	ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
15	CTTTGTGAAG	CCGGCACGGT	CAGGTTTCGTC	CTTTGGCGTA	ACCAAAGTAA	550
	ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
	GGAAAAATCT	TAATTGAGCA	AGCGATTTTCG	GGCTGTGAGG	TCGGCTGCGC	650
	GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
	GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
20	GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
	ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
	GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
	GTTCTAAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
	TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
25	GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 1714

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

35

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*

(B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714

45	GCACAGGTTC	AGTTGGGCTT	GATCTTGCTT	TAGGTATAGG	CGGTGTTCCA	50
	AAAGGAAGAA	TTATAGAAAT	TTATGGRCCT	GAAAGTTCAG	GTAAAACCAC	100
	TCTAACTCTA	CACATTATCG	CAGAATGCCA	AAAAGCAGGT	GGRGTTTGTG	150
	CTTTTATCGA	TGCAGAACAT	GCRCTTGATG	TRAAATATGC	TAAAAATTTG	200
	GGTGTAATA	CAGATGATTT	GTATGTTTCT	CAGCCTGATT	TTGGAGARCA	250
50	AGCCTTAGAA	ATTGTAGAAA	CTATAGCAAG	AAGTGGCGCA	GATAGATCTTA	300
	TCGTAGTAGA	TAGCGTTGCA	GCGCTTACCC	CAAAAGCAGA	AATTGAAGGC	350
	GATATGGGTG	ATCAACATGT	AGGACTTCAA	GCAAGACTTA	TGTCTCAAGC	400
	TCTAAGAAAA	CTTACAGGTA	TAGTTCATAA	AATGAATACC	ACAGTAATTT	450

	TYATCAACCA	AATTCGTATG	AAAATCGGTG	CTATGGGTTA	TGGTACTCCT	500
	GAAACCACAA	CAGGTGGAAA	TGCATTAAAA	TTTTATGCTT	CTGTGCGTTT	550
	AGATGTTAGA	AAAGTAGCAA	CCTTAAAACA	AAACGAAGAA	CCTATAGGAA	600
	ACCGCGTTAA	AGTAAAAGTA	GTTAAAAATA	AAGTTGCTCC	TCCATTGAGA	650
5	CAAGCTGAAT	TTGATGTGAT	GTTTGGAGAG	GGTTTAAGCC	GTGAAGGTGA	700
	ATTGATCGAT	TATGGTGTAA	AACTTGATAT	CGTAGATAAA	AGTGGTGCCT	750
	GGTTTTCTTA	TAAAGATAAA	AACTTGGAC	AAGGTAGAGA	AAATTCAAAA	800
	GCTTTCCTAA	AAGAAAAC				818

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2) INFORMATION FOR SEQ ID NO: 1715

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175
 25 (C) ACCESSION NUMBER: AF124224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715

	TGGTGCTATC	TTAGTAGTAT	CTGCAGCTGA	TGGTCCAATG	CCTCAAACAC	50
30	GTGAACACAT	CTTATTATCA	CGTCAAGTAG	GTGTTCTTCTTA	CATCGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
	ACACTCCAGT	TGTTGCAGGT	TCTGCTTTAC	GCGCTTTAGA	AGGCGACGCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ACGAATACAT	300
35	TCCAACCTCCA	GAACGYGACG	TTGACAAACC	ATTCATGATG	CCAGTTGAAG	350
	ACGTGTTCTC	AATCACAGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGTGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTTTCTGTA	450
	AGAAACTTCA	AAAACAACCTG	TAAGTGGTGT	TGAAATGTTC	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGG	GATAACATTG	GTACATTATT	ACGTGGTGTGTT	550
40	ACACGTGACA	ACATCGAACG	TGGACAAGTT	CTTGCTAAAC	CAGGAACAAT	600
	CACTCCACAT	ACTAAATTCA	AAGCTGAAGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACATCAC	TGGTGTGTTG	GTGTTACCAG	AAGGCGTTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATTCACC	800
45	CAGTAGCGA					809

2) INFORMATION FOR SEQ ID NO: 1716

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(B) STRAIN: ATCC 49176

(C) ACCESSION NUMBER: AF124225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716

	CGGCGCGATC	CTCGTTGTAT	CTGCTGCTGA	CGGCCCAATG	CCACAAACTC	50
	GTGAACACAT	CCTCTTGTCT	CGTCAAGTTG	GTGTTCCCTTA	CATCGTAGTA	100
15	TTCTTGAACA	AAGTTGACAT	GGTTGACGAC	GAAGAATTGC	TCGAATTAGT	150
	TGAAATGGAA	GTTCTGTACC	TCTTGTCTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
	AACTACGAAG	CTAAAGTTTT	AGAATTGATG	GAACAAGTTG	ATGCTTACAT	300
	TCCAGAACCA	GAACGTGACA	CTGACAAGCC	ATTCATGATG	CCAGTCGAAG	350
20	ACGTATTCTC	TATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGTCAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCGAAGA	450
	AGAAACTTCT	AAGACTACCG	TTACCGGTGT	TGAAATGTTC	CGTAAGTTAT	500
	TGGATTACGC	TGAAGCTGGG	GACAACGTTG	GTACCTTGTT	ACGTGGTGTA	550
	ACTCGTGACC	AAATCCAACG	TGGTCAAGTA	TTATCTAAAC	CAGGTTCAAT	600
25	CACTCCGYAC	ACTAAGTTCG	AAGCTGAAGT	GTACGTATTG	TCTAAAGAAG	650
	AAGGTGGTCTG	TCACACTCCA	TTCTTCTCTA	ACTACCGTCC	ACAATTCTAC	700
	TTCCGTACAA	CTGACGTAAAC	TGGTGTGTTT	ACTTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCAGGCGACA	ACGTACAAAT	GGTTGTTGAA	TTGATCCACC	800
30	CAATCGCGAT	CGAAGAA				817

2) INFORMATION FOR SEQ ID NO: 1717

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium accolens*

(B) STRAIN: ATCC 49725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717

	CGGCGCTATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
50	GCGAGCACGT	TCTGCTTGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTCGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	GGAGATGGAG	ATCTCCGAGC	TGCTCGCAGA	GCAGGACTAC	GATGAGGAAG	200
	CTCCTATCGT	TCACATCTCC	GCTCTGAAGG	CACTCGAGGG	TGACGAGAAG	250

	TGGGTACAGT	CCATCGTTGA	CCTGATGGAT	GCCTGCGACA	ACTCCATCCC	300
	TGATCCGGAG	CGCGCTACCG	ATCAGCCGTT	CTTGATGCCT	ATCGAGGACA	350
	TCTTCACCAT	TACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGTCGTCTGA	ACGTCAACGA	GGACGTTGAG	ATCATCGGTA	TCCAGGAGAA	450
5	GTCCCAGAAC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGC	AAGATGATGG	500
	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTGCG	TGGTACCAAG	550
	CGTGAGGACG	TTGAGCGTGG	CCAGGTTGTT	ATCAAGCCGG	GCGCTTACAC	600
	CCCTCACACC	AAGTTCGAGG	GTTCCGTCTA	CGTCCTGAAG	AAGGAAGAGG	650
	GCGGCCGCCA	CACCCCGYTC	ATGAACAAC	ACCGTCCTCA	GTTCTACTTC	700
10	CGCACCACCG	ACGTTACCGG	TGTTGTGAAC	CTGCCTGAGG	GCACCGAGAT	750
	GGTTATGCC	GGCGACAACG	TTGAGATGTC	TGTTGAGCTC	ATCCAGCCTG	800
	TTGCTATGGA	CGAG				814

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2) INFORMATION FOR SEQ ID NO: 1718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium genitalium*
 (B) STRAIN: ATCC 33031

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718

	CGGCGCCATC	CTGGTTGTTG	CTGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GTGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCGTA	CATCCTAGTT	100
	GCACTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAGCTGC	TGGAGCTCGT	150
35	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CACCTGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
	TGGGCTAAGC	AGATCCTGGA	GCTCATGGAG	GCTTGCGACA	ACTCCATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGRGGACA	350
	TCTTCACCAT	TACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
40	GGCGTCCTGA	ACCTGAACGA	CGAGGTCGAG	ATCCTGGGCA	TCCGCGAGAA	450
	GTCCACCAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
	ACACCGCAGA	GGCTGGCGAC	AACGCCGCAC	TGCTGCTGCG	TGGCCTGAAG	550
	CGCGAAGATG	TTGAGCGTGG	TCAGATCGTT	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
45	GTGGCCGCCA	CACCCCGTTC	TTCGACAAC	ACCGTCCGCA	GTTCTATTTT	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCGGAGG	GCACCGAGAT	750
	GGTTATGCCG	GGCGACAACG	TTGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

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2) INFORMATION FOR SEQ ID NO: 1719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*
 (B) STRAIN: ATCC 43216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719

15	CGGCGCCATC	CTGGTTGTTG	CCGCAACCGA	TGGCCCGATG	CCGCAGACCC	50
	GCGAGCACGT	TCTGCTGGCY	CGCCAGGTTG	GCGTTCCGTA	CATCCTGGTT	100
	GCACTGAACA	AGTGTGACAT	GGTTGACGAT	GAGGAGCTGC	TGGAGCTCGT	150
	CGAGATGGAG	GTCCGCGAGC	TGCTGGCTGA	GCAGGACTTC	GACGAGGAAG	200
	CTCCGGTTGT	TCACATCTCC	GCACTGAAGG	CCCTGGAGGG	CGACGAGAAG	250
20	TGGGCTAACC	AGATTCTCGA	GCTGATGCAG	GCTTGCGACG	AGTCTATCCC	300
	GGATCCGGAG	CGCGAGACCG	ACAAGCCGTT	CCTGATGCCG	GTTGWGGACA	350
	TCTTCACCAT	TACCGGTCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCATCCTGA	ACCTGAACGA	CGAGGTTGAG	ATCCTGGGTA	TCCGCGAGAA	450
	GTCCCAGAAG	ACCACCGTTA	CCTCCATCGA	GATGTTCAAC	AAGCTGCTGG	500
25	ACACCGCAGA	GGCTGGCRAC	AACGCTGCAC	TGCTGCTGCG	TGGTCTGAAG	550
	CGCGAGGACG	TTGAGCGTGG	CCAGATCATC	GCTAAGCCGG	GCGAGTACAC	600
	CCCGCACACC	GAGTTCGAGG	GCTCCGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTCGACAACT	ACCGTCCGCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTGCCTGAGG	GCACCGAGAT	750
30	GGTTATGCCG	GGCGACAACG	TYGACATGTC	CGTCACCCTG	ATCCAGCCGG	800
	TTGCTATGGA	CGAG				814

35 2) INFORMATION FOR SEQ ID NO: 1720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720

50	CGGCGCTATC	TTGGTTGTTG	CAGCTACCGA	CGGCCCAATG	CCACAGACTC	50
	GCGAGCACGT	TCTGCTGGCT	CGCCAGGTTG	GCGTTCCTTA	CATCCTGGTT	100
	GCACTAAACA	AGTGCGACAT	GGTTGACGAC	GAGGAAATCC	TCGAGCTCGT	150

	CGAGATGGAG	ATCCGCGAAT	TGCTGGCTGA	CCAGGAATTC	GACGAAGAAG	200
	CTCCAATCGT	TCACATCTCC	GCAGTCGGCG	CCTTGGAAGG	CGAAGAGAGG	250
	TGGGTTAACG	CCATCGTTGA	ACTGATGGAT	GCTTGTGACG	AGTCGATCCC	300
	TGATCCAGAC	CGTGCTACCG	ACAAGCCATT	CCTGATGCCT	ATCGAGGACA	350
5	TCTTCACCAT	TACCGGTCGT	GGCACC GTT	TTACGGGTCG	TGTTGAGCGT	400
	GGTTCCTGA	AGGTCAACGA	AGAAGTCGAG	ATCATCGGCA	TCAAGGAAAA	450
	GTCCCAGAAG	ACCACCATCA	CCGGTATCGA	AATGTTCCGC	AAGATGCTGG	500
	ACTACACCGA	GGCCGGCGAC	AACGCTGGTC	TGCTGCTTCG	CGGTACCAAG	550
	CGTGAAGACG	TTGAGCGTGG	ACAGGTTATC	GTTGCTCCAG	GTGCTTACAG	600
10	CACCCACAAG	AAGTTCGAAG	GTTCCGTCTA	CGTTCTTTCC	AAGGACGAGG	650
	GCGGCCGCCA	CACCCCGTTC	TTGACAACCT	ACCGTCCTCA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTTACC	CTGCCTGAGG	GCACCGAG	748

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2) INFORMATION FOR SEQ ID NO: 1721

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 813 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Corynebacterium striatum*
- (B) STRAIN: ATCC 6940

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721

	GGCGCTATCT	TGGTTGTTGC	TGCAACCGAT	GGCCCGRTGC	CGCAGACCCG	50
	CGAGCACGTT	CTTCTGGCTC	GCCAGGTTGG	CGTTCCTTAC	ATCCTCGTTG	100
	CACTGAACAA	GTGCGACATG	GTTGACGACG	AGGAAATTAT	CGAGCTCGTC	150
35	GAGATGGAGA	TCCGCGAACT	GCTCGCAGAG	CAGGACTACG	ATGAGGAAGC	200
	TCCGATCGTT	CACATCTCTG	CTCTGAAGGC	TCTTGAGGGC	GRCGAGAAGT	250
	GGGTACAGGC	TATCGTTGAC	CTGATGCAGG	CTTGCGATGA	CTCCATCCCCG	300
	GATCCGGAGC	GCGAGCTGGA	CAAGCCGTTT	CTGATGCCAA	TCGAGGACAT	350
	CTTCACCATC	ACCGGCCGCG	GTACCGTTGT	TACTGGCCGT	GTTGAGCGTG	400
40	GCTCCCTGAA	CGTCAACGAG	GACGTTGAGA	TCATCGGTAT	CCAGGACARG	450
	TCCATCTCCA	CCACCGTTAC	CGGTATCGAG	ATGYTCCGCA	AGATGATGGA	500
	CTACACCGAG	GCTGGCGACA	ACTGTGGTCT	GCTTCTGCGT	GGTACCAAGC	550
	GTGAAGAGGT	TGAGCGCGGC	CAGGTTGTTA	TTAAGCCGGG	CGCTTACACC	600
	CCTCACACCC	AGTTCGAGGG	TTCCGTCTAC	GTCCTGAAGA	AGGAAGAGGG	650
45	CGGCCGCCAC	ACCCCGTTCA	TGGACAACCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACCACCGA	CGTTACCGGC	GTCATCAAGC	TGCCTGAGGG	CACCGAGATG	750
	GTTATGCCTG	GCGACAACGT	CGAGATGTCY	GTCGAGCTGA	TCCAGCCGGT	800
	CGCTATGGAC	GAG				813

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2) INFORMATION FOR SEQ ID NO: 1722

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025
 (C) ACCESSION NUMBER: AF124220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722

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15 CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCTATG CCTCAAAC TC      50
   GTGAACACAT CTTGTTATCT CGTAACGTTG GTGTTCCCTA CATCGTTGTA      100
   TTCTTAAACA AAATGGATAT GGTTGACGAT GAAGAATTAC TTGAATTAGT      150
   TGAAATGGAA GTTCGTGACT TATTAAC TGA      200
20 ACACTCCAGT TATCGCAGGT TCAGCGTTGA AAGCTTTAGA AGGCGACGCT      250
   TCATACGAAG AAAAATCTT AGAATTAATG GCTGCTGTTG ACGAATATAT      300
   CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGTCGAAG      350
   ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACTGG TCGTGTGAA      400
   CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATCGCTGA      450
25 CGAAACTGCT AAAACAAC TGACAGGTGT TGAAATGTTC CGTAAATTGT      500
   TAGACTACGC TGAAGCAGGT GACAACATCG GTGCTTTGTT ACGTGGTGT      550
   GCACGTGAAG ATATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT      600
   CACTCCACAT ACAAATTCT CTGCAGAAGT TTATGTTCTA ACTAAAGAAG      650
   AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC      700
30 TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA      750
   AATGGTWATG CCTGGGGATA ACGTAACTAT GGAAGTTGAA TTGATYCACC      800
   CAATYCGCGT AGAAGAC                                     817

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2) INFORMATION FOR SEQ ID NO: 1723

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*
 (B) STRAIN: ATCC 14018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723

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TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC      50
GTGAACACGT CTTGCTTGCT AAGCAGGTCG GCGTTCCAAA AATTCTTGTT      100

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	GCTTTGAACA	AGTGCGATAT	GTTTGACGAC	GAAGAGCTTA	TCGATCTCGT	150
	TGAAGAAGAG	GTCCGTGACC	TCCTCGAAGA	AAACGGCTTC	GATCGCGATT	200
	GCCCAGTCYT	CCGTACTTCC	GCTTACGGCG	CTTTGCATGA	TGACGCTCCA	250
	GACCACGACA	AGTGGGTAGA	GACCGTCAAG	GAATCATGA	AGGCTGTTGA	300
5	CGAGTACATC	CCAACCCCAA	CTCACGATCT	TGACAAGCCA	TTCTTGATGC	350
	CAATCGAAGA	TGTGTTTACC	ATCTCCGGTC	GTGGTYCCGT	TGTCACCGGT	400
	CGTGTTGAGC	GTGGTAAGCT	CCCAATCAAC	ACCCCAGTTG	AGATCGTTGG	450
	TTTGCGCGAT	ACCCAGACCA	CCACCGTCAC	CTCTATCGAG	ACCTTCCACA	500
	AGCAGATGGA	TGAGGCAGAG	GCTGGCGATA	ACACTGGTCT	TCTTCTCCGC	550
10	GGTATCAACC	GTACCGACGT	TGAGCGTGGT	CAGGTTGTGG	CTGCTCCAGG	600
	TTCTGTGACT	CCACACACCA	AGTTCGAAGG	CGAAGTTTAC	GTCTTGACCA	650
	AGGACGAAGG	TGGCCGTCAC	TCGCCATTCT	TCTCCAACTA	CCGTCCACAG	700
	TTCTACTTCC	GTACCACCGA	TGTTACTGGC	GTTATCACCT	TGCCAGACGG	750
	CATCGAAATG	GTTCAGCCAG	GCGATCACGC	AACCTTCACT	GTTGAGTTGA	800
15	TCCAGGCTAT	CGCAATGGAA	GAG			823

2) INFORMATION FOR SEQ ID NO: 1724

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Listeria innocua*
- (B) STRAIN: ATCC 33090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCTGTATC	TATTAACCTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCTGT	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
40	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
45	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGT	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTACTA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
50	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1725

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACATAT	TCTTACTTTC	ACGTCAAGTT	GGTGTTCAT	ACATCGTTGT	100
	ATTCATGAAC	AAATGTGACA	TGGTTGACGA	TGAAGAATTA	CTTGAATTAG	150
20	TTGAAATGGA	AATTCGTGAT	CTATTAAGTG	AATATGAATT	CCCTGGCGAC	200
	GACATTCCTG	TAATCAAAGG	TTCAGCTCTT	AAAGCACTTC	AAGGTGAAGC	250
	TGATTGGGAA	GCTAAAATTG	ACGAGTTAAT	GGAAGCTGTA	GATTCTTACA	300
	TTCCAAGTCC	AGAACGTGAT	ACTGACAAAC	CATTCATGAT	GCCAGTTGAG	350
	GATGTATTCT	CAATCACTGG	TCGTGGAACA	GTTGCAACTG	GACGTGTTGA	400
25	ACGTGGACAA	GTTAAAGTTG	GTGACGAAGT	AGAAGTTATC	GGTATTGAAG	450
	AAGAAAGCAA	AAAAGTAGTA	GTAAGTGGAG	TAGAAATGTT	CCGTAAATTA	500
	CTAGACTACG	CTGAAGCTGG	CGACAACATT	GGCGCACTTC	TACGTGGTGT	550
	TGCTCGTGAA	GATATCCAAC	GTGGTCAAGT	ATTAGCTAAA	CCAGGTTCGA	600
	TTACTCCACA	TACTAACTTC	AAAGCTGAAA	CTTATGTTTT	AACTAAAGAA	650
30	GAAGGTGGAC	GTCATACTCC	ATTCTTCAAC	AACTACCGCC	CACAATTCTA	700
	TTTCCGTACT	ACTGACGTAA	CTGGTATTGT	TACACTTCCA	GAAGGTACTG	750
	AAATGGTAAT	GCCTGGTGAT	AACATTGAGC	TTGCAGTTGA	ACTAATTGCA	800
	CCAATCGCTA	TCGAAGAC				818

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2) INFORMATION FOR SEQ ID NO: 1726

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: LSPQ 5093202
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726

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CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGCGATG	200
	ACATTCCGTG	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
5	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCW	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATCGAAGA	450
	AGAAAGCAAA	AAAGTAGTAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
10	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACR	TGGTCAAGTA	TTAGCTAAAC	CAGGTTCGAT	600
	TACTCCACAC	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTAATA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
15	AATGGTAAAYG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1727

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria seeligeri*
 (B) STRAIN: ATCC 35967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727

35	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAACATAT	CTTACTTTCA	CGTCAAGTTG	GTGTTCCATA	CATCGTTGTA	100
	TTCATGAACA	AATGTGACAT	GGTTGACGAT	GAAGAATTAC	TTGAATTAGT	150
	TGAAATGGAA	ATTCGTGATC	TATTAAGTGA	ATATGAATTC	CCTGGTGATG	200
40	ACATTCCGTG	AATCAAAGGT	TCAGCTCTTA	AAGCACTTCA	AGGTGAAGCT	250
	GACTGGGAAG	CTAAAATTGA	CGAGTTAATG	GAAGCTGTAG	ATTCTTACAT	300
	TCCAACCTCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ATGTATTCTC	AATCACTGGT	CGTGGAACAG	TTGCAACTGG	ACGTGTTGAA	400
	CGTGGACAAG	TTAAAGTTGG	TGACGAAGTA	GAAGTTATCG	GTATTGAAGA	450
45	AGAAAGCAAA	AAAGTAATAG	TAAGTGGAGT	AGAAATGTTC	CGTAAATTAC	500
	TAGACTACGC	TGAAGCTGGC	GACAACATTG	GCGCACTTCT	ACGTGGTGTG	550
	GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTAGCTAAAC	CAGGTTCGAT	600
	TACTCCACAT	ACTAACTTCA	AAGCTGAAAC	TTATGTTTTA	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGCCC	ACAATTCTAT	700
50	TTCCGTAATA	CTGACGTAAC	TGGTATTGTT	ACACTTCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACATTGAGCT	TGCAGTTGAA	CTAATTGCAC	800
	CAATCGCTAT	CGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1728

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 814 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: ATCC 25923

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728

	CGGTGGTATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
20	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAR	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTARTG	GAAGCTGTAG	ATACTTACAT	300
	TCCAACCTCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
25	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	450
	CACATCTAAA	ACAACGTGTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	550
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	600
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	650
30	GTGGACGTCA	CACTCCATTC	TTCTCAAAC	ATCGTCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACCTG	TGTTGTTTAC	TTACCAGAAG	GTAAGTAAAT	750
	GGTAATGCCT	GGTGATAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCAA	800
	TCGCGATTGA	AGAC				814

35

2) INFORMATION FOR SEQ ID NO: 1729

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 15305

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729

	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCACAAACTC	50
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	GTGAACACAT	TCTTTTATCA	CGTRACGTTG	GTGYTCCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAY	GAAGAATTAT	TAGAATTRGT	150
	AGAAATGGAA	GTTTCGTGRCT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	200
	ATGTACCTGT	AATCTCTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACGCT	250
5	GACTATGAGC	AAAAAATCTT	AGACTTAATG	CAAGCTGTTG	ATGACTYCAT	300
	TCCAACACCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAATC	GARATCATCG	GTATGCAAGA	450
	AGAATCAAGC	AAAACAACCTG	TTACTGGTGT	AGAAATGTTC	CGTAAATTAT	500
10	TAGACTACGC	TGAAGCTGGT	GACAACATTG	GTGCATTATT	ACGTGGTGT	550
	TCACGTGATG	ATGTACAACG	TGGTCAAGTT	TTAGCTGCTC	CTGGTACTAT	600
	CACACCACAT	ACAAAATTCA	AAGCGGATGT	TTACGTTTTA	TCTAAAGATG	650
	AAGGTGGTCG	TCATACGCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAT	700
	TTCCGTAATA	CTGACGTAAC	TGGTGTGT	AACTTACCAG	AAGGTACTGA	750
15	AATGGTTATG	CCTGGCGATA	ACGTTGAAAT	GGATGTTGAA	TTAATTTCTC	800
	CAATCGCTAT	TGAAGAC				817

20 2) INFORMATION FOR SEQ ID NO: 1730

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus simulans*
 (B) STRAIN: ATCC 27848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730

35	CGGCGGTATC	TTAGTAGTAT	CTGCTGCAGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	TTTAGTTGTA	100
	TTCTTAAACA	AAGCTGACAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTATCTGA	ATACGACTTC	CCTGGTGACG	200
40	ATGTACCAGT	TATCGTTGGT	TCTGCATTAA	AAGCTTTAGA	AGGCGACCCA	250
	GAATACGAAC	AAAAAATCTT	AGACTTAATG	CAAGCTGTAG	ATGACTACAT	300
	CCCAACTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TAGCAACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAGTT	GAAATCATCG	GTATCACTGA	450
45	AGAAAGCAAG	AAAACAACAG	TTACAGGTGT	AGAAATGTTC	CGTAAATTAT	500
	TAGACTACGC	TGAAGCTGGT	GACAACATCG	GTGCTTTATT	ACGTGGTGT	550
	GCACGTGAAG	ACGTACAACG	TGGACAAGTA	TTAGCAGCTC	CTGGCTCTAT	600
	TACTCCACAC	ACAAAATTCA	AAGCTGATGT	TTACGTTTTA	TCTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
50	TTCCGTAATA	CTGACGTAAC	TGGCGTTGTT	CACTTACCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACGTAGAAAT	GACTGTTGAA	TTGATCGCTC	800
	CAATCGCGAT	TGAAGAC				817

2) INFORMATION FOR SEQ ID NO: 1731

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731

CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC 50
 GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA 100
 20 TTCATGAACA AAGTTGACCT TGTGATGAT GAAGAATTGC TTGAATTGGT 150
 TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG 200
 ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA 250
 AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT 300
 TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG 350
 25 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC 400
 CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA 450
 AGATATCCAA AAAGCAGTTG TTAGTGGTGT TGAAATGTTC CGTAAACAAC 500
 TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGT 550
 CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
 30 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG 650
 AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC 700
 TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA 750
 AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTACAC 800
 CAATCGCCGT AGAACAA 817

2) INFORMATION FOR SEQ ID NO: 1732

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Streptococcus pneumoniae*
 50 (B) STRAIN: ATCC 27336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732

	CGGAGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAC	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TATTGTCAGA	ATACGACTTC	CCAGGTGACG	200
5	ATCTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGACTCT	250
	AAATACGAAG	ACATCGTTAT	GGAATTGATG	AACACAGTTG	ATGAGTATAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTATCG	TTAAAGTCAA	CGACGAAATC	GAAATCGTTG	GTATCAAAGA	450
10	AGAAACTCRA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGAAGG	TCTTGCTGGA	GATAACGTAG	GTGTCCTTCT	TCGTGGTGTT	550
	CAACGTGATG	AAATCGAACG	TGGACAAGTT	ATCGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	CTACATCCTT	ACTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAATTCTAC	700
15	TTCCGTAATA	CTGACGTTAC	AGGTTCAATC	GAAGTTCCAG	CAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTGACAAT	CGACGTTGAG	TTGATTCCACC	800
	CAATCGCCGT	AGAACAA				817

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2) INFORMATION FOR SEQ ID NO: 1733

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733

	CGGTGCGATC	CTTGTAGTAG	CATCTACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAGGTTG	GTGTTAAACA	CCTTATCGTC	100
	TTCATGAACA	AAGTTGACTT	GGTTGACGAT	GAAGAATTGC	TTGAATTGGT	150
40	TGAAATGGAA	ATCCGTGACC	TTCTTTTCTA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCTCTTA	AAGCTCTTGA	AGGTGATTCT	250
	AAATACGAAG	ACATCATCAT	GGACTTGATG	AACACTGTTG	ACGAATACAT	300
	CCCAGAACCA	GAACGTGACA	CTGACAAACC	ATTGTTGCTT	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
45	CGTGGTGTTG	TTCGTGTCAA	TGACGAAGTT	GAAATCGTTG	GTCTTAAAGA	450
	AGACATCCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAAC	500
	TTGACGRAGG	TATTGCCGGA	GATAACGTCG	GTGTTCTTCT	TCGTGGTATC	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTA	TTGGCTGCAC	CTGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACATCCTT	TCTAAAGAAG	650
50	AAGGTGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAAC	AGGTTCAATC	GAAGTTCTTG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAA				817

2) INFORMATION FOR SEQ ID NO: 1734

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Agrobacterium tumefaciens*
 (C) ACCESSION NUMBER: x99673
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734

	AACATGATCA	CCGGTGCTGC	CGAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
	GGCTGCCGAC	GGCCCGATGC	CACAGACCCG	CGAGCACATC	CTGCTTGCCC	100
	GTCAGGTGGG	CGTTCCGGCC	ATCGTCGTGT	TCCTCAACAA	GGTCGACCAG	150
20	GTTGACGACG	CCGAGCTTCT	CGAGCTCGTC	GAGCTTGAAG	TTCGCGAACT	200
	TCTGTCGTCC	TACGACTTCC	CGGGCGACGA	TATCCCGATC	ATCAAGGGTT	250
	CGGCACTTGC	TGCTCTTGAA	GATTCTGACA	AGAAGATCGG	TGAAGACGCG	300
	ATCCGCGAGC	TGATGGCTGC	TGTCGACGCC	TACATCCCGA	CGCCTGAGCG	350
	TCCGATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
25	CGGGTCGTGG	TACGGTTGTG	ACGGGTCGCG	TTGAGCGCGG	TATCGTCAAG	450
	GTTGGTGAAG	AAGTCGAAAT	CGTCGGCATC	CGTCCGACCT	CGAAGACGAC	500
	TGTTACCGGC	GTTGAAATGT	TCCGCAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACAT	CGGTGCACTC	GTTCGCGGCG	TTACCCGTGA	CGGCGTCGAG	600
	CGTGGTCAGA	TCCTGTGCAA	GCCGGGTTCG	GTCAAGCCGC	ACAAGAAGTT	650
30	CATGGCAGAA	GCCTACATCC	TGACGAAGGA	AGAAGGCGGC	CGTCATACGC	700
	CGTTCTTCAC	GAActACCGT	CCGCAGTTCT	ACTTCCGTAC	GA CTGACGTT	750
	ACCGGTATCG	TTTCGCTTCC	TGAAGGCACG	GAAATGGTTA	TGCCTGGCGA	800
	CAACGTCACT	GTTGAAGTCG	AGCTGATCGT	TCCGATCGCG	ATGGAAGAAA	850
	AGCTGCGCTT	CGCTATCCGC	GAAGGCGGCC	GTACCGTCGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1735

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 885 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus subtilis*
 (B) STRAIN: 168
 (C) ACCESSION NUMBER: Z99104
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735

	ATGATCACTG	GTGCTGCGCA	AATGGACGGA	GCTATCCTTG	TAGTATCTGC	50
	TGCTGATGGC	CCAATGCCAC	AAACTCGTGA	GCACATCCTT	CTTTCTAAAA	100
	ACGTTGGTGT	ACCATACATC	GTTGTATTCT	TAAACAAATG	CGACATGGTA	150
5	GACGACGAAG	AGCTTCTTGA	ACTAGTTGAA	ATGGAAGTTC	GCGATCTTCT	200
	TAGCGAATAC	GACTTCCCTG	GTGATGATGT	ACCAGTTGTT	AAAGGTTCTG	250
	CTCTTAAAGC	TCTTGAAGGA	GACGCTGAGT	GGGAAGCTAA	AATCTTCGAA	300
	CTTATGGATG	CGGTTGATGA	GTACATCCCA	ACTCCAGAAC	GCGACACTGA	350
	AAAACCATTC	ATGATGCCAG	TTGAGGACGT	ATTCTCAATC	ACTGGTCGTG	400
10	GTACAGTTGC	TACTGGCCGT	GTAGAACGCG	GACAAGTTAA	AGTCGGTGAC	450
	GAAGTTGAAA	TCATCGGTCT	TCAAGAAGAG	AACAAGAAAA	CAACTGTTAC	500
	AGGTGTTGAA	ATGTTCCGTA	AGCTTCTTGA	TTACGCTGAA	GCTGGTGACA	550
	ACATTGGTGC	CCTTCTTCGC	GGTGTATCTC	GTGAAGAAAT	CCAACGTGGT	600
	CAAGTACTTG	CTAAACCAGG	TACAATCACT	CCACACAGCA	AATTCAAAGC	650
15	TGAAGTTTAC	GTTCTTTCTA	AAGAAGAGGG	TGGACGTCAT	ACTCCATTCT	700
	TCTCTAACTA	CCGTCCTCAG	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	750
	ATCATCCATC	TTCCAGAAGG	CGTAGAAATG	GTTATGCCTG	GAGATAACAC	800
	TGAAATGAAC	GTTGAACTTA	TTTCTACAA	CGCTATCGAA	GAAGGAACTC	850
	GTTTCTCTAT	TCGTGAAGGC	GGACGTACTG	TTGGT		885
20						

2) INFORMATION FOR SEQ ID NO: 1736

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 882 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacteroides fragilis*
 - (B) STRAIN: DSM 2151
 - (C) ACCESSION NUMBER: P33165
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736

40	ATGGTTACTG	GTGCTGCTCA	GATGGACGGT	GCTATCATTG	TAGTTGCTGC	50
	TACTGATGGT	CCGATGCCTC	AGACTCGTGA	GCACATCCTT	TTGGCTCGTC	100
	AGGTAAACGT	TCCGAAGCTG	GTTGTATTCA	TGAACAAGTG	CGATATGGTT	150
	GAAGATGCTG	AGATGTTGGA	ACTTGTTGAA	ATGGAAATGA	GAGAATTGCT	200
	TTCATTCTAT	GATTTGACG	GTGACAATAC	TCCGATCATT	CAGGGTTCTG	250
45	CTCTTGGTGC	ATTGAACGGC	GTAGAAAAAT	GGGAAGACAA	AGTAATGGAA	300
	CTGATGGAAG	CTGTTGATAC	TTGGATTCCA	CTGCCTCCGC	GCGATGTTGA	350
	TAAACCTTTC	TTGATGCCGG	TAGAAGACGT	GTTCTCTATC	ACAGGTCGTG	400
	GTACTGTAGC	TACAGGTCGT	ATCGAAACTG	GTGTTATCCA	TGTAGGTGAT	450
	GAAATCGAAA	TCCTCGGTTT	GGGTGAAGAT	AAGAAATCAG	TTGTAACAGG	500
50	TGTTGAAATG	TTCCGCAAAC	TTCTGGATCA	GGGTGAAGCT	GGTGACAACG	550
	TAGGTCTGTT	GCTTCGTGGT	GTTGACAAGA	ACGAAATCAA	ACGTGGTATG	600
	GTTCTTTGTA	AACCGGGTCA	GATTAAACCT	CACTCTAAAT	TCAAAGCAGA	650
	GGTTTATATC	CTGAAGAAAG	AAGAAGGTGG	TCGTACACT	CCATTCCATA	700

ACAAATATCG	TCCTCAGTTC	TACCTGCGTA	CTATGGACTG	TACAGGTGAA	750
ATCACTCTTC	CGGAAGGAAC	TGAAATGGTA	ATGCCGGGTG	ATAACGTAAC	800
TATCACTGTA	GAGTTGATCT	ATCCGGTTGC	ACTGAACATC	GGTCTTCGTT	850
TCGCTATCCG	CGAAGGTGGA	CGTACAGTAG	GT		882

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2) INFORMATION FOR SEQ ID NO: 1737

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 20 (B) STRAIN: U78183
 (C) ACCESSION NUMBER: U78183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737

25	AATATGATTA	CAGGAGCAGC	TCAAATGGAT	GCAGCGATAC	TTTtagTTGC	50
	TGCTGATAGT	GGTGCTGAGC	CTCAAACAAA	AGAGCATTTG	CTTCTTGCTC	100
	AAAGAATGGG	AATAAAGAAA	ATAATAGTTT	TTTTAAATAA	ATTGGACTTA	150
	GCAGATCCTG	AACTTGTTGA	GCTTGTTGAA	GTTGAAGTTT	TAGAACTTGT	200
	TGAAAAATAT	GGCTTTTCAG	CTGATACTCC	AATAATCAAA	GGTTCAGCTT	250
30	TTGGGGCTAT	GTCAAATCCA	GAAGATCCTG	AATCTACAAA	ATGCGTTAAA	300
	GAACTTCTTG	AATCTATGGA	TAATTATTTT	GATCTTCCAG	AAAGAGATAT	350
	TGACAAGCCA	TTTTTGCTTG	CTGTTGAAGA	TGTATTTTCT	ATTTTCAGGAA	400
	GAGGCACTGT	TGCTACTGGG	CGTATTGAAA	GAGGTATTAT	TAAAGTTGGT	450
	CAAGAAGTTG	AAATAGTTGG	AATTAAAGAA	ACCAGAAAAA	CTACTGTTAC	500
35	TGGTGTTGAA	ATGTTCCAGA	AAATTCTTGA	GCAAGGTCAA	GCAGGGGATA	550
	ATGTTGGTCT	TCTTTTGAGA	GGCGTTGATA	AAAAAGACAT	TGAGAGGGGG	600
	CAAGTTTTGT	CAGCTCCAGG	TACAATTACT	CCACACAAGA	AATTTAAAGC	650
	TTCAATTTAT	TGTTTGACTA	AAGAAGAAGG	CGGTAGGCAC	AAGCCATTTT	700
	TCCCAGGGTA	TAGACCACAG	TTCTTTTTTA	GAACAACCGA	TGTTACTGGA	750
40	GTTGTTGCTT	TAGAGGGCAA	AGAAATGGTT	ATGCCTGGTG	ATAATGTTGA	800
	TATTATTGTT	GAGCTGATCT	CTTCAATAGC	TATGGATAAG	AATGTAGAAT	850
	TTGCTGTTCG	AGAAGGTGGA	AGAACCGTTG	CTTCAGGA		888

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2) INFORMATION FOR SEQ ID NO: 1738

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevibacterium linens*
 5 (B) STRAIN: DSM 20425
 (C) ACCESSION NUMBER: X76863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738

10	AACATGATCA	CCGGTGCCGC	TCAGATGGAC	GGTGCGATCC	TCGTCTCGTCGC	50
	CGCTACCGAC	GGACCGATGC	CCCAGACCCG	TGAGCACGTG	CTGCTCGCGC	100
	GTCAGGTCGG	CGTTCCCTAC	ATCGTCGTGG	CTCTGAACAA	GTCCGACATG	150
	GTCGATGACG	AGGAGCTCCT	CGAGCTCGTC	GAATTCGAGG	TCCGCGACCT	200
	GCTCTCGAGC	CAGGACTTCG	ACGGAGACAA	CGTCCGGTC	ATTCCGGTGT	250
15	CCGCTCTCAA	GGCGCTGGAA	GGCGACGAGA	AGTGGGTCAA	GAGCGTTCAG	300
	GATCTCATGG	CTGCCGTCGA	TGACAACGTT	CCGGAGCCGG	AGCGCGATGT	350
	CGACAAGCCG	TTCCTCATGC	CCGTCGAGGA	CGTCTTCACG	ATCACCGGTC	400
	GTGGAACCGT	CGTCACCGGT	CGTGTCGAGC	GCGGCGTGCT	CCTGCCTAAC	450
	GACGAAATCG	AAATCGTCGG	CATCAAGGAG	AAGTCGTCCA	AGACGACTGT	500
20	CACCGCTATC	GAGATGTTCC	GCAAGACCCCT	GCCGGATGCC	CGTGCAGGTG	550
	AGAACGTCGG	TCTGCTCCTC	CGCGGCACCA	AGCGCGAGGA	TGTTGAGCGC	600
	GGTCAGGTCA	TCGTGAAGCC	GGGTTCGATC	ACCCCGCACA	CCAAGTTCGA	650
	GGCTCAGGTC	TACATCCTGA	GCAAGGACGA	GGGCGGACGT	CACAACCCGT	700
	TCTACTCGAA	CTACCGTCCG	CAGTTCTACT	TCCGGACCAC	GGACGTCACC	750
25	GGTGTCATCA	CGCTGCCCCG	GGGCACCGAG	ATGGTCATGC	CCGGCGACAA	800
	CACCGATATG	TCGGTCGAGC	TCATCCAGCC	GATCGCTATG	GAGGACCGCC	850
	TCCGCTTCGC	AATCCGCGAA	GGTGGCCGCA	CCGTCGGCGC	CGGT	894

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2) INFORMATION FOR SEQ ID NO: 1739

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
 35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: F/IC-Cal-13
 45 (C) ACCESSION NUMBER: L22216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739

	ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
	AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
50	AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
	GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
	GTCGAAGTAC	GACTTCCCGG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
	CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300

	ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
	AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
	GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCTG	AGCGCGGCAT	CGTGAAGGTC	450
	GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
5	CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
	ACAACGTCCG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
	GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
10	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
	CGTGTCTGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
	TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCGGC		888

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2) INFORMATION FOR SEQ ID NO: 1740

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fibrobacter succinogenes*
 (B) STRAIN: S85
 (C) ACCESSION NUMBER: X76866

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740

	AACATGGTGA	CTGGTGCTGC	TCAGATGGAC	GGCGCTATCC	TCGTTGTTGC	50
	CGCTACTGAC	GGTCCGATGC	CGCAGACTCG	CGAACACATC	CTTCTCGCTC	100
35	ACCAGGTTGG	CGTGCCGAAG	ATCGTCGTGT	TCATGAACAA	GTGCGACATG	150
	GTTGACGATG	CTGAAATTCT	CGACCTCGTC	GAAATGGAAG	TTCGCGAACT	200
	CCTCTCCAAG	TATGACTTCG	ACGGTGACAA	CACCCCGATC	ATCCGTGGTT	250
	CCGCTCTCAA	GGCCCTCGAA	GGCGATCCGG	AATACCAGGA	CAAGGTCATG	300
	GAACATCATGA	ACGCTTGCGA	CGAATACATC	CCGCTCCCGC	AGCGCGATAC	350
40	CGACAAGCCG	TTCCTCATGC	CGATCGAAGA	CGTGTTACAG	ATTACTGGCC	400
	GCGGCACTGT	CGCTACTGGC	CGTATCGAAC	GCGGTGTCGT	TCGCTTGAAC	450
	GACAAGGTTG	AACGTATCGG	TCTCGGTGAA	ACCACCGAAT	ACGTCATCAC	500
	CGGTGTTGAA	ATGTTCCGTA	AGCTCCTCGA	CGACGCTCAG	GCAGGTGACA	550
	ACGTTGGTCT	CCTCCTCCGT	GGTGCTGAAA	AGAAGGACAT	CGTCCGTGGC	600
45	ATGGTTCTCG	CAGCTCCGAA	GTCTGTCACT	CCGCACACCG	AATTTAAGGC	650
	TGAAATCTAC	GTTCTCACGA	AGGACGAAGG	TGGCCGTCAC	ACGCCGTTCA	700
	TGAATGGCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTTACTGGT	750
	ACGATCCAGC	TCCCGGAAGG	TGTCGAAATG	GTTACTCCGG	GTGACACGGT	800
	CACGATCCAC	GTGAACCTCA	TCGCTCCGAT	CGCTATGGAA	AAGCAGCTCC	850
50	GCTTCGCTAT	CCGTGAAGGT	GGACGTACTG	TTGGTGCTGG	C	891

2) INFORMATION FOR SEQ ID NO: 1741

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Flavobacterium ferrugineum*
 (B) STRAIN: DSM 13524
 (C) ACCESSION NUMBER: X76867

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741

	AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGTGCTATCT	TAGTTGTGGC	50
	TGCATCAGAC	GGTCCTATGC	CTCAAACAAA	AGAACACATC	CTGCTTGCTG	100
20	CCCAGGTAGG	TGTACCTAAA	ATGGTTGTGT	TTCTGAATAA	AGTTGACCTC	150
	GTTGACGACG	AAGAGCTCCT	GGAGCTGGTT	GAGATCGAGG	TTCGCGAAGA	200
	ACTGACTAAA	CGCGGTTTCG	ACGGCGACAA	CACTCCAATC	ATCAAAGGTT	250
	CCGCTACAGG	CGCCCTCGCT	GGTGAAGAAA	AGTGGGTAA	AGAAATTGAA	300
	AACCTGATGG	ACGCTGTTGA	CAGCTACATC	CCACTGCCTC	CTCGTCCGGT	350
25	TGATCTGCCG	TTCCTGATGA	GCGTAGAGGA	CGTATTCTCT	ATCACTGGTC	400
	GTGGTACTGT	TGCTACCGGT	CGTATCGAGC	GTGGCCGTAT	CAAAGTTGGT	450
	GAGCCTGTTG	AGATCGTAGG	TCTGCAGGAG	TCTCCCCTGA	ACTCTACCGT	500
	TACAGGTGTT	GAGATGTTCC	GCAAACCTCT	CGACGAAGGT	GAAGCTGGTG	550
	ATAACGCCGG	TCTCCTCCTC	CGTGGTGTTG	AAAAACACA	GATCCGTCGC	600
30	GGTATGGTAA	TCGTTAAACC	CGGTTCCATC	ACTCCGCACA	CGGACTTCAA	650
	AGGCGAAGTT	TACGTACTGA	GCAAAGACGA	AGGTGGCCGT	CACACTCCAT	700
	TCTTCAACAA	ATACCGTCCT	CAATTCTACT	TCCGTACAAC	TGACGTTACA	750
	GGTGAAGTAG	AACTGAACGC	AGGAACAGAA	ATGGTTATGC	CTGGTGATAA	800
	CACCAACCTG	ACCGTTAAAC	TGATCCAACC	GATCGCTATG	GAAAAAGGTC	850
35	TGAAATTCCG	GATCCGCGAA	GGTGGCCGTA	CCGTAGGTGC	AGGA	894

2) INFORMATION FOR SEQ ID NO: 1742

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Helicobacter pylori*
 (B) STRAIN: 26695
 (C) ACCESSION NUMBER: AE000626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742

	AACATGATCA	CCGGTGCGGC	GCAAATGGAC	GGAGCGATTT	TGGTTGTTTC	50
	TGCAGCTGAT	GGCCCTATGC	CTCAAAC TAG	GGAGCATATC	TTATTGTCTC	100
5	GTCAAGTAGG	CGTGCC TCAC	ATCGTTGTTT	TCTTAAACAA	ACAAGACATG	150
	G TAGATGACC	AAGAATTGTT	AGAACTTGTA	GAAATGGAAG	TGCGCGAATT	200
	GTTGAGCGCG	TATGAATTTT	CTGGCGATGA	CACTCCTATC	G TAGCGGGTT	250
	CAGCTTTAAG	AGCTTTAGAA	GAAGCAAAGG	CTGGTAATGT	GGGTGAATGG	300
	GGTGAAAAAG	TGCTTAAACT	TATGGCTGAA	GTGGATGCCT	ATATCCCTAC	350
10	TCCAGAAAGA	GACACTGAAA	AAACTTTCTT	GATGCCGGTT	GAAGATGTGT	400
	TCTCTATTGC	GGGTAGAGGG	ACTGTGGTTA	CAGGTAGGAT	TGAAAGAGGC	450
	GTGGTGAAAG	TAGGCGATGA	AGTGGAATC	GTTGGTATCA	GACCTACACA	500
	AAAAACGACT	GTAACCGGTG	TAGAAATGTT	TAGGAAAGAG	TTGGAAAAAG	550
	GTGAAGCCGG	CGATAATGTG	GGCGTGCTTT	TGAGAGGAAC	TAAAAAAGAA	600
15	GAAGTGGAAC	GCGGTATGGT	TCTATGCAAA	CCAGGTTCTA	TCACTCCGCA	650
	CAAGAAATTT	GAGGGAGAAA	TTTATGTCCT	TTCTAAAGAA	GAAGGCGGGA	700
	GACACACTCC	ATTCTTCACC	AATTACCGCC	CGCAATTCTA	TGTGCGCACA	750
	ACTGATGTGA	CTGGCTCTAT	CACCTTCCT	GAAGGCGTAG	AAATGGTTAT	800
	GCCTGGCGAT	AATGTGAAAA	TCACTGTAGA	GTTGATTAGC	CCTGTTGCGT	850
20	TAGAGTTGGG	AACTAAATTT	GCGATTCTGT	AAGGCGGTAG	GACCGTTGGT	900
	GCTGGT					906

25 2) INFORMATION FOR SEQ ID NO: 1743

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus luteus*
 (B) STRAIN: IFO 3333
 (C) ACCESSION NUMBER: M17788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743

	AACATGATCA	CCGGCGCCGC	TCAGATGGAC	GGCGCGATCC	TCGTGGTCGC	50
	CGCTACCGAC	GGCCCGATGG	CCCAGACCCG	TGAGCACGTG	CTCCTGGCCC	100
	GCCAGGTCGG	CGTGCCCGCC	CTGCTCGTGG	CCCTGAACAA	GTCGGACATG	150
45	GTGGAGGACG	AGGAGCTCCT	CGAGCGTGTC	GAGATGGAGG	TCCGGCAGCT	200
	GCTGTCTCTC	AGGAGCTTCG	ACGTGACGCA	GGCCCCGGTC	ATCCGCACCT	250
	CCGCTCTGAA	GGCCCTCGAG	GGCGACCCCC	AGTGGGTCAA	GTCCGTCGAG	300
	GACCTCATGG	ATGCCGTGGA	CGAGTACATC	CCGGACCCGG	TGCGCGACAA	350
	GGACAAGCCG	TTCCTGATGC	CGATCGAGGA	CGTCTTCACG	ATCACCGGCC	400
50	GTGGCACCGT	GGTGACCGGT	CGCGCCGAGC	GCGGCACCCT	GAAGATCAAC	450
	TCCGAGGTCG	AGATCGTCGG	CATCCGCGAC	GTGCAGAAGA	CCACTGTCAC	500
	CGGCATCGAG	ATGTTCCACA	AGCAGCTCGA	CGAGGCCTGG	GCCGGCGAGA	550
	ACTGCGGTCT	GCTCGTGCGC	GGTCTGAAGC	GCGACGACGT	CGAGCGCGGC	600

	CAGGTGCTGG	TGGAGCCGGG	CTCCATCACC	CCGCACACCA	ACTTCGAGGC	650
	GAACGTCTAC	ATCCTGTCCA	AGGACGAGGG	TGGGCGTCAC	ACCCCGTTCT	700
	ACTCGAACTA	CCGCGCGCAG	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	750
	GTCATCACGC	TGCCCCGAGGG	CACCGAGATG	GTCATGCCCCG	GCGACACCAC	800
5	CGAGATGTCG	GTCGAGCTCA	TCCAGCCGAT	CGCCATGGAG	GAGGGCCTCG	850
	GCTTCGCCAT	CCGCGAGGGT	GGCCGCACCG	TGGGCTCCGG	C	891

10 2) INFORMATION FOR SEQ ID NO: 1744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: Erdmann
 (C) ACCESSION NUMBER: X63539

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744

	AACATGATCA	CCGGCGCCGC	GCAGATGGAC	GGTGCGATCC	TGGTGGTTCGC	50
	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	CGAGCACGTT	CTGCTGGCGC	100
	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	CGCTGAACAA	GGCCGACGCA	150
30	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	GAGATGGAGG	TCCGCGAGCT	200
	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	CCCGGTTGTG	CGGGTCTCGG	250
	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	GGGTTGCCTC	TGTCGAGGAA	300
	CTGATGAACG	CGGTCGACGA	GTCGATTCCG	GACCCGGTCC	GCGAGACCGA	350
	CAAGCCGTTT	CTGATGCCCG	TCGAGGACGT	CTTCACCATT	ACCGGCCCGC	400
35	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	GCGTGATCAA	CGTGAACGAG	450
	GAAGTTGAGA	TCGTGCGCAT	TCGCCCATCG	ACCACCAAGA	CCACCGTCAC	500
	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	CCAGGGCCAG	GCGGGCGACA	550
	ACGTTGGTTT	GCTGCTGCGG	GGCGTCAAGC	GCGAGGACGT	CGAGCGTGCC	600
	CAGGTTGTCA	CCAAGCCCGG	CACCACCACG	CCGCACACCG	AGTTCGAAGG	650
40	CCAGGTCTAC	ATCCTGTCCA	AGGACGAGGG	CGGCCGGCAC	ACGCCGTTCT	700
	TCAACAACCTA	CCGTCCGCAG	TTCTACTTCC	GCACCACCGA	CGTGACCGGT	750
	GTGGTGACAC	TGCCCGAGGG	CACCGAGATG	GTGATGCCCCG	GTGACAACAC	800
	CAACATCTCG	GTGAAGTTGA	TCCAGCCCGT	CGCCATGGAC	GAAGGTCTGC	850
45	GTTTCGCGAT	CCGCGAGGGT	GGCCGCACCG	TGGGCGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1745

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycoplasma genitalium*

(B) STRAIN: G37

(C) ACCESSION NUMBER: U39732

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745

	AATATGATCA	CAGGTGCTGC	ACAAATGGAT	GGAGCTATTC	TAGTTGTTTC	50
	AGCAACTGAT	AGTGTGATGC	CCCAAACCCG	CGAGCACATC	TTACTTGCCC	100
	GCCAAGTAGG	GGTTCCTAAA	ATGGTAGTTT	TTCTAAACAA	GTGTGATATT	150
15	GCTAGTGATG	AAGAGGTACA	AGAACTTGTT	GCTGAAGAAG	TACGTGATCT	200
	GTAACTTCC	TATGGTTTTG	ATGGTAAGAA	CACTCCTATT	ATTTATGGCT	250
	CAGCTTTAAA	AGCATTGGAA	GGTGATCCAA	AGTGGGAGGC	TAAGATCCAT	300
	GATTTGATTA	AAGCAGTTGA	TGAATGGATT	CCAACTCCTA	CACGTGAAGT	350
	AGATAAACCT	TTCTTATTAG	CAATTGAAGA	TACGATGACC	ATTACTGGTA	400
20	GAGGTACAGT	TGTTACAGGA	AGAGTTGAAA	GAGGTGAACT	CAAAGTAGGT	450
	CAAGAAGTTG	AAATTGTTGG	TTTAAACCA	ATTAGAAAAG	CAGTTGTTAC	500
	TGGAATTGAA	ATGTTCAAAA	AGGAACTTGA	TTCAGCAATG	GCTGGTGACA	550
	ATGCTGGGGT	ATTATTACGT	GGTGTGAAC	GTAAAGAAGT	TGAAAGAGGT	600
	CAAGTTTTAG	CAAACCCAGG	CTCTATTAAA	CCGCACAAGA	AATTTAAAGC	650
25	TGAGATCTAT	GCTTTAAAGA	AAGAAGAAGG	TGGTAGACAC	ACTGGTTTTT	700
	TAAACGGTTA	CCGTCCTCAA	TTCTATTTCC	GTACCACTGA	TGTAAGTGGT	750
	TCTATTGCTT	TAGCTGAAAA	TACTGAAATG	GTTCTACCTG	GTGATAATGC	800
	TTCTATTACT	GTTGAGTTAA	TTGCTCCTAT	CGCTTGTGAA	AAAGGTAGTA	850
	AGTTCTCAAT	TCGTGAAGGT	GGTAGAACTG	TAGGGGCAGG	C	891

2) INFORMATION FOR SEQ ID NO: 1746

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

45 (B) STRAIN: MS11

(C) ACCESSION NUMBER: L36380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746

50	AACATGATTA	CCGGCGCCGC	ACAAATGGAC	GGTGCAATCC	TGGTATGTTT	50
	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	CGAACACATC	CTGCTGGCCC	100
	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	TCATGAACAA	ATGCGACATG	150
	GTGACGATG	CCGAGCTGTT	CCAAGTGTTT	GAAATGGAAA	TCCGCGACCT	200

	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	CTGCCCCGATC	GTACAAGGTT	250
	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	CTTACGAAGA	AAAAATCTTC	300
	GAAGTGGCTA	CCGCATTGGA	CAGATACATC	CCGACTCCCG	AGCGTGCCGT	350
	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	CGTGTTCTCC	ATTTCCGGCC	400
5	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	GAGGTATCAT	CCACGTTGGT	450
	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	ACCCAAAAAA	CCACCTGTAC	500
	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGTCAG	GCGGGCGACA	550
	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	GTGAAGACGT	AGAACGCGGT	600
	CAGGTATTGG	CCAAACGGGG	TACTATCACT	CCTCACACCA	AGTTCAAAGC	650
10	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	CGGCCCCCAT	ACCCCGTTTT	700
	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	GTACCACTGA	CGTAACCGGC	750
	ACGATTACTT	TGGAAAAAGG	TGTGGAAATG	GTAATGCCGG	GTGAGAACGT	800
	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	CGCTATGGAA	GAAGGTCTGC	850
15	GCTTTGCGAT	TCGCGAAGGC	GGCCGTACCG	TGGGTGCCGG	C	891

2) INFORMATION FOR SEQ ID NO: 1747

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 891 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Rickettsia prowazekii*
 - (B) STRAIN: Madrid E
 - (C) ACCESSION NUMBER: Z54170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747

35	AATATGATAA	CTGGTGCCGC	TCAGATGGAT	GGTGCTATAT	TAGTAGTTTC	50
	TGCTGCTGAT	GGTCCTATGC	CTCAAACCTAG	AGAACATATA	TTACTGGCAA	100
	AACAGGTAGG	TGTACCTGCT	ATGGTAGTAT	TTTTGAATAA	AGTAGATATG	150
	GTAGATGATC	CTGACCTATT	AGAATTAGTT	GAGATGGAAG	TAAGAGAATT	200
	ATTATCAAAA	TATGGTTTCC	CTGGTAATGA	AATACCTATT	ATTAAAGGTT	250
40	CTGCACTTCA	AGCTTTAGAA	GGAAAACCTG	AAGGTGAAAA	AGCTATTAAT	300
	GAGTTAATGA	ATGCAGTAGA	TACGTATATA	CCTCAGCCTA	TAGAGCTACA	350
	AGATAAACCT	TTTTTAATGC	CAATAGAGGA	TGTATTTTCT	ATTTTCAGGCA	400
	GAGGTACCGT	TGTAACCTGGT	AGAGTGAGGT	CAGGCATAAT	TAAGGTGGGT	450
	GAAGAAATTG	AAATAGTAGG	TCTAAAAAAT	ACGCAAAAAA	CGACTTGTAC	500
45	AGGTGTAGAA	ATGTTTCAAG	AATTACTTGA	TGAAGGACAA	TCTGGAGATA	550
	ATGTCGGTAT	ATTACTACGT	GGTACAAAAA	GAGAAGAAGT	AGAAAGAGGA	600
	CAAGTACTTG	CAAAACCTGG	GAGCATAAAA	CCGCATGATA	AATTTGAAGC	650
	TGAAGTGTAT	GTGCTTAGTA	AAGAGGAAGG	TGGACGTCAT	ACCCCATTTA	700
	CTAATGATTA	TCGCCCACAG	TTCTATTTTA	GAACAACAGA	TGTTACCGGC	750
50	ACAATAAAAT	TGCCTTCTGA	TAAGCAGATG	GTTATGCCTG	GAGATAATGC	800
	TACTTTTTTCA	GTAGAATTAA	TTAAGCCGAT	TGCTATGCAA	GAAGGGTTAA	850
	AATTCTCTAT	ACGTGAAGGT	GGTAGAACAG	TAGGAGCCGG	T	891

2) INFORMATION FOR SEQ ID NO: 1748

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 891 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Typhimurium
- (B) STRAIN: LT2 trpE91
- (C) ACCESSION NUMBER: X55116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748

	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	GGCGCGATCC	TGGTTGTTGC	50
20	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	TGAGCACATC	CTGCTGGGTC	100
	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	ATGCGACATG	150
	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	TTCGCGAACT	200
	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	GTTCGTGGTT	250
	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	GAAAATCATC	300
25	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	CCGGAACCAG	AGCGTGCGAT	350
	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	ATCTCCGGTC	400
	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	CAAAGTGGGC	450
	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACTCAGAAGT	CTACCTGTAC	500
	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	GCCGGTGAGA	550
30	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	CGAACGTGGT	600
	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	CCGCACACCA	AGTTCGAATC	650
	TGAAGTGTA	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	ACTCCGTTCT	700
	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	CGTGACTGGT	750
	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	GCGACAACAT	800
35	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	GACGGTCTGC	850
	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	TTGGCGCGGG	C	891

40 2) INFORMATION FOR SEQ ID NO: 1749

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: DSM 50426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749

	ATGATCACTG	GTGCTGCACA	GATGGACGGC	GCGATTCTGG	TAGTCGCTTC	50
	AACAGACGGT	CCAATGCCAC	AGACTCGTGA	GCACATCCTG	CTTTCTCGTC	100
5	AGGTTGGCGT	ACCATTTCATC	ATCGTATTCA	TGAACAAATG	TGACATGGTA	150
	GATGACGAAG	AGCTGTTAGA	GCTAGTTGAG	ATGGAAGTGC	GTGAACTGTT	200
	ATCAGAATAC	GATTTCCCAG	GTGATGACTT	ACCGGTAATC	CAAGGTTGAG	250
	CTCTGAAAGC	GCTAGAAGGC	GAGCCAGAGT	GGGAAGCAAA	AATCCTTGAA	300
	TTAGCAGCGG	CGCTGGATTC	TTACATTCCA	GAACCACAAC	GTGACATCGA	350
10	TAAGCCGTTT	CTACTGCCAA	TCGAAGACGT	ATTCTCAATT	TCAGGCCGTG	400
	GTACAGTAGT	AACAGGTCGT	GTTGAGCGTG	GTATTGTACG	CGTAGGCGAC	450
	GAAGTTGAAA	TCGTTGGTGT	ACGTGCGACA	ACTAAGACAA	CGTGTACTGG	500
	TGTAGAAATG	TTCCGTAAAC	TGCTTGACGA	AGGTCGTGCA	GGTGAGAACT	550
	GTGGTATTTT	GTTACGTGGT	ACTAAGCGTG	ATGACGTAGA	ACGTGGTCAA	600
15	GTATTAGCGA	AGCCAGGTTC	AATCAACCCA	CACACTACTT	TTGAATCAGA	650
	AGTTTACGTA	CTGTCAAAAG	AAGAAGGTGG	TCGTACACAG	CCATTCTTCA	700
	AAGGCTACCG	TCCACAGTTC	TACTTCCGTA	CAACTGACGT	AACCGGTACT	750
	ATCGAACTGC	CAGAAGGCGT	AGAGATGGTA	ATGCCAGGCG	ATAACATCAA	800
	GATGGTAGTG	ACACTGATTT	GCCCAATCGC	GATGGACGAA	GGTTTACGCT	850
20	TCGCAATCCG	TGAAGGCGGT	CGTACAGTGG	T		881

2) INFORMATION FOR SEQ ID NO: 1750

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stigmatella aurantiaca*
 (B) STRAIN: DW4
 (C) ACCESSION NUMBER: X82820

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750

40

	AACATGATCA	CGGGCGCGGC	GCAGATGGAC	GGAGCGATTC	TGGTGGTGTC	50
	CGCGGCCGAC	GGCCCGATGC	CCCAGACGCG	TGAGCACATC	CTGCTGGCCA	100
	GGCAGGTGGG	CGTGCCCTAC	ATCGTCGTCT	TCCTGAACAA	GGTGGACATG	150
	CTGGACGATC	CGGAGCTGCG	CGAGCTGGTG	GAGATGGAGG	TGCGCGACCT	200
45	GCTCAAGAAG	TACGAGTTCC	CGGGCGACAG	CATCCCCATC	ATCCCTGGCA	250
	GCGCGCTCAA	GGCGCTGGAG	GGAGACACCA	GCGACATCGG	CGAGGGAGCG	300
	ATCCTGAAGC	TGATGGCGGC	GGTGGACGAG	TACATCCCGA	CGCCGCAGCG	350
	TGCGACGGAC	AAGCCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCCATCG	400
	CAGGCCGAGG	AACGGTGGCG	ACGGGCCGAG	TGGAGCGCGG	CAAGATCAAG	450
50	GTGGGCGAGG	AAGTGGAGAT	CGTGGGGATC	CGTCCGACGC	AGAAGACGGT	500
	CATCACGGGG	GTGGAGATGT	TCCGCAAGCT	GCTGGACGAG	GGCATGGCGG	550
	GAGACAACAT	CGGAGCGCTG	CTGCGAGGCC	TGAAGCGCGA	GGACCTGGAG	600
	CGTGGGCAGG	TGCTGGCGAA	CTGGGGGAGC	ATCAACCCGC	ACACGAAGTT	650

	CAAGGCGCAG	GTGTACGTGC	TGTCGAAGGA	AGAGGGAGGG	CGGCACACGC	700
	CGTTCTTCAA	GGGATACCGG	CCGCAGTTCT	ACTTCCGGAC	GACGGACGTG	750
	ACCGGAACGG	TGAAGCTGCC	GGACAACGTG	GAGATGGTGA	TGCCGGGAGA	800
	CAACATCGCC	ATCGAGGTGG	AGCTCATTAC	TCCGGTCGCC	ATGGAGAAGG	850
5	AGCTGCCGTT	CGCCATCCGT	GAGGGTGGCC	GCACGGTGGG	CGCCGGC	897

2) INFORMATION FOR SEQ ID NO: 1751

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiomonas cuprina*
 (B) STRAIN: Hoe5
 (C) ACCESSION NUMBER: x76871

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1751

25

	AACATGATCA	CCGGTGCGGC	CCAGATGGAC	GGCGCCATCC	TGGTCGTGTC	50
	CGCCGCCGAC	GGCCCCATGC	CCCAAACCCG	CGAGCACATC	CTGCTGGCGC	100
	GTCAGGTGGG	CGTGCCCTAC	ATCATCGTGT	TCCTCAACAA	GTGCGACATG	150
	GTCGACGACG	CCGAGCTGCT	CGAACTCGTC	GAGATGGAAG	TGCGCGAGCT	200
30	GCTGTCCAAG	TACGACTTCC	CCGGTGACGA	CACCCCATC	ATCAAGGGCT	250
	CGGCCAAGCT	GGCCCTCGAA	GGCGACAAGG	GCGAACTGGG	CGAAGGCGCC	300
	ATTCTCAAGC	TGGCCGAGGC	CCTGGACACC	TACATCCCCA	CGCCCGAGCG	350
	GGCCGTGAC	GGCGCGTTCC	TCATGCCCGT	GGAAGACGTG	TTCTCCATCT	400
	CCGGGCGCGG	CACGGTGGTC	ACCGGGCGTG	TGGAGCGCGG	CATCATCAAG	450
35	GTCGGCGAGG	AAATCGAGAT	TGTCGGCCTC	AAGCCCACCC	TCAAGACCAC	500
	CTGCACCGGC	GTGGAATGT	TCAGGAAGCT	GCTCGACCAG	GGCCAGGCCG	550
	GCGACAACGT	CGGCATCTTG	CTGCGCGGCA	CCAAGCGCGA	GGAAGTCGAG	600
	CGCGGCCAGG	TGCTGTGCAA	ACCGGCTCG	ATCAAGCCCC	ACACCCACTT	650
	CACCGCCGAG	GTGTACGTGC	TGAGCAAGGA	CGAGGGCGGC	CGCCACACCC	700
40	CCTTCTTCAA	CAACTACCGC	CCGCAGTTCT	ACTTCCGCAC	CACCGACGTC	750
	ACCGGCGCCA	TCGAACTGCC	CAAGGACAAG	GAAATGGTCA	TGCCCGGCGA	800
	TAATGTGAGC	ATCACCGTCA	AGCTCATCGC	CCCCATCGCC	ATGGAAGAAG	850
	GCCTGCGCTT	CGCCATCCGC	GAAGGCGGCC	GCACCGTCGG	CGCCGGC	897

45

2) INFORMATION FOR SEQ ID NO: 1752

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 (C) ACCESSION NUMBER: AE001202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752

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10 AATATGATCA CGGGTGCTGC GCAGATGGAC GGTGGTATTC TCGTCGTGTC 50
   TGC GCCTGAC GGC GTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC 100
   GTCAGGTTGG TGTTCCCTCC ATCATTGTTT TTTTGAACAA GGTTGATTG 150
   GTTGATGATC CTGAGTTGCT AGAGCTGGTG GAAGAAGAGG TCGGTGATGC 200
15 GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC AAGGGGTCTG 250
   CGTTTAAAGC TCTGCAGGAT GCGCCTTCCC CGGAGGATGC AGCTTGATT 300
   GAGGAAGTGC TTGCGGCCAT GGATTCCTAC TTTGAAGACC CAGTGCGTGA 350
   CGACGCAAGA CCTTCTTGC TCTCTATCGA GGATGTGTAC ACTATTTCTG 400
   GGC GTGGTAC CGTTGTACG GGGCGCATCG AATGTGGGGT AATTAGTCTG 450
20 AATGAAGAGG TCGAGATCGT CGGGATTAAG CCCACTAAGA AAACAGTGGT 500
   TACTGGCATT GAGATGTTTA ATAAGTTGCT TGATCAGGGA ATTG CAGGTG 550
   ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAGA GGTTGAGCGC 600
   GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA 650
   GGCGCAGATC TACGTGCTCT CTAAGGAAGA GGGTGGCCGT CACAGTCCCT 700
25 TTTTTC AAGG TTATCGTCCG CAGTTTTATT TTAGAACTAC TGACATTACC 750
   GGTACGATTT CTCTTCCTGA AGGGGTAGAC ATGGTGAAGC CGGGGGATAA 800
   CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG GACAAGGGTC 850
   TGAAGCTTGC GATTCGTGAA GGGGGGCGCA CTATTGCTTC TGGT 894

```

30

2) INFORMATION FOR SEQ ID NO: 1753

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Ureaplasma urealyticum*
 (B) STRAIN: ATCC 33697
 (C) ACCESSION NUMBER: Z34275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753

```

50 AATATGATTA CAGGGGCAGC ACAAATGGAT GGAGCAATTT TAGTTATTGC 50
   TGCATCTGAT GGGGTTATGG CTCAAATAA AGAACATATT TTATTAGCAC 100
   GTCAAGTTGG TGTTCCAAAA ATCGTTGTTT TCTTAAACAA ATGTGATTTC 150
   ATGACAGATC CAGATATGCA AGATCTTGTT GAAATGGAAG TTCGTGAATT 200
   ATTATCTAAA TATGGATTG ATGGCGATAA CACACCAGTT ATTCGTGGTT 250

```

	CAGGTCTTAA	GGCTTTAGAA	GGAGATCCAG	TTTGAGAAGC	AAAAATTGAT	300
	GAATTAATGG	ACGCAGTTGA	TTCATGAATT	CCATTACCAG	AACGTAGTAC	350
	TGACAAACCA	TTCTTATTAG	CAATTGAAGA	TGTATTCACA	ATTTCAGGAC	400
	GTGGTACAGT	AGTAACTGGA	CGTGTTGAAC	GTGGTGTATT	AAAAGTTAAT	450
5	GATGAGGTTG	AAATTGTTGG	TCTAAAAGAC	ACTCAAAAAA	CTGTTGTTAC	500
	AGGAATTGAA	ATGTTTAGAA	AATCATTAGA	TCAAGCTGAA	GCTGGTGATA	550
	ATGCTGGTAT	TTTATTACGT	GGTATTAAAA	AAGAAGATGT	TGAACGTGGT	600
	CAAGTACTTG	TAAAACCAGG	ATCAATTAAA	CCTCACCGTA	CTTTTACTGC	650
	TAAAGTTTAT	ATTCTTAAAA	AAGAAGAAGG	TGGACGTCAT	ACACCTATTG	700
10	TTTCAGGATA	CCGTCCACAA	TTCTATTTTA	GAACAACAGA	TGTAACAGGT	750
	GCTATTTTCAT	TACCTGCTGG	TGTTGATTTG	GTTATGCCAG	GTGATGACGT	800
	TGAAATGACT	GTAGAATTAA	TTGCTCCAGT	TGCGATTGAA	GATGGATCTA	850
	AATTCTCAAT	CCGTGAAGGT	GGTAAACTG	TAGGTCATGG	T	891

15

2) INFORMATION FOR SEQ ID NO: 1754

- (i) SEQUENCE CHARACTERISTICS:
- 20 (A) LENGTH: 909 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Wolinella succinogenes*
- (B) STRAIN: DSM 1740
- 30 (C) ACCESSION NUMBER: X76862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754

	AACATGATTA	CAGGTGCTGC	TCAAATGGAT	GGCGCGATTC	TTGTTGTTTC	50
35	TGCGGCGGAT	GGCCCCATGC	CCCAAAC TAG	GGAGCACATT	CTTCTTTCTC	100
	GACAAGTAGG	CGTTCCTTAC	ATCGTGGTTT	TCTTGAACAA	AGAAGATATG	150
	GTTGATGACG	CTGAGCTTCT	TGAGCTTGTT	GAAATGGAAG	TTAGAGAACT	200
	TCTTAGCAAC	TACGACTTCC	CTGGAGATGA	CACTCCTATC	GTTGCAGGTT	250
	CCGCTCTTAA	AGCTCTTGAA	GAGGCTAACG	ACCAGGAAAA	TGTTGGCGAG	300
40	TGGGGCGAGA	AAGTATTGAA	GCTTATGGCT	GAGGTTGACC	GATATATTCC	350
	TACGCCTGAG	CGAGATGTGG	ATAAGCCTTT	CCTTATGCCT	GTTGAAGACG	400
	TATTCTCCAT	CGCGGGTCGT	GGAACCGTTG	TGACAGGAAG	AATTGAAAGA	450
	GGCGTGTTA	AAGTCGGTGA	CGAAGTAGAA	ATCGTTGGTA	TCCGAAACAC	500
	ACAAAAACA	ACCGTAACTG	GCGTTGAGAT	GTTCCGAAAA	GAGCTCGACA	550
45	AGGGTGAGGC	GGGTGACAAC	GTTGGTGTTT	TTTTGAGAGG	CACCAAGAAA	600
	GAAGATGTTG	AGAGAGGTAT	GGTTCTTTGT	AAAATAGGTT	CTATCACTCC	650
	TCACACTAAC	TTTGAAGGTG	AAGTTTACGT	TCTTTCCAAA	GAGGAAGGCG	700
	GACGACACAC	TCCATTCTTC	AATGGATACC	GACCTCAGTT	CTATGTTAGA	750
	ACTACAGACG	TTACCGGTTT	TATCTCTCTT	CCTGAGGGCG	TAGAGATGGT	800
50	TATGCCTGGT	GACAACGTTA	AGATCAATGT	TGAGCTTATC	GCTCCTGTAG	850
	CCCTCGAAGA	GGGAACACGA	TTGCGGATCC	GTGAAGGTGG	TGGAACCGTT	900
	GGTGCGGGT					909

2) INFORMATION FOR SEQ ID NO: 1755

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755

15

ATGATCACGG	GCGCAGCGCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
AGCAGACGGC	CCGATGCCGC	AAACGCGTGA	GCACATCCTG	CTGGCGCGTC	100
AGGTTGGTGT	TCCGTACATC	ATCGTGTTCC	TGAACAAGTG	CGACAGTGTG	150
GACGACGCTG	AACTGCTCGA	GCTGGTCGAG	ATGGAAGTTC	GCGAACTCCT	200
20 GTCGAAGTAC	GAATTCCCCG	GCGACGACAC	GCCGATCGTG	AAGGGTTCGG	250
CCAAGCTGGC	GCTGGAAGGC	GACACGGGCG	AGCTGGGCGA	AGTGGCGATC	300
ATGAGCCTGG	CAGACGCGCT	GGACACGTAC	ATCCCGACGC	CGGAGCGTGC	350
AGTTGACGGC	GCGTTCCTGA	TGCCGGTGGA	AGACGTGTTC	TCGATCTCGG	400
GCCGTGGTAC	GGTGGTGACG	GGTCGTGTCG	AGCGCGGCAT	CGTGAAGGTC	450
25 GGCGAAGAAA	TCGAAATCGT	CGGTATCAAG	CCGACGGTGA	AGACGACCTG	500
CACGGGCGTT	GAAATGTTCC	GCAAGCTGCT	GGACCAAGGT	CAGGCAGGCG	550
ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	AGCGTGAAGA	CGTGGAGCGT	600
GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	ACGCCGCACA	CGCACTTCAC	650
GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	AGGCGGCCGT	CACACGCCGT	700
30 TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	TCCGTACGAC	GGACGTGACG	750
GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	ATGGTGATGC	CGGGCGACAA	800
CGTGTCGATC	ACGGTGAAGC	TGATTGCTCC	GATCGCGATG	GAAGAAGGTC	850
TGCGCTTCGC	AATCCGTGAA	GGCGGCCGTA	CGGTCGGC		888

35

2) INFORMATION FOR SEQ ID NO: 1756

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756

TGAAAGTTCA GGTAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50

AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 5 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1757

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 388 bases
 - 15 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 20 (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus anthracis*
 - (B) STRAIN: ATCC 4229

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757

TGAAAGTTCA GGTAACAAC CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 30 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

35

2) INFORMATION FOR SEQ ID NO: 1758

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 388 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Bacillus cereus*
 - 50 (B) STRAIN: ATCC 7064
 - (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758

5 TGAAAGTTCA GGTAAAACAA CAGTTTCATT ACACGCAATT GCAGAAGTAC 50
 AGCGTCAAGG TGGACAAGCA GCGTTCATTG ATGCTGAGCA TGCAATGGAT 100
 CCTGTATATG CACAAAAACT AGGTGTTAAC ATCGATGAAT TACTATTATC 150
 10 ACAACCTGAT ACAGGGGAGC AAGGTTTAGA AATCGCAGAA GCACTTGTAC 200
 GAAGTGGTGC GGTGATATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 CCGAAAGCTG AAATTGAAGG AGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCTCGTCTA ATGTCTCAAG CACTTCGTAA ACTTTCAGGT GCAATCAATA 350
 AATCAAAAAC AATCGCAATC TTTATTAACC AAATTCGT 388

2) INFORMATION FOR SEQ ID NO: 1759

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus cereus*
 25 (B) STRAIN: ATCC 13472
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759

30 TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC 50
 AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT 100
 CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC 150
 ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC 200
 GAAGTGGTGC GGTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA 250
 35 CCGAAAGCAG AGATTGAAGG TGACATGGGT GACTCACACG TAGGTTTACA 300
 AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA 350
 AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT 388

2) INFORMATION FOR SEQ ID NO: 1760

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 50 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760

```

5  AAACGACAGT TTCATTACAT GCAATTGCAG AAGTACAACG TCAAGGTGGA      50
   CAAGCAGCAT TCATCGATGC GGAGCACGCA ATGGATCCTG TATATGCACA      100
   AAAATTAGGC GTTAACATAG ATGAATTACT ATTATCACAG CCTGATACAG      150
   GGGAGCAAGG ATTAGAAATC GCAGAAGCAC TTGTACGAAG TGGTGCGGTT      200
   GACATTATCG TAATTGACTC TGTAGCAGCT CTTGTACCGA AAGCAGAGAT      250
   TGAAGGAGAC ATGGGTGACT CACACGTAGG TTTACAAGCA CGTTTAATGT      300
10  CACAAGCACT TCGTAAGCTT TCAGGAGCAA TCAACAAATC AAAAACAATT      350
   GCAATCTTTA TTAACCAAAT TCGT                                374

```

15 2) INFORMATION FOR SEQ ID NO: 1761

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 381 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomyoides*
 (B) STRAIN: NRRL BD-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761

```

30  GGAAAGTTCA GGTAACAACAA CGGTTTCCTT ACATGCGATT GCAGAAAGTGC      50
   AACGTCAAGG TGGACAAGCG GCATTTATTG ATGCGGAGCA TGCGATGGAT      100
   CCTGTATATG CACAAAAGTT AGGTGTTAAT ATTGATGAGT TACTATTATC      150
   GCAGCCTGAT ACAGGAGAAC AAGGTTTAGA AATCGCAGAA GCATTAGTAC      200
35  GAAGCGGTGC GATTGATATC ATTGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCAAAGCAG AAATCGAAGG GGAAATGGGT GACTCCCACG TTGGTTTACA      300
   AGCGCGTTTA ATGTCACAAG CACTTCGTAA GCTTTCTGGT GCGATTAACA      350
   AATCAAAAAC AATTGCAATC TTCATTAACC A                                381

```

40

2) INFORMATION FOR SEQ ID NO: 1762

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*

(B) STRAIN: HER 1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762

```

5  TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATCG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
   ACAGCCTGAT ACAGGGGAGC AAGGATTAGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
10  CCGAAAGCAG AGATTGAAGG CGACATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

15

2) INFORMATION FOR SEQ ID NO: 1763

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 388 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

     (A) ORGANISM: Bacillus thuringiensis
     (B) STRAIN: HER 1418

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763

```

35  TGAAAGTTCA GGTAAAACGA CAGTTTCATT ACATGCAATT GCAGAAGTAC      50
   AACGTCAAGG TGGACAAGCA GCATTCATTG ATGCGGAGCA CGCAATGGAT      100
   CCTGTATATG CACAAAAATT AGGCGTTAAC ATAGATGAAT TACTATTATC      150
   ACAGCCTGAT ACAGGGGAGC AAGGATTGGA AATCGCGGAA GCACTTGTAC      200
   GAAGTGGTGC GGTTGACATT ATCGTAATTG ACTCTGTAGC AGCTCTTGTA      250
   CCGAAAGCAG AGATTGAAGG CGATATGGGT GACTCACACG TAGGTTTACA      300
   AGCACGTTTA ATGTCACAAG CACTTCGTAA GCTTTCAGGA GCAATCAACA      350
   AATCAAAAAC AATTGCAATC TTTATTAACC AAATTCGT      388

```

40

2) INFORMATION FOR SEQ ID NO: 1764

(i) SEQUENCE CHARACTERISTICS:

```

45  (A) LENGTH: 358 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764

5 CTCCTATCTG GATTATGCGA TGTCGGTCAT TGTTGGCCGT GCGCTGCCGG 50
 ATGTCCGAGA TGGCCTGAAG CCGGTACACC GTCGCGTACT ATACGCCATG 100
 AACGTATTGG GCAATGACTG GAACAAAGCC TATAAAAAAT CTGCCCGTGT 150
 CGTGGGTGAC GTCATCGGTA AATACCACCC TCATGGTGAT ACTGCCGTAT 200
 10 ACGACACCAT TGTACGTATG GCGCAGCCCT TCTCCCTGCG TTACATGCTG 250
 GTAGATGGCC AGGGTAACTT TGGTTCGGTC GACGGCGACT CCGCCGCAGC 300
 GATGCGTTAT ACGGAAATCC GTATGTGCGAA GATCGCCCAT GAACTGATGG 350
 CCGACCTC 358

15

2) INFORMATION FOR SEQ ID NO: 1765

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 365 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765

TTAAGAACTC TTATCTGGAT TATGCGATGT CGGTCAATTGT TGGCCGTGCG 50
 CTGCCGGATG TCCGAGATGG CCTGAAGCCG GTACACCGTC GCGTACTTTA 100
 35 CGCCATGAAC GTATTGGGCA ATGACTGGAA CAAAGCCTAT AAAAAATCAG 150
 CCCGTGTCTG TGGTGACGTA ATCGGTAAAT ACCACCCGCA CGGCGACTCC 200
 GCGGTATACG ACACCATCGT GCGTATGGCG CAGCCGTTCT CGCTGCGTTA 250
 CATGCTGGTG GACGGCCAGG GTAACCTTGG TTCCATCGAC GGCGACTCCG 300
 CCGCGGCGAT GCGTTATACC GAAATTCGTC TGGCGAAAAT CGCTCATGAG 350
 40 CTGATGGCCG ATCTT 365

2) INFORMATION FOR SEQ ID NO: 1766

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766

```

AAGAGCTCGT ATCTGGATTA TGCATGTCG GTCATTGTTG GCCGTGCGCT      50
GCCGGATGTC CGAGATGGCC TGAAACCGGT ACACCGTCGC GTACTTTACG      100
CCATGAACGT ATTGGGCAAT GACTGGAACA AAGCCTATAA AAAATCCGCC      150
10 CGTGTCGTTG GTGACGTAAT CCGTAAATAC CACCCTCATG GTGATACCGC      200
CGTTTATGAC ACCATTGTAC GTATGGCACA GCCATTCTCC TTGCGTTATA      250
TGCTGGTCGA TGGCCAGGGT AACTTCGGTT CTGTTCGATGG CGACTCCGCC      300
GCAGCGATGC GTTATACGGA AATCCGTATG TCGAAAATCG CCCA          344

```

15

2) INFORMATION FOR SEQ ID NO: 1767

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 345 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767

```

AACTCTTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
GGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
35 TGAACGTATT GGGCAATGAC TGGAACAAAG CCTATAAAAA ATCAGCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAC CCGCACGGCG ACTCCGCGGT      200
ATACGACACC ATCGTGCGTA TGGCGCAGCC GTTCTCGCTG CGTTACATGC      250
TGGTGGACGG CCAGGGTAAC TTTGGTTCCA TCGACGGCGA CTCCGCCGCG      300
GCGATGCGTT ATACCGAAAT TCGTCTGGCG AAAATCGCTC ATGAG          345

```

40

2) INFORMATION FOR SEQ ID NO: 1768

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 356 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768

5 CTTATCTGGA TTATGCGATG TCGGTCATTG TTGGCCGTGC GCTGCCGGAT 50
GTCCGAGATG GCCTGAAGCC GGTACACCGT CGCGTACTTT ACGCCATGAA 100
CGTATTGGGC AATGACTGGA ACAAAGCCTA TAAAAAATCA GCCCGTGTCTG 150
TTGGTGACGT AATCGGTAAA TACCACCCGC ACGGCGACTC CGCGGTATAC 200
10 GACACCATCG TCGGTATGGC GCAGCCGTTT TCGCTGCGTT ACATGCTGGT 250
GGACGGCCAG GGTAACCTTG GTTCCATCGA CGGCGACTCC GCCGCGGCGA 300
TGCGTTATAC CGAAATTCGT CTGGCGAAAA TCGCTCATGA GCTGATGGCC 350
GATCTT 356

15

2) INFORMATION FOR SEQ ID NO: 1769

- (i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 361 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
30 (B) STRAIN: ATCC 29011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769

TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC 50
TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC 100
35 GCCATGAACG TATTGGGCAA TGACTGGAAC AAAGCCTATA AAAAATCAGC 150
CCGTGTCGTT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG 200
CGGTATACGA CACCATCGTG CGTATGGCGC AGCCGTTCTC GCTGCGTTAC 250
ATGCTGGTGG ACGGCCAGGG TAACCTTGGT TCCATCGACG GCGACTCCGC 300
CGCGGCGATG CGTTATACCG AAATTCGTCT GGCGAAAATC GTCATGAGC 350
40 TGATGGCCGA T 361

2) INFORMATION FOR SEQ ID NO: 1770

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis
 (B) STRAIN: ATCC 13824

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770

```

10  TAAGAACTCT TATCTGGATT ATGCGATGTC GGTCATTGTT GGCCGTGCGC      50
    TGCCGGATGT CCGAGATGGC CTGAAGCCGG TACACCGTCG CGTACTTTAC      100
    GCCATGAACG TATTGGGCAA TGACTGGAAC AAAGCCTATA AAAAATCAGC      150
    CCGTGTCGTT GGTGACGTAA TCGGTAAATA CCACCCGCAC GGCGACTCCG      200
    CGGTATACGA CACCATCGTG CGTATGGCGC AGCCGTTCTC GCTGCGTTAC      250
    ATGCTGGTGG ACGGCCAGGG TAACTTTGGT TCCATCGACG GCGATTCCGC      300
    CGCGGCGATG CGTTATACCG AAATTCGTCT GGCGAAAATC GTCATGAGC      350
15  TGATGGCCGA TCTTG                                     365
  
```

2) INFORMATION FOR SEQ ID NO: 1771

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella terrigena*
 (B) STRAIN: ATCC 33257

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771

```

35  TCGTATCTGG ATTATGCGAT GTCGGTCATT GTTGGCCGTG CGCTGCCGGA      50
    TGTCCGAGAT GGGTTGAAAC CCGTACACCG TCGCGTACTT TACGCCATGA      100
    ACGTATTGGG CAATGACTGG AACAAAGCCT ATAAAAAATC CGCCCGTGTC      150
    GTTGGTGACG TAATCGGTAA ATATCACCTT CACGGTGATA CCGCCGTTTA      200
    TGACACCATT GTACGTATGG CGCAGCCATT CTCCTTGCGT TATATGCTGG      250
40  TCGATGGCCA GGGTAACTTC GGTTCTGTCG ATGGCGACTC CGCCGCAGCG      300
    ATGCGTTATA CGGAAATCCG TATGTCGAAA ATCGCCACG AGCTGATGGC      350
    CGACCTC                                     357
  
```

45

2) INFORMATION FOR SEQ ID NO: 1772

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 5 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772

```

10 CAGTACACAG GCGAGTTCTT TTTGCGATGA GTGAGTTAAG TAATGATTGG      50
    AATAAGCCGT ATAAAAAATC TGCTCGTGTA GTAGGGGATG TCATTGGTAA      100
    ATATCATCCT CATGGGGATA CAGCTGTTTA TGACACTATT GTTCGTATGG      150
    CTCAGCCCTT TTCCATGCGT TATATGCTGA TTGATGGGCA GGGTAATTTT      200
    GGCTCTGTAG ATGGAGATGC TCCAGCTGCC ATGCGTTACA CTGAAGTAAG      250
    AATGTCCAAA GTGGCGCATG CTTTACTGGC TGATTTGGAT AAGGAAACCG      300
15 TTGATTTTATG TCCTAACTAT GATGAAACAG AATTTGCTCC AGTGGTATTG      350
    CCATCGAGAA TTCCCAATTT ACTAGTTAAT GGCTCTTCCG GTATTGCGGT      400
    AGGGATGGCT ACTAATATTC CACCACATAA TCTTACCGAA GTAATCAATG      450
    CATGTATTGC TTTAGTGGAT GAACCTGACA CGAGTCTTGA AGATTTAATG      500
    GAAATTATTC CTGGCCCTGA TTTTCCTACA GCCGCAATTA TTAATGGTCG      550
20 TGCTGGAATT ATTGAAGGTT ATCGTACTGG AAAAGGGCGG GTTGTTATCA      600
    GGGCACGCAC AGAAATTGAA ACGGATGAAA GTTCAGGCCG TCAGTCAATT      650
    ATTATTCAGG AATTACCCTA TCAGGTGAAT AAAGCGCGTT TGATCGAGCG      700
    TATTGCTGAA TTGGTAAGGG ACAAGAAAAAT CGAAGGAATT TCCGGCTTGA      750
    GAGATGAGTC AGACAAGCAA GGAATGAGAG TAGTCATTGA ATTAACACGC      800
25 AATGAAGTAG CAGATGTGGT ATTGAATAAC CTGTTTCGCTC ATACTCAAAT      850
    GCAAAATGTA TTCGGAATTA ATATGGTTGC TCTGGTGGAT GGCCAACCGC      900
    GTACTTTGAA TTTGAAGCAA ATACTGGAAT ATTTTATAAA ACATCGAAGA      950
    GAGGTTGTTA CCAGACGC                                     968
  
```

30

2) INFORMATION FOR SEQ ID NO: 1773

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 967 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*
 45 (B) STRAIN: ATCC 25933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773

```

50 CACCGCCGAG TGCTATTTGC GATGAATGTA CTGGGAAACG ATTGGAATAA      50
    ACCTTATAAA AAATCAGCCC GTGTTGTTGG GGATGTAATC GGTAATATC      100
    ACCCGCACGG TGACAGTGCT GTCTATGAAA CGATTGTTCG TTTAGCACAG      150
    CCTTTTCTA TGCGCTACAT GTTGGTTGAC GGTCAGGGTA ACTTCGGGTC      200
    AGTTGATGGT GACTCCGCGG CGGCTATGCG TTATACCGAA GTTCGTATGG      250
    CGAAGATCGC CCATGAACTG CTGGCGGATT TGGAAAAAGA GACGGTCGAC      300
  
```



```

TTTGTTTCCTA ACTATGATGG AACAGAAAAT ATACCGGCTG TTATGCCAAC 350
CCGTATTCCA AACTTGTTAG TTAATGGCTC TTCAGGTATT GCCGTGGGA 400
TGGCAACGAA TATCCCTCCG CATAACCTCG GTGAAGTTAT CGACGGTTGT 450
CTTGCCTATG TTGATAATGA AGACATCACC ATAGAAGAAT TAATGGAATA 500
5 TATTACCGGG CCTGATTTTC CGACTGCTGC GATTATTAAT GGTCGCAGAG 550
GAATATTAGA TGCTTATCGT ACAGGGCGTG GAAAGATTTA TATCCGTGCT 600
CAGGCTGATA TTGAAACTGA TGAGAAAACA GGTCGCGAAA CCATTATCGT 650
GACAGAAATT CCTTATCAGG TGAATAAAGC CCGTTTAATT GAAAAAATTG 700
CGGAGCTTGT AAAAGATAAA CGTATTGAAG GTATCAGCGG ATTACGTGAC 750
10 GAGTCTGATA AAGACGGTAT GCGTATTGTT GTTGAGATCA AACGTGATGC 800
AGTCGGTGAA GTAGTATTAA ATCACCTCTT TTCACAACT CAAATGCAAG 850
TCTCTTTTGG TATTAATATG GTTGCGCTTC ATCAAGGCCA ACCAAAATTA 900
TTGAACCTAA AAGAAATTAT CGCAGCCTTT ATTCGCCATC GTCGTGAAGT 950
GGTGACTCGC CGTACCA 967
15

```

2) INFORMATION FOR SEQ ID NO: 1774

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
- (B) STRAIN: ATCC 9250

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774

```

CCAGTACACC GCAGAGTATT GTATGCGATG AATGTATTGG GAAATGATTG 50
35 GAATAAACCC TATAAAAAAT CTGCCCCTAT TGTTGGGGAC GTCATCGGTA 100
AATACCATCC ACATGGTGAT AGCGCTGTTT ACGAGACAAT CGTTCGTCTT 150
GCTCAGCCTT TCTCAATGCG TTACATGCTG GTTGATGGTC AGGGAAACTT 200
CGGTTCTGTT GACGGAGACT CCGCAGCGGC AATGCGTTAT ACGGAAATCC 250
GTATGGCGAA AATTGCCCAT GAACTACTTG CTGACCTTGA AAAAGAAACC 300
40 GTTGATTTCG TTCCTAACTA TGACGGAACA GAGCACATTC CTGAAGTTAT 350
GCCAACGAAA ATCCCAAACC TTTTGGTTAA TGGGTCGTCA GGTATTGCTG 400
TTGGGATGGC AACCAATATC CCACCTCACA ATTTAGGGGA GGTGATTAAT 450
GGTTGTCTTG CCTATATAGA AGACGAAGAC ATCAGCATTG ATGTTTAAAT 500
GGAACACATT CCAGGGCCTG ATTTCCCAAC CGCAGCTATT ATTAATGGCC 550
45 GTCGTGGGAT TATTGATGCG TATCGCACAG GCGGTGGCAA GGTCTATATC 600
CGTGCAAGCG CTGAAGTGGA AGTCGATGAG AAAAATGGTC GCGAAACCAT 650
TATTGTCAGC GAAATTCCTT ATCAAGTGAA TAAAGCTCGC TTGATTGAAA 700
AAATTGCTGA GTTAGTTAAA GACAAGCGTG TTGAAGGTAT CAGTGCACTG 750
CGTGACGAGT CTGATAAAGA CCGTATGCGT ATTGTTATTG AAATCAAACG 800
50 CGATGCGGTG GGTGAAGTTG TACTGAACAA CTTATATTCC CTGACCCAAT 850
TGCAAGTTTC TTTTGGTATC AATATGGTAG CTCTACACCA AGGGCAGCCG 900
AAAATACTGA ATTTAAAAGA TATCATTGCT GCTTTTGTGC GTCACCGCCG 950
TGAAGTCGTC ACTCGTCGTA CGATTTTC 978

```

2) INFORMATION FOR SEQ ID NO: 1775

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 978 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775

CCAGTACACC GTCGCGTTCT TTTCGCGATG AATGTATTAG GAAACGATTG 50
 GAATAAACCT TATAAAAAAT CAGCCCGTGT TGTTGGGGAT GTTATCGGTA 100
 AATATCACCC GCACGGTGAC AGTGCTGTTT ATGAAACGAT AGTTCGTTTA 150
 20 GCACAGCCTT TTTCTATGCG TTACATGTTG GTTGACGGGC AGGGTAACTT 200
 CGGGTCAGTT GATGGTGACT CGGCGGCTGC AATGCGTTAT ACCGAAGTTC 250
 GTATGGCGAA AATCGCCCAT GAACTGCTGG CGGATTTGGA AAAAGAAACG 300
 GTTGATTTTG TTCCTAACTA TGATGGAACA GAGCATATCC CGGCAGTCAT 350
 GCCAACCCGT ATTCCAAAC TATTAGTCAA TGGTTCTTCA GGTATCGCAG 400
 25 TCGGGATGGC AACAAACATT CCTCCGCATA ACCTAGGTGA AGTTATCGAC 450
 GGCTGTCTTG CTTATGTTGA TAACGAAGAC ATCACTATTG AAGAGTTGAT 500
 GGAGCATATC ACGGGGCCTG ATTTCCCAAC TGCCGCTATT ATTAATGGCC 550
 GCAGAGGAAT TTTAGATGCT TACCGTACTG GCGCGGAAA AATTTATATT 600
 CGTGCACAAG CTGATGTAGA AACCGATGAG AAAACTGGTC GCGAAACAAT 650
 30 TATCGTGACG GAAATTCCCTT ATCAGGTGAA CAAAGCTCGC TTAATTGAAA 700
 AAATTGCAGA GCTTGTTAAA GATAAACGTA TTGAAGGCAT TAGCGGATTA 750
 CGTGATGAGT CAGATAAAGA TGGTATGCGC ATTGTTGTTG AAATTAAGCG 800
 TGATGCTGTT GGTGAAGTTG TACTAAATCA CTTATTTTCT CAGACTCAGA 850
 TGCAGGTTTC TTTTGGTATT AACATGGTTG CACTGCATCA AGGTCAACCG 900
 35 AAAGTGTTAA ACCTGAAAGA AATTATTTCA GCCTTTATTC GTCACCGTCG 950
 TGAAGTGGTG ACTCGTCGTA CTATTTTTT 978

40 2) INFORMATION FOR SEQ ID NO: 1776

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 940 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776

	TGGGTAATGA	CTGGAATAAG	CCATACAAAA	AATCGGCCCCG	TGTAGTCGGG	50
	GACGTTATCG	GTAAATATCA	CCCGCATGGT	GACAGCGCGG	TCTACGACAC	100
5	AATTGTGCGT	ATGGCCCAGC	CGTTCTCACT	GCGCTATATG	CTGGTGATG	150
	GGCAGGGCAA	CTTCGGTTCC	GTTGATGGCG	ACTCCGCCGC	AGCGATGCGT	200
	TATACCGAAA	TCCGTATGTC	TAAAATTGCT	CACGAATTGT	TGGCGGACTT	250
	AGAAAAAGAT	ACCGTCGACT	TCGTGCCGAA	CTATGACGGT	ACGGAGCAAA	300
	TTCCTGCCGT	AATGCCAACC	CGAATCCCTA	ACTTGCTGGT	TAACGGCTCG	350
10	TCAGGTATTG	CTGTCGGTAT	GGCAACCAAT	ATTCCGCCGC	ATAACCTTTC	400
	TGAGGTTATT	GATGGCTGTC	TGGCCTATAT	CGAAGATGAA	AACATCACCA	450
	TTGAAGGGTT	GATGGAGTAC	ATCCCGGGGC	CAGATTTCCC	AACTGCTGCG	500
	ATTATCAATG	GTCCCGTGG	TATTGAAGAA	GCTTATCGTA	CTGGCCGTGG	550
	CAAGGTGTAT	ATCCGTGCCC	GTGCTGAAGT	TGAGGCTGAC	GCTTAAACCG	600
15	GTCCGCAAAAC	CATTATTGTT	CACGAGATCC	CGTATCAGGT	GAACAAGGCG	650
	CGGTTGATTG	AAAAAATCGC	CGAGCTGGTT	AAAGAAAAAC	GCGTAGAAGG	700
	CATCAGTGCG	TTGCGTGATG	AGTCTGATAA	AGACGGCATG	CGTATCGTGA	750
	TTGAAATCAA	ACGTGATGCT	GTCCGGGAAG	TGGTTCTGAA	CAACCTCTAT	800
	TCTCTGACGC	AATTGCAGGT	GACTTTCGGT	ATCAATATGG	TGGCTCTGTC	850
20	TCAAGGGCAG	CCTAAGTTGC	TTAACCTGAA	AGACATTTTG	GTTGCTTTCG	900
	TGCGCCACCG	CCGTGAAGTG	GTGACTCGCC	GTACCATTTT		940

25 2) INFORMATION FOR SEQ ID NO: 1777

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--------------------------|
| | (A) LENGTH: 668 bases |
| | (B) TYPE: Nucleic acid |
| 30 | (C) STRANDEDNESS: Double |
| | (D) TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- | | |
|--|---|
| | (A) ORGANISM: <i>Klebsiella oxytoca</i> |
| | (B) STRAIN: ATCC 13182 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777

40	CCGTTTATTG	GCGATGGCCT	GAAGCCGGTC	CAGCGTCGCA	TCGTCTATGC	50
	GATGTCTGAA	CTGGGTCTGA	ACGCCAGCGC	GAAGTTCAAA	AAGTCCGCC	100
	GCACCGTCGG	TGACGTGCTG	GGTAAATACC	ATCCCCACGG	CGACAGCGCG	150
	TGCTATGAAG	CCATGGTGCT	GATGGCTCAG	CCCTTCTCCT	ACCGCTATCC	200
45	GCTGGTTGAC	GGTCAGGGAA	ACTGGGGGGC	GCCGGACGAT	CCTAAATCCT	250
	TCGCCGCAAT	GCGTTATACC	GAATCCCGTT	TGTCGAAGTA	TGCTGAACTG	300
	CTGCTGAGCG	AACTGGGGCA	AGGCACCGTT	GACTGGGTAC	CAAACCTCGA	350
	CGGCACTTTG	CAGGAGCCGA	AGATGCTGCC	TGCGCGCCTG	CCCAATATTC	400
	TGCTAAACGG	TACTACCGGC	ATTGCCGTTG	GGATGGCGAC	GGACATTCCG	450
50	CCGCACAACC	TGCGTGAAGT	GGCCCGGGCG	GCCATTACCC	TGATTGAAAA	500
	GCCGCAAAC	TCGCTGGATG	ACCTGCTGGA	TATCGTGCAG	GGGCCGGATT	550
	ATCCTACCGA	AGCGGAAATC	ATTACCCCCC	GTGCCGAAAT	CCGCAAAATC	600
	TACCAGAATG	GCCGCGGTTT	GGTGCGGATG	CGCGCGGTAT	GGGCCAAAGA	650

AGACGGCGCG GTGGTGAT

668

5 2) INFORMATION FOR SEQ ID NO: 1778

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778

20 GTTTATTGGC GATGGCCTGA AGCCGGTCCA GCGTCGCATC GTCTATGCGA 50
 TGTCTGAACT GGGTCTGAAC GCCAGCGCGA AGTTCAAAAA GTCCGCCCCG 100
 ACCGTCGGTG ACGTGCTGGG TAAATACCAT CCCCACGGCG ACAGCGCGTG 150
 CTATGAAGCC ATGGTGCTGA TGGCTCAGCC CTTCTCCTAC CGCTATCCGC 200
 25 TGGTTGACGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC TAAATCCTTC 250
 GCCGCAATGC GTTATAACCGA ATCCCGTTTG TCGAAGTATG CTGAACTGCT 300
 GCTGAGCGAA CTGGGGCAAG GCACCGTTGA CTGGGTACCA AACTTCGACG 350
 GCACTTTGCA GGAGCCGAAG ATGCTGCCTG CGCGCCTGCC CAATATTCTG 400
 CTAAACGGTA CTACCGGCAT TGCCGTTGGG ATGGCGACGG ACATTCCGCC 450
 30 GCACAACCTG CGTGAAGTGG CCCGGGCGGC CATTACCCTG ATTGAAAAGC 500
 CGCAAACCTC GCTGGATGAC CTGCTGGATA TCGTGCAGGG GCCGGATTAT 550
 CCTACCGAAG CGGAAATCAT TACCCCCCGT GCCGAAATCC GCAAAAATCTA 600
 CCAGAATGGC CGCGGTTCCG TCGCGATGCG CGCGGTATGG GCCAAAAGAAG 650
 ACGGCGCGGT GGTGATTAGC GCGCTGCCGC ATCAGGTTTC CGGCGCCCCG 700
 35 GTGCTTGAGC AGAT 714

2) INFORMATION FOR SEQ ID NO: 1779

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779

```

TTGGCGATGG CTTAAAACCG GTCCAGCGTC GCATCGTCTA TGCGATGTCC      50
GAGCTGGGGC TGAACGCCAG CGCGAAATTC AAAAAGTCCG CCCGCACCGT      100
CGGCGACGTG TTGGGTAAAT ATCACCCGCA CGGCGACAGC GCCTGCTATG      150
5  AAGCGATGGT GCTGATGGCG CAGCCGTTCT CTTACCGCTA TCCGCTGGTG      200
GATGGTCAGG GAAACTGGGG GGCGCCGGAC GATCCCAAAT CTTTCGCCGC      250
CATGCGTTAC ACCGAATCCC GCCTGTCGAA GTATGCCGAG CTGCTGCTCA      300
GCGAGCTGGG GCAGGGGACG GTCGACTGGG TGCCAAACTT TGACGGTACG      350
CTGCAGGAGC CGAAAATGCT GCCAGCGCGT TTGCCGAACA TCCTGCTGAA      400
10 CGGCACCACC GGCATCGCGG TAGGTATGGC GACCGATATT CCTCCGCACA      450
ACCTGCGGGA AGTGGCCAAA GCGGCGATTA CGCTGATTGA GCAGCCGAAA      500
ACCACCCTCG ACGAACTGCT GGATATCGTA CAGGGGCCGG ATTTCCCGAC      550
CGAGGCGGAG ATCATCACCT CGCGGGCGGA AATTCGAAAA ATCTACCAGA      600
ACGGGCGCGG CTCAGTGCGC ATGCGCGCGG TGTGGAGTAA AGAGGACGGC      650
15 GCGGTGGTGA TCAGCGCGCT GCCGCATCAG GTCTCCGGCG CCAAAGTGCT      700
GGAGCAGATT GCGGCGCAGA TG      722

```

20 2) INFORMATION FOR SEQ ID NO: 1780

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 692 bases
    (B) TYPE: Nucleic acid
25  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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30  (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Klebsiella planticola
    (B) STRAIN: ATCC 33531

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780

```

35  GTCCAGCGTC GCATCGTTTA TGCGATGTCT GAGCTGGGGC TGAACGCCAG      50
CGCGAAGTTC AAAAAGTCCG CCCGCACCGT GGGTGATGTG CTGGGTAAAT      100
ATCACCCGCA CGGCGATAGC GCATGCTATG AAGCTATGGT GCTGATGGCG      150
CAGCCATTCT CCTACCGCTA CCCGCTGGTG GATGGGCAGG GGAAGTGGGG      200
40  GGCACCGGAC GATCCTAAAT CTTTCGCCGC GATGCGTTAT ACCGAATCCC      250
GTTTGTGCGAA GTATGCGGAA CTGCTGCTGG GCGAACTGGG GCAGGGAACC      300
GTCGACTGGG TGCCGAACTT CGACGGGACG ATGCAGGAGC CGAAAATGCT      350
GCCTGCGCGT CTGCCGAATA TTCTGCTGAA CGGCACTACC GGCATCGCCG      400
TCGGTATGGC AACCGATATT CCTCCGCACA ACCTGCGTGA AGTGGCGCAG      450
45  GCGGCGATTA CCCTGATCGA AAAACCGCAG ACCTGCGCTG ACGAACTGCT      500
GGATATCGTT CACGGACCCG ACTACCCGAC CGAAGCCGAA ATCATTACTC      550
CACGCGCGGA GATCCGCAA ATCTACCAGA ACGGCCGCGG TTCGGTGCGG      600
ATGCGCGCGG TATGGAAAAA AGAGGACGGC GCGGTCGTGA TTACGGCGTT      650
50  GCCGCATCAG GTTTCCGGCG CCCGCGTGCT GGAGCAAATT GC      692

```

2) INFORMATION FOR SEQ ID NO: 1781

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 700 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 27336
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781

```

15  GTTTATTGGC GATGGCTTAA AACCGGTCCA GCGTCGCATC GTCTATGCGA      50
    TGTCCGAGCT GGGGCTGAAC GCCAGCGCGA AATTCAAAAA GTCCGCCCCG      100
    ACCGTCGGCG ACGTGTTGGG TAAATATCAC CCGCACGGCG ACAGCGCCTG      150
    CTATGAAGCG ATGGTGCTGA TGGCGCAGCC GTTCTCTTAC CGCTATCCGC      200
20  TGGTGGATGG TCAGGGAAAC TGGGGGGCGC CGGACGATCC CAAATCTTTC      250
    GCCGCCATGC GTTACACCGA ATCCCGCCTG TCGAAGTATG CCGAGCTGCT      300
    GCTCAGCGAG CTGGGGCAGG GGACGGTCGA CTGGGTGCCA AACTTTGACG      350
    GCACGCTGCA GGAGCCGAAA ATGCTGCCAG CGCGTTTGCC GAACATCCTG      400
    CTGAACGGCA CCACCGGCAT CGCGGTAGGC ATGGCGACCG ATATTCCTCC      450
25  GCACAACCTG CGGGAAGTGG CCAAAGCGGC GATTACGCTG ATTGAGCAGC      500
    CGAAAACCAC CCTCGACGAA CTGCTGGATA TCGTACAGGG GCCGGATTTC      550
    CCGACCGAGG CGGAGATCAT CACCTCGCGG GCGGAAATTC GCAAAATCTA      600
    CCAAACGGG CGCGGCTCAG TGCGCATGCG CGCGGTGTGG AGTAAAGAGG      650
    ACGGCGCGGT GGTGATCAGC GCGCTGCCGC ATCAGGTCTC CGGCGCCAAA      700
30

```

2) INFORMATION FOR SEQ ID NO: 1782

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 726 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782

```

50  ATTGGCGATG GCTTAAAACC GGTCCAGCGT CGCATCGTCT ATGCGATGTC      50
    CGAGCTGGGG CTGAACGCCA GCGCGAAATT CAAAAGTCC GCCCGCACCG      100
    TCGGCGACGT GTTGGGTAAA TATCACCCGC ACGGCGACAG CGCCTGCTAT      150
    GAAGCGATGG TGCTGATGGC GCAGCCGTTT TCTTACCGCT ATCCGCTGGT      200
    GGATGGTCAG GGAAACTGGG GGGCGCCGGA CGATCCCAA TCTTTCGCCG      250

```

	CCATGCGTTA	CACCGAATCC	CGCCTGTCTGA	AGTATGCCGA	GCTGCTGCTC	300
	AGCGAGCTGG	GGCAGGGGAC	GGTCGACTGG	GTGCCAAACT	TTGACGGCAC	350
	GCTGCAGGAG	CCGAAAATGC	TGCCAGCGCG	TCTGCCGAAC	ATCCTGCTGA	400
	ACGGCACCAC	CGGCATCGCG	GTAGGCATGG	CGACCGATAT	TCCTCCGCAC	450
5	AACCTGCGGG	AAGTGGCCAA	AGCGGCGATT	ACGCTGATTG	AGCAGCCGAA	500
	AACCACCCTC	GACGAACTGC	TGGATATCGT	ACAGGGGCCG	GATTTCCCGA	550
	CCGAGGCGGA	GATCATCACC	TCGCGGGCGG	AAATTCGCAA	AATCTACCAG	600
	AACGGGCGCG	GCTCAGTGCG	CATGCGCGCG	GTGTGGAGTA	AAGAGGACGG	650
	CGCGGTGGTG	ATCAGTGCGC	TGCCGCATCA	GGTCTCTGGC	GCCAAAGTGC	700
10	TGGAGCAGAT	TGCGGCGCAG	ATGCGC			726

2) INFORMATION FOR SEQ ID NO: 1783

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 29011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783

30	GGCTTAAAC	CGGTCCAGCG	TCGCATCGTC	TATGCGATGT	CCGAGCTGGG	50
	GCTGAACGCC	AGCGCGAAAT	TCAAAAAGTC	CGCCCGCACC	GTCGGCGACG	100
	TGTTGGGTAA	ATATCACCCG	CACGGCGACA	GCGCCTGCTA	TGAAGCGATG	150
	GTGCTGATGG	CGCAGCCGTT	CTCTTACCGC	TATCCGCTGG	TGGATGGTCA	200
	GGGAAACTGG	GGGGCGCCGG	ACGATCCCAA	ATCTTTTGCC	GCCATGCGTT	250
35	ACACCGAATC	CCGCCTGTCT	AAGTATGCCG	AGCTGCTGCT	CAGCGAGCTG	300
	GGGCAGGGGA	CGGTCTGACTG	GGTGCCAAAC	TTTGACGGCA	CGCTGCAGGA	350
	GCCGAAAATG	CTGCCAGCGC	GTCTGCCGAA	CATCCTGCTG	AACGGCACCA	400
	CCGGCATCGC	GGTAGGCATG	GCGACCGATA	TTCCTCCGCA	CAACCTGCGG	450
	GAAGTGGCCA	AAGCGGCGAT	TACGCTGATT	GAGCAGCCGA	AAACCACCCT	500
40	CGACGAACTG	CTGGATATCG	TACAGGGGCC	GGATTTCCCG	ACCGAGGCGG	550
	AGATCATCAC	CTCGCGGGCG	GAAATTCGCA	AAATCTACCA	GAACGGGCGC	600
	GGCTCAGTGC	GATGCGCGC	GGTGTGGAGT	AAAGAGGACG	GCGCGGTGGT	650
	GATCAGTGCG	CTGCCGCATC	AGGTCTCCGG	CGCCAAAGTG	CTGGAGCAGA	700
	TTGCGG					706

45

2) INFORMATION FOR SEQ ID NO: 1784

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

(B) STRAIN: ATCC 13884

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784

```

TTGGCGATGG CTTAAAACCG GTCCAGCGTC GCATCGTCTA TGCGATGTCC      50
GAGCTGGGGC TGAACGCCAG CGCGAAATTC AAAAAGTCCG CCCGCACCGT      100
CGGCGACGTG TTGGGTAAAT ATCACCCGCA CGGCGACAGC GCCTGCTATG      150
15 AAGCGATGGT GCTGATGGCG CAGCCGTTCT CTTACCGCTA TCCGCTGGTG      200
GATGGTCAGG GAAACTGGGG GGCGCCGGAC GATCCCAAAT CTTTCGCCGC      250
CATGCGTTAC ACCGAATCCC GCCTGTGCGAA GTATGCCGAG CTGCTGCTCA      300
GCGAGCTGGG GCAGGGGACG GTCGACTGGG TGCCAAACTT TGACGGCACG      350
CTGCAGGAGC CGAAAATGCT GCCAGCGCGT CTGCCGAACA TCCTGCTGAA      400
20 CGGCACCACC GGCATCGCGG TAGGCATGGC GACCGATATT CCTCCGCACA      450
ACCTGCGGGA AGTGGCCAAA GCGGCGATTA CGCTGATTGA GCAGCCGAAA      500
ACCACCCTCG ACGAACTGCT GGATATCGTA CAGGGGCCGG ATTTCCCGAC      550
CGAGGCGGAG ATCATCACCT CGCGGGCGGA AATTTCGCAA ATCTACCAGA      600
ACGGGCGCGG CTCA                                         614
25

```

2) INFORMATION FOR SEQ ID NO: 1785

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella terrigena*

40 (B) STRAIN: ATCC 33257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785

```

GCCTGAAACC GGTCCAGCGG CGCATCGTTT ATGCGATGTC CGAACTGGGT      50
45 CTGAACGCCA CCGCTAAATT CAAAAAATCC GCGCGCACCG TCGGCGACGT      100
GCTGGGTAAA TATCACCCGC ACGGCGATAG CGCCTGCTAT GAGGCGATGG      150
TGCTGATGGC GCAGCCGTTT TCTTACCGCT ACCCGCTGGT GGACGGTCAG      200
GGCAACTGGG GCGCCCCGGA CGATCCCAA TCCCTCGCCG CGATGCGTTA      250
TACCGAATCC CGCCTGTCAA AGTATGCGGA GCTGCTGCTG GGCGAGCTGG      300
50 GTCAGGGAAC CGTTGACTGG GTACCTAACT TTGACGGTAC GATGCAGGAG      350
CCGAAAATGC TGCCTGCGCG TTTGCCGAAT ATTCTGCTCA ACGGCACCAC      400
CGGTATCGCC GTGGGGATGG CCACCGATAT TCCGCCGCAC AACCTGCGCG      450
AAGTGGCCAA AGCGGCCATC ACCCTGATTG AAAAGCCGCA GACCTCGCTC      500

```


GACGAACTGC TGGATATCGT TCACGGGCGG GACTACCCCA CCGAAGCTGA 550
AATCATCACC CCGCGCGCCG AGATCCGCAA AATCTATCAG AACGGTCGCG 600
GCTCGGTTTC CATGCGTGCG GTGTGGAAAA AAGAGGACGG CGCGGTGGTG 650
ATTAGCGCCC TGCCGCAT 668

5

2) INFORMATION FOR SEQ ID NO: 1786

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 7064

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786

25 CATTACGTTT TAACACTCAA GGACGCGGAA CATTCTCTAT GGTGTTTGAC 50
CACTATGAAG AAGTACCAAA GTCTGTTTCT GAAGAAATTA TCAAAAAAAA 100
TAAAGGTGAA TAA 113

30 2) INFORMATION FOR SEQ ID NO: 1787

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787

45

AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT 50
TTGACCACTA TGAAGAAGTA CCAAGTCTG TTTCTGAAGA AATTATCAAA 100
AAAAATAAAG GTGAATAA 118

50

2) INFORMATION FOR SEQ ID NO: 1788

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788

15	GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT	50
	GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA	100
	AAAAAATAAA AGGTGAATAA	120

20

2) INFORMATION FOR SEQ ID NO: 1789

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789

35	AACGTCATTA CGTTCTAACA CTCAAGGACG CGGAACATTC TCTATGGTGT	50
	TTGACCACTA TGAAGAAGTA CCAAAGTCTG TTTCTGAAGA AATTATCAAA	100
	AAAAATAAAG GTGAATAA	118

40

2) INFORMATION FOR SEQ ID NO: 1790

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

50

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790

5 GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1791

- (i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomycooides*
(B) STRAIN: NRRL B-617

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791

GCAACGTCAT TACGTTCTAA CACGCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATCA 100
30 AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1792

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 49064

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792

50 CGTCATTACG TTCTAACACT CAAGGACGCG GAACATTCTC TATGGTGTTT 50
GACCACTATG AAGAAGTACC AAAGTCTGTT TCTGAAGAAA TTATCAAAAA 100
AAATAAAGGT GAATAA 116

2) INFORMATION FOR SEQ ID NO: 1793

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1794

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 15816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794

CACTCAAGGA CGCGGAACAT TCTCTATGGT GTTTGATCAC TATGAAGAAG 50
40 TACCAAAGTC TGTTTCTGAA GAAATTATCA AAAAAATAA AGGTGAATAA 100

2) INFORMATION FOR SEQ ID NO: 1795

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795

GCAACGGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCTGAA GAAATTATTA 100
AAAAAATAA AGGTGAATAA 120

10

2) INFORMATION FOR SEQ ID NO: 1796

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
25 (B) STRAIN: ATCC 6462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796

GCGACAGCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCAATGAC 50
30 ATTTGATCAT TATGAAGAAG TACCGAAGTC TGTTTCAGAA GAAATTATTA 100
AAAAAATAA AGGCGAATAA 120

35 2) INFORMATION FOR SEQ ID NO: 1797

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus thuringiensis*
(B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797

50

GCAACGTCAT TACGTTCTAA CACTCAAGGA CGCGGAACAT TCTCTATGGT 50
GTTTGACCAC TATGAAGAAG TACCAAAGTC TGTTTCTGAA GAAATTATCA 100
AAAAAATAA AGGTGAATAA 120

2) INFORMATION FOR SEQ ID NO: 1798

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
10

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus weihenstephanensis*
(B) STRAIN: WSBC 10204

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798

TTGATTTT	TCGATTGT	TCAAGTATA	ACTTATGT	AAGCTTAGAA	AG	50
TGAGACGC	AA	GTTTCACT	TT	CTAGTCTAA	AATATAA	100
CTAAGGAG	GA	ATTAGA				117

20

2) INFORMATION FOR SEQ ID NO: 1799

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Bacillus thuringiensis*
35 (B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799

TTGATTTT	TCGATTGT	TCAAGTATA	ACTTATGT	AAGCTTAGAA	AG	50
TGGGACGT	AA	GTTTCACT	TT	CTAGTCTAA	AATATAA	100
CTAAGGAG	GA	ATTAGA				117

40

45 2) INFORMATION FOR SEQ ID NO: 1800

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: ATCC 4229

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
10 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1801

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Bacillus pseudomycoides*
(B) STRAIN: NRRL B-617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801

30 TTGATTTTTA TCGATTGTTT AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACTTAA GTTTCACCTTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

35

2) INFORMATION FOR SEQ ID NO: 1802

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
40 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9444

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100

CTAAGGAGGA ATTTAGA

117

5 2) INFORMATION FOR SEQ ID NO: 1803

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803

20 TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGAGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

25

2) INFORMATION FOR SEQ ID NO: 1804

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM *Bacillus cereus*
(B) STRAIN: ATCC 49064

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCACCTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
45 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1805

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus mycoides*
- (B) STRAIN: ATCC 6462

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805

TTGATTTT	TTC	GAGTATA	ACTTATGTAA	GCTTAGAAAG	50
TGGGACGTAA	GTTTCGCTTT	CTAGTCTAAA	TATAAAATAA	CCTATATAAA	100
CTAAGGAGGA	ATTAGA				117

15

2) INFORMATION FOR SEQ ID NO: 1806

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 14579

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806

TTGATTTT	TTC	AAGTATA	ACTTATGTAA	GCTTAGAAAG	50
TGGGACGTAA	GTTTCACTTT	CTAGTCTAAA	TATAAAATAA	CCTATATAAA	100
CTAAGGAGGA	ATTAGA				117

35

40 2) INFORMATION FOR SEQ ID NO: 1807

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
5 CTAAGGAGGA ATTTAGA 117

2) INFORMATION FOR SEQ ID NO: 1808

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 13472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808

25 TTGATTTTTA TCGATTGTTT AAGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGTAA GTTTCACCTT CTAGTCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAGA 117

30

2) INFORMATION FOR SEQ ID NO: 1809

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809

TTGATTTTTA TCGATTCTTC ACGTATAACT ACTTATGTAA GCTTAGAAAG 50
TGGGACGCAA GTTTCGCTTT CTAGCCTAAA TATAAAATAA CCTATATAAA 100
CTAAGGAGGA ATTTAG 117
50

2) INFORMATION FOR SEQ ID NO: 1810

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus mycoides*
 (B) STRAIN: ATCC 6462
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810

15 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GACGCTGCTC CAGAAGAAAAG AGAGCGCGGA ATCACAATCT CAACTGCACA 200
 20 CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

25 2) INFORMATION FOR SEQ ID NO: 1811

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 bases
 (B) TYPE: Nucleic acid
 30 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Bacillus thuringiensis*
 (B) STRAIN: ATCC 10792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811

40 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 45 CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

50 2) INFORMATION FOR SEQ ID NO: 1812

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
- (B) STRAIN: ATCC 15816

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTCTG	GCGATCACTA	100
15	CAGTACTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
	GATGCTGCTC	CAGAAGAAAAG	AGAGCGCGGT	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCACGCTGA	CTATGTTAAA				270

20

2) INFORMATION FOR SEQ ID NO: 1813

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus weihenstephanensis*
- (B) STRAIN: WSBC 10204

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813

	ATGGCTAAAG	CTAAATTCGA	ACGTTCTAAA	CCCCATGTTA	ACATCGGTAC	50
	AATCGGCCAC	GTTGACCATG	GTAAAACTAC	ATTAAGTCTG	GCGATCACTA	100
40	CAGTTCTTGC	AAAAGCTGGT	GGTGCTGAAG	CACGCGGATA	CGATCAAATC	150
	GACGCTGCTC	CAGAAGAAAAG	AGAGCGCGGA	ATCACAATCT	CAACTGCACA	200
	CGTTGAGTAC	GAAACTGAAA	CTCGTCACTA	TGCACACGTT	GACTGCCCAG	250
	GTCATGCTGA	CTATGTTAAA	AACATGAT			278

45

2) INFORMATION FOR SEQ ID NO: 1814

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 266 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacillus anthracis*
(B) STRAIN: CIP 9440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814

10	ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC	50
	AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA	100
	CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC	150
	GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA	200
	CGTTGAGTAC GAAACTGAAA CTCGTCCTA TGCACACGTT GACTGCCCAG	250
15	GTCACGCTGA CTATGT	266

2) INFORMATION FOR SEQ ID NO: 1815

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Bacillus cereus*
(B) STRAIN: ATCC 7064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815

35	ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC	50
	AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTGCT GCGATCACTA	100
	CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC	150
	GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA	200
	CGTTGAGTAC GAAACTGAAA CTCGTCCTA TGCACACGTT GACTGCCCAG	250
40	GTCACGCTGA CTATGTTAA	269

2) INFORMATION FOR SEQ ID NO: 1816

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 13472

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816

```

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA      100
CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
10 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTATGTTA                                268
  
```

15

2) INFORMATION FOR SEQ ID NO: 1817

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: ATCC 4229

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817

```

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA      100
CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
35 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
GTCACGCTGA CTATGTTAAA AACATGAT                                278
  
```

40

2) INFORMATION FOR SEQ ID NO: 1818

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818

```

10  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
    5  AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTG GCGATCACTA      100
      CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
      GATGCTGCTC CAGAAGAAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
      CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
      GTCACGCTGA CTATGTTA                                268

```

2) INFORMATION FOR SEQ ID NO: 1819

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
- (B) STRAIN: CIP 9444

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819

```

30  ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC      50
    AATCGGCCAC GTTGACCATG GTAAAACTAC ATTAAGTCTG GCGATCACTA      100
    CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC      150
    GATGCTGCTC CAGAAGAAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA      200
    CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCCAG      250
    GTCACGCTGA CTATGTTAAA AACATGAT                                278
35

```

2) INFORMATION FOR SEQ ID NO: 1820

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus pseudomyoides*
- (B) STRAIN: NRRL B-617

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820

ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTTCTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGACCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 5 CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCAG 250
 GTCACGCTGA CTATGTTAAA AACATGAT 278

10 2) INFORMATION FOR SEQ ID NO: 1821

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 49064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821

25 ATGGCTAAAG CTAAATTCGA ACGTTCTAAA CCCCATGTTA ACATCGGTAC 50
 AATCGGCCAC GTTGACCATG GTAAACTAC ATTAAGTCT GCGATCACTA 100
 CAGTACTTGC AAAAGCTGGT GGTGCTGAAG CACGCGGATA CGATCAAATC 150
 GATGCTGCTC CAGAAGAAAG AGAGCGCGGT ATCACAATCT CAACTGCACA 200
 30 CGTTGAGTAC GAAACTGAAA CTCGTCACTA TGCACACGTT GACTGCCAG 250
 GTCACGCTGA CTA 263

35 2) INFORMATION FOR SEQ ID NO: 1822

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
 (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822

50 CAATCGAAGT ACAACGTTCT CTTGCGWTAT TGGACGGTGC GGTTACTGTT 50
 CTTGACTCAC AATCAGGTGT TGAGCCTCAA ACTGAAACAG TTTGGCGTCA 100
 AGCAACTGAG TACGGAGTTC CACGTATCGT ATTTGCTAAC AAAATGGACA 150

	AAATCGGTGC	TGACTTCCTT	TACTCAGTAA	GCACACTTCA	CGACCGTCTT	200
	CAAGCAAACG	CACACCCAAT	CCAATTGCCA	ATCGGTGCTG	AAGATGACTT	250
	CCGTGGTATC	ATCGACTTGA	TCAAGATGAA	AGCTGAAATC	TATACTAACG	300
	ACCTTGGTAC	AGATATCCTT	GAAGAAGATA	TTCCAGCTGA	ATACCTTGAC	350
5	CAAGCTCAAG	AATACCGTGA	AAAATTGGTT	GAAGCAGTCG	CTGAAACTGA	400
	TGAAGACTTG	ATGATGAAAT	ACCTTGAAGG	TGAAGAAATC	ACTAACGAAG	450
	AATTGAAAGC	TGCTATCCGT	AAAGCAACTA	TCAACGTTGA	ATTCTTCCCA	500
	GTATTGTGTG	GTTCTGCCTT	CAAGAACAAG	GGTGTTCAT	TGATGCTTGA	550
	TGCGGTTATC	GACTACCTTC	CAAGCCCACT	TGATATCCCA	GCGATCAAAG	600
10	GTATCAACCC	AGATWCAGAT	GAAGAAGAAA	CTCGTCCAGC	ATCTGACGAA	650
	GAGCCATTCT	CAGCTCTTGC	CTTCAAGATC	ATGACGGACC	CATTTGTAGG	700
	TCGTTTGACA	TTCTTCCGTG	TATACTCARG	TGTTCTCCAA	TCARGKTCTT	750
	ACGTATTGAA	CACATCTAAA	GGTAAACGTG	AACGTATCGG	ACGTATCCTT	800
	CAAATGCACG	CTAACAGCCG	TCAAGAAATT	GACACTGTTT	ACTCAGGTGA	850
15	TATCGCTGCT	GCCGTTGGTT	TGAAAGATAC	TYCAACTGGT	GACTCATTGM	900
	CAGATGAAAA	AGCTAAAATC	ATCCTTGAGT	CAATCAACGT	TCCAGAMCCA	950
	GTTATCCAAT	TGATGGTTGA	GCCAAAATCT	AAAGCTGACC	AAGATAAGAT	1000
	GGGTATCGCC	CTTCAAAAAT	TGGCTGAAGA	AGATCCAACA	TTCCGCGTTG	1050
	AAMCAAACGT	TGAAACTGGT	GAAMCAGTTA	TCTCAGGTAT	GGGTGAGCTT	1100
20	CACTTGGACG	TCCTTGTTGA	CCGTATGCGT	CGTGAGTTCA	AAGTGGGAAGC	1150
	GAACGTAGGT	GCTCCTCAAG	TATCTTACCG	TGAAACATTC	CGCGCTTCTA	1200
	CTCAAGCACG	TGGATTCTTC	AAACGTCAGT	CTGGTGGTAA	AGGTCAATTC	1250
	GGTGATGTAT	GGATTGAATT	TACTCCAAAC	GAAGAAGGTA	AAGGATTCTGA	1300
	ATTCGAAAAC	GCAATCGTCG	GTGGTGTGGT	TCCTCGTGAA	TTTATCCCAG	1350
25	CGGTTGAAAA	AGGTTTGGTA	GAATCTATGG	CTAACGGTGT	TCTTGCAGGT	1400
	TACCCAATGG	TTGACGTTAA	AGCTAAGCTT	TACGATGGTT	CATACCACGA	1450
	TGTCGACTCA	TCTGAAACTG	CCTTCAAGAT	CGCGGCTTCA	CTTGCCCTTA	1500
	AAGAAGCTGC	TAAGTCAGCA	CAACCAGCTA	TCCTTGAGCC	AATGATGCTT	1550
	GTAACCATCA	CTGTTCCAGA	AGAAAACCTT	GGTGATGTTA	TGGGTCACGT	1600
30	AACTGCTCGT	CGTGGACGTG	TAGATGGTAT	GGAAGCACWC	GGTAACAGCC	1650
	AAATCGTTCT	TGCTTACG				1668

35 2) INFORMATION FOR SEQ ID NO: 1823

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 115 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823

50	AGACCTGCGT	TCACAAACAC	AGGGTCGTGC	TTCTTACTCT	ATGGAGTTCT	50
	TGAAGTACAA	CGAAGCGCCA	AACAACGTTG	CTACAGCAAT	CATTGAAGCT	100
	CGTAAGGCTA	GATAA				115

2) INFORMATION FOR SEQ ID NO: 1824

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Buttiauxella agrestis*
(B) STRAIN: ATCC 33320
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824

CTGCGTTCAC TGACCAAGGT CGTGCATCTT ACTCCATGGA ATTCCTGAAG 50
TATGATGACG CGCCAAACAA CGTAGCTCAG GCCGTAATCG AAGCTCGCGG 100
TAAATAA 107

2) INFORMATION FOR SEQ ID NO: 1825

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825

TTACTCCATG GAGTTCCTGA AGTATGATGA TGCGCCGAAC AACGTTGCTC 50
AGGCCGTAAT CGAAGCCCGT GGTAATAA 79

2) INFORMATION FOR SEQ ID NO: 1826

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
 (B) STRAIN: ATCC 14029

5. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826

CAGCTGCGTT CTCTGACCAA AGGTCGTGCA TCATACACTA TGGAAATTCCT 50
 GAAGTATGAT GATGCGCCAA ACAACGTTGC TCAGGCCGTT ATTGAAGCCC 100
 GTGGTAAGTA A 111

10

2) INFORMATION FOR SEQ ID NO: 1827

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
 (B) STRAIN: ATCC 8071

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827

GATTTGCGCT CTGCAACTCA TGGGCGTGCT TCGTACTCCA TGGAGTTCTT 50
 30 GAAGTACTCT GATGCACCGC AAAACATTGC GAAAGCGATT ATTGAATCTC 100
 GTAGCTAA 108

35 2) INFORMATION FOR SEQ ID NO: 1828

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
 (B) STRAIN: ATCC 12841

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828

50

CTCAGCTGCG TTCTCTGACC AAAGGTCGTG CATCTTACTC CATGGAATTC 50
 CTGAAGTATG ATGATGCGCC TAACAACGTT GCTCAGGCCG TTATTGAAGC 100
 TCGTGGCAAA TAA 113

2) INFORMATION FOR SEQ ID NO: 1829

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: ATCC 13182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829

GCCGCAGGGT TAAACCAAA GTCCCGTGCT CTCTCCTGAA GGGGAGAGCA 50
CTATAGTAAG GAATATAGCC 70

20

2) INFORMATION FOR SEQ ID NO: 1830

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Budvicia aquatica*
(B) STRAIN: ATCC 35567

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830

GCCTCGGGTA AAACCTATAT CCCAGTCCCC CTCGTATAGA GGGGGATAGA 50
GTAAAGGAAG ATAATC 66

40

2) INFORMATION FOR SEQ ID NO: 1831

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
(B) STRAIN: ATCC 14029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831

5

TCCACAGGAT TAAACCCAG GTTTAAACCT AAGTCCCGTG CTCTCTCCTC 50
AGGGGAGAGC ACAATAGTAA GGAATATAGC C 81

10

2) INFORMATION FOR SEQ ID NO: 1832

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 70 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Obesumbacterium proteus*
(B) STRAIN: ATCC 12841

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832

GCTACTAGTT TAAACATTG ATCCCGTGCT CTCTCTATGA AGGGAGAGCA 50
CAAGAGTAAG GAATAAAGCC 70

30

2) INFORMATION FOR SEQ ID NO: 1833

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putrefaciens*
(B) STRAIN: ATCC 8071

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833

TTTCCAGTTA CGACATAAAT GTTATTATGG TCCAGCTTTG ACTGGACTAT 50
TCTGAAAAGA AAGGAATATA TC 72

50

2) INFORMATION FOR SEQ ID NO: 1834

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 bases
 (B) TYPE: Nucleic acid
 5 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Buttiauxella agrestis*
 (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834

15 GCCCCGGGTT TTAAAAACA TTGATCCCGT GCTCTCTCCA GAAGGGGAGA 50
 GCGCAACAGT AAGGAATATA GCC 73

20 2) INFORMATION FOR SEQ ID NO: 1835

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 795 bases
 25 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter coli*
 (B) STRAIN: ATCC 43479

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835

CTGCAGCTGA TGGTCCTATG CCACAACTA GAGAGCACAT CCTTCTATCA 50
 CGCCAAGTAG GTGTTCCATA TATCGTTGTA TTTATGAATA AAGCAGATAT 100
 GGTTGATGAT GCTGAACTTT TAGAATTGGT TGAAATGGAA ATTAGAGAAT 150
 40 TATTAAGCTC TTATGATTTC CCAGGTGATG ACACACCTAT TATTTCAGGT 200
 TCTGCTTTAA AAGCTCTTGA AGAAGCAAAA GCTGGACAAG ATGGCGAATG 250
 GTCAGCGAAA ATTATGGATC TTATGGCTGC TGTTGATAGC TATATTCCAA 300
 CTCCAACCTCG TGACACTGAA AAAGATTCT TAATGCCAAT TGAAGATGTT 350
 TTCTCAATTT CAGGTCGTGG TACTGTTGTT ACAGGTAGAA TTGAAAAAGG 400
 45 TATTGTAAAA GTTGGTGATA CTATAGAAAT CGTTGGTATT AAAGATACTC 450
 AAACAACAAC TGTAACCTGGC GTTGAAATGT TTAGAAAAGA AATGGACCAA 500
 GGTGAAGCAG GGGATAATGT TGGTGTCTT CTTGCGTGGT CAAAAAAGA 550
 AGAAGTTATC CGCGGTATGG TTCTTGCTAA ACCAAAATCA ATTACTCCAC 600
 ATACTGATTT CGAAGCTGAA GTTTATATCC TAAATAAAGA TGAGGGTGGT 650
 50 AGACATACTC CATTCTTTAA TAACTATAGA CCGCAATTCT ATGTAAGAAC 700
 AACAGATGTA ACAGGTTCTA TTAAATTAGC TGATGGCGTT GAAATGGTTA 750
 TGCCTGGTGA AAATGTAAGA ATTACTGTAA GCTTGATTGC ACCAG 795

2) INFORMATION FOR SEQ ID NO: 1836

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836

```

GCCATACTAG TTGTTTCTGC AGCTGATGGC CCAATGCCAC AACTAGAGA      50
GCACATTTTG CTATCTCGTC AAGTTGGTGT TCCATATATA GTTGTTTTTA     100
TGAACAAAGC TGATATGGTA GATGACGCAG AGTTGCTAGA ATTAGTTGAA      150
20 ATGGAGATCA GAGAGTTATT AAGCGAATAT GACTTCCCTG GTGATGATAC     200
TCCTATTATA AGCGGATCAG CACTTCAAGC TCTTGAAGAA GCTAAAGCTG      250
GTAATGATGG CGAATGGTCA GCTAAGATTA TGGATCTTAT GGCTGCTGTT      300
GATAGCTACA TACCAACTCC AGTTCGTGCT ACTGATAAAG ATTTCTTAAT      350
GCCGATTGAA GACGTATTCT CAATTTCTGG CCGTGGTACT GTTGTTACTG      400
25 GTAGAATTGA AAAAGGTATA GTTAAAGTTG GTGATACTAT CGAAATCGTA     450
GGTATTAGAG ATACACAAAC TACAACAGTT ACCGGCGTTG AAATGTTTAG      500
AAAAGAAATG GATCAAGGCG AGGCTGGTGA TAACGTTGGT GTTCTTTTAC      550
GCGGTACAAA GAAAGAAGAC GTTGAAAGAG GTATGGTTCT TTGTAAGCCA      600
AAATCAATTA CTCCTCATAC TAAATTTGAG GGAGAAGTTT ATATCTTGAC      650
30 TAAGGAAGAG GGCGGTAGAC ATACTCCATT CTTCAACAAC TATAGACCAC     700
AATTTTATGT AAGAACAACA GATGTTACTG GATCAATCAC TCTTCCAGAG      750
GGTACTGAGA TGGTTATGCC TGGTGATAAC TTAAAAATCA CTGTTGAGTT      800
AATCAACCCA GTTGCTC                                           817

```

35

2) INFORMATION FOR SEQ ID NO: 1837

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837

50

```

CCATACTAGT TGTTTCTGCA GCTGATGGCC CAATGCCACA AACTAGAGAG      50

```

	CACATTTTGC	TATCTCGTCA	AGTTGGTGT	CCATATATAG	TTGTTTTTAT	100
	GAACAAAGCT	GATATGGTAG	ATGACGCAGA	GTTGCTAGAA	TTAGTTGAAA	150
	TGGAGATCAG	AGAGTTATTA	AGCGAATATG	ACTTCCCTGG	TGATGATACT	200
	CCTATTATAA	GCGGATCAGC	ACTTCAAGCT	CTTGAAGAAG	CTAAAGCTGG	250
5	TAATGATGGC	GAATGGTCAG	CTAAGATTAT	GGATCTTATG	GCTGCTGTTG	300
	ATAGCTACAT	ACCAACTCCA	GTTTCGTGCTA	CTGATAAAGA	TTTCTTAATG	350
	CCGATTGAAG	ACGTATTCTC	GATTTCTGGC	CGTGGTACTG	TTGTTACTGG	400
	TAGAATTGAA	AAAGGTATAG	TTAAAGTTGG	TGATACTATC	GAAATCGTAG	450
	GTATTAGAGA	TACACAAACT	ACAACAGTTA	CCGGCGTTGA	AATGTTTAGA	500
10	AAAGAAATGG	ATCAAGGCGA	GGCTGGTGAT	AACGTTGGTG	TTCTTTTACG	550
	CGGTACAAAG	AAAGAAGACG	TTGAAAGAGG	TATGGTTCTT	TGTAAGCCAA	600
	AATCAATTAC	TCCTCATACT	AAATTTGAGG	GAGAAGTTTA	TATCTTGACT	650
	AAGGAAGAGG	GCGGTAGACA	TACTCCATTC	TTCAACAACT	ATAGACCACA	700
	ATTTTATGTA	AGAACAACAG	ATGTTACTGG	ATCAATCACT	CTTCCAGAGG	750
15	GTACTGAGAT	GGTTATGCCT	GGTGATAACT	TAAAAATCAC	TGTTAGTT	798

2) INFORMATION FOR SEQ ID NO: 1838

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Buttiauxella agrestis*
- (B) STRAIN: ATCC 33320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838

35	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCCGGTAC	50
	TATCGGCCAC	GTTGACCATG	GTAAACTAC	TCTGACTGCA	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGCGGTTCTG	CACGCGCATT	CGACCAGATC	150
	GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
	CGTTGAATAT	GACACCCCGA	CTCGTCACTA	CGCGCACGTT	GACTGCCCGAG	250
40	GGCAGCCCGA	CTACGTTAAA	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCGATGC	CACAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCATTC	ATGATCGTGT	400
	TCATGAACAA	ATGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	450
	GAAATGGAAG	TTCTGTGAAC	TCTGTCTGCT	TATGATTTC	CGGGCGACGA	500
45	CATCCCAGTG	GTTTCGTGGT	CAGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	550
	AGTGGGAAGC	TAAAATCATC	GAGCTGGCTG	GTCACCTGGA	TAAGTACATC	600
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCA	TTCTGCTGCT	CAATCGAAGA	650
	CGTATTCTCC	ATCTCCGGCC	GTGGTACTGT	TGTTACTGGT	CGTGTAGAGC	700
	GTGGTATCAT	TAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAT	750
50	ACCGTGAAAT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATTAAAC	850
	GTGAAGATAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCTATCAAG	900
	CCGCACACTC	AGTTCGAATC	AGAAGTTTAT	ATCCTGTCCA	AAGATGAAGG	950

CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	1050
GTAATGCCGG	GCGACAACAT	TCAAATGGTT	GTTACCCTGA	TCCACCCAAT	1100
CGCAATGGAC	GACGGT				1116

5

2) INFORMATION FOR SEQ ID NO: 1839

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella oxytoca*
- (B) STRAIN: ATCC 13182

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTCGGTAC	50
25 TATCGGCCAC	GTTGACCATG	GTAAAACTAC	TCTGACCGCT	GCAATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTGCTG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCCCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GA CTGCCCGG	250
GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
30 GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	350
TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	400
TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	450
GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	500
CACTCCGATC	GTTCGTGGTT	CTGCTCTGAA	AGCTCTGGAA	GGCGACGCTG	550
35 AGTGGGAATC	TAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTATATT	600
CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	650
CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTG TAGAGC	700
GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	750
ACTGCTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
40 CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	850
GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	900
CCGCACACCA	AGTTCGAATC	TGAAGTTTAT	ATCCTGTCCA	AAGACGAAGG	950
CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	1000
GTACAACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	1050
45 GTTATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	1100
CGCGATGGA					1109

50 2) INFORMATION FOR SEQ ID NO: 1840

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plesiomonas shigelloides*
- (B) STRAIN: ATCC 14029

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840

	GTGTCTAAAG	AAAAATTTGA	ACGTACTAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAACTAC	CCTGACTGCA	GCTATCACTA	100
15	CCGTACTGTC	TAAAGTATAC	GGTGGTCAGG	CTCGTGCAAT	CGATCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTAGAGTAC	GACACCCCAA	CTCGTCACTA	CGCGCACGTT	GA CTGCC CAG	250
	GTCACGCCGA	CTACGTGAAG	AACATGATCA	CTGGTGCTGC	TCAGATGGAC	300
	GGCGCTATCC	TGGTAGTAGC	TGCGACTGAC	GGCCCAATGC	CTCAGACTCG	350
20	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAGCTGCT	GGA ACTGGTA	450
	GAAATGGAAG	TACGTGAGCT	GCTGTCTCAG	TACGACTTCC	CAGGCGACGA	500
	TACTCCAGTT	GTTCGCGGTT	CTGCACTGAA	AGCGCTGGAA	GGCGATGCTC	550
	AGTGGGAAGA	GAAGATTGTT	GA ACTGGCAG	GCTACCTGGA	CAGCTACATC	600
25	CCTGAGCCAG	AGCGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATCTCCGGCC	GTGGTACTGT	AGTAACTGGT	CGTG TAGAGC	700
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTAG	AAATCGTTGG	TATCAAAGAG	750
	ACTACCAAGA	CTACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGCTGCTGGA	800
	CGAAGGTCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	850
30	GTGATGACGT	AGAGCGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCAATCAAC	900
	CCACACACCA	ACTTTGTAGC	AGAAGTTTAT	ATTCTGTCCA	AAGATGAAGG	950
	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050
	GTAATGCCAG	GTGACAACAT	TCAAATGGTT	GTTACCCTGA	TTGCACCAAT	1100
35	CGCGATGG					1108

2) INFORMATION FOR SEQ ID NO: 1841

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Shewanella putrefaciens*
- (B) STRAIN: ATCC 8071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841

	TGGCAAAAGC	TAAATTTGAA	CGTATTAAGC	CTCACGTAAA	CGTGGGCACC	50
	ATTGGTCACG	TTGACCATGG	TAAAACCACT	CTGACTGCAG	CTATCTCTCA	100
	CGTACTGGCT	AAGACCTACG	GTGGCGAAGC	TAAAGACTTC	TCTCAAATCG	150
5	ATAACGCTCC	AGAAGAGCGT	GAGCGCGGTA	TTACCATCAA	TACCTCTCAC	200
	ATCGAATATG	ACACGCCATC	ACGCCACTAC	GCCCACGTAG	ACTGCCCAGG	250
	CCACGCTGAC	TATGTTAAAA	ACATGATCAC	TGGTGCTGCA	CAGATGGACG	300
	GCGCGATTCT	GGTAGTCGCT	TCAACAGACG	GTCCAATGCC	ACAGACTCGT	350
	GAGCACATCC	TGCTTTCTCG	TCAGGTTGGC	GTACCATTCA	TCATCGTATT	400
10	CATGAACAAA	TGTGACATGG	TAGATGACGA	AGAGCTGTTA	GAGCTAGTTG	450
	AGATGGAAGT	GCGTGAAGT	TTATCAGAAT	ACGATTTCCC	AGGTGATGAC	500
	TTACCGGTAA	TCCAAGGTTT	AGCTCTGAAA	GCGCTAGAAG	GCGAGCCAGA	550
	GTGGGAAGCA	AAAATCCTTG	AATTAGCAGC	GGCGCTGGAT	TCTTACATTC	600
	CAGAACCACA	ACGTGACATC	GATAAGCCGT	TCCTACTGCC	AATCGAAGAC	650
15	GTATTCTCAA	TTTCAGGCCG	TGGTACAGTA	GTAACAGGTC	GTGTTGAGCG	700
	TGGTATTGTA	CGCGTAGGCG	ACGAAGTTGA	AATCGTTGGT	GTACGTGCGA	750
	CAACTAAGAC	AACGTGTACT	GGTGTAGAAA	TGTTCCGTAA	ACTGCTTGAC	800
	GAAGGTCGTG	CAGGTGAGAA	CTGTGGTATT	TTGTTACGTG	GTACTAAGCG	850
	TGATGACGTA	GAACGTGGTC	AAGTATTAGC	GAAGCCAGGT	TCAATCAACC	900
20	CACACACTAC	TTTTGAATCA	GAAGTTTACG	TACTGTCAAA	AGAAGAAGGT	950
	GGTCGTCACA	CGCCATTCTT	CAAAGGCTAC	CGTCCACAGT	TCTACTTCCG	1000
	TACAAC TGAC	GTAACCGGTA	CTATCGAACT	GCCAGAAGGC	GTAAGATGG	1050
	TAATGCCAGG	CGATAACATC	AAGATGGTAG	TGACACTGAT	TTGCCCAATC	1100
	GCGATGG					1107
25						

2) INFORMATION FOR SEQ ID NO: 1842

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1116 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Obesumbacterium proteus*
 - 40 (B) STRAIN: ATCC 12841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1842

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
45	AATCGGCCAC	GTTGACCACG	GTAAACTAC	CCTGACTGCT	GCAATCACTA	100
	CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CACGTGCATT	CGACCAGATC	150
	GATAACGCGC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCAG	250
	GCCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	GCAGATGGAC	300
50	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTAT	400
	TCCTGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAGCTGGTA	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CAGGCAATGA	500

	TACTCCAATC	ATCCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCGTA	GAAGTGGCTG	AACTCTGGA	TTCTTACATC	600
	CCAGAACCAG	AACGTGCTAT	CGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTTACCGGT	CGTGTAGAGC	700
5	GCGGTATCGT	TAAAGTTGGT	GAAGAAGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTTAAAT	CAACTTGTAC	CGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	800
	CGAAGGTCGT	GCAGGCGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	850
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCTATCAAA	900
	CCACACACCA	AGTTCGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
10	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTGGAAATG	1050
	GTAATGCCAG	GCGATAACAT	CAAATGATC	GTTACCCTGA	TCCACCCAAT	1100
	CGCAATGGAC	GATGGT				1116

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2) INFORMATION FOR SEQ ID NO: 1843

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1129 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Budvicia aquatica*
 (B) STRAIN: ATCC 35567

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843

	GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
	TATCGGCCAC	GTTGACCACG	GTAAAACAAC	TCTGACTGCT	GCTATCACCA	100
35	GCGTTTTAGC	TAAAACTTAT	GGCGGTAACG	CTCGTGCAAT	CGATCAAATC	150
	GATAATGCAC	CAGAAGAAAA	AGCACGTGGT	ATCACCATCA	ACACTTCTCA	200
	CGTTGAGTAT	GATACTCCTG	CTCGCCACTA	CGCACACGTA	GACTGCCCCAG	250
	GACACGCCGA	CTATGTGAAA	AACATGATCA	CCGGTGCTGC	TCAAATGGAC	300
	GGCGCGATCT	TAGTTGTTGC	GGCAACTGAT	GGTCCTATGC	CACAGACTCG	350
40	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCTTAC	ATCATCGTGT	400
	TCCTGAACAA	GTGTGACATG	GTTGATGACG	AAGAACTGTT	AGAATTAGTT	450
	GAAATGGAAG	TTCGTGAGCT	TCTTTCTGCT	TATGATTTC	CTGGTGACGA	500
	TACTCCAGTT	GTTCGTGGTT	CTGCGCTGAA	AGCGTTAGAA	GGCGAAGCTG	550
	AGTGGGAAGC	TAAGATCAT	GAATTAGCCG	GATATCTGGA	TAGCTACATC	600
45	CCAGAGCCAG	AGCGTGCGAT	TGACCGTCCG	TTCCTGCTGC	CAATCGAAGA	650
	CGTATTCTCT	ATTTCAGGCC	GTGGTACAGT	TGTTACCGGT	CGTGTAGAGC	700
	GCGGAATCGT	TAAAGTCGGT	GAAGCCGTTG	AGATTGTTGG	TATCAAAGAT	750
	ACCGTACAAA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGTA	AGTTACTTGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	850
50	GTGAAGAAAT	CGAACGCGGT	CAAGTACTGG	CTAAGCCAGG	TTCAATCAAC	900
	CCGCACACCA	ACTTTGTATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	950
	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	1000
	GTACAACCTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTAGAGATG	1050

GTGATGCCTG GTGACAACAT TCAGATGACT GTAACCTCTGA TTGCACCAAT 1100
 CGCGATGGAC GAAGGTTTAC GCTTCGCTA 1129

5

2) INFORMATION FOR SEQ ID NO: 1844

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844

ATATTCATAA TGCATTACAA GTTGTGAAAA CAACAAGTGA CGGAAGTGAA 50
 AAGACTGTTA CATTGGAAAC TGCTGTAGAA TTAGGGGATG GTGCAGTTCG 100
 TACGATTGCC ATGGAATCTA CAGATGGTTT GCAACGTGGC ATGAAAGTAG 150
 25 TGGACTTAGG ACGCACAATT AGCGTTCCTG TGGGACCTGA AACATTAGGT 200
 CGTGTATTCA ACGTTTTAGG AGATACAATC GACTTGAAAG AACCATTCCC 250
 AGAAGACTTT ACAAGACATG AAATCCATAA ACCAGCACCA AAATTTGAAG 300
 AATTAAACAG TCAATATGAA ATTCTACAAA CAGGGATTAA AGTTATTGAC 350
 CTTTTAGCAC CTTATCTTAA AGGTGGTAAA ATCGGTTTAT TCGGTGGTGC 400
 30 CGGTGTAGGG AAAACCGTAT TAATTCAAGA ATTAATTCAT AATATCGCTG 450
 AAGAACTTGG TGGTATTTCA GTATTTACAG GGGTAGGGGA ACGTACTCGT 500
 GAAGGGAATG ACCTTTACCA TGAAATGCAA GAATCAGGCG TATCTGCTAA 550
 AACAGCGATG GTGTTTGGGC AAATGAACGA ACCACCAGGA GCTCGTATGC 600
 GTGTAGCACT AACAGGGTTA ACTATTGCGG AATACTTCCG TGATATGGAA 650
 35 AAACAAGACG TGCTTTTATT CATCGATAAC ATTTATCGTT TCACGCAAGC 700
 AGGTTTCAGAA GTGTCAGCGT TACTTGGTCG TATGCCTTCT GCCGTAGGGT 750
 ATCAACCAAC ATTAGCGACA GAAATGGGTC AATTACAAGA ACGTATCAGT 800
 TCAACTAAAG 810

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2) INFORMATION FOR SEQ ID NO: 1845

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arcanobacterium haemolyticum*

(B) STRAIN: ATCC 9345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845

5	TGCTCTGCCA	GAAATTAACA	ACGCCCTCCT	CACCGAAGTA	GACCTCTCCG	50
	GCCAAGGCGA	AGGCGAAAGC	GTTCTCAAGA	TGACTCTTGA	GGTTGCTCAG	100
	CACCTCGGCG	ATAACATCGT	CCGTACCATC	GCCATGAAGC	CAACCGACGG	150
	TCTGGTTTCG	GGCGCCACCG	TTATCGATAC	CGGCGCCCCA	ATCACCGTGC	200
	CAGTTGGCGA	CGCAACTAAA	GGTCATGTTT	TCAACGTGAC	CGGTGATGTC	250
10	CTAAACTTGG	GCGAAGGCGA	AACCCTTGAC	GTCAAGGAAC	GGTGGCCAAT	300
	CCACCGCAAG	GCTCCACAGT	TCGACGAACT	CGAACCGGAA	ACCAAGATGT	350
	TCGAAACAGG	CATCAAGGTG	ATCGATCTCC	TCACCCCAT	CGTACAGGGC	400
	GGCAAGATCG	GTCTGTTTGG	CGGTGCTGGT	GTTGGTAAGA	CCGTTCTTAT	450
	CCAGGAAATG	ATCCAGCGTG	TTGCACAGGA	TCATGGCGGT	GTGTCCGTGT	500
15	TCGCGGGTGT	GGGTGAACGT	ACCCGTGAAG	GTAACGATCT	TATCCACGAA	550
	ATGGAAGATG	CGGGCGTTCT	TGATAAGACC	GCGCTTGTGT	TCGGCCAGAT	600
	GGATGAACCG	CCAGGGGTTC	GTTTGCATAT	TGCACTTTCC	GGCCTGACCA	650
	TGGCGGAATA	CTTCCGTGAC	GTGCAAAACC	AGGACGTGCT	TTTGTTCATC	700
	GATAACATCT	TCCGCTTCAC	CCAGGCAGGT	TCGGAAGTGT	CCACGTTGCT	750
20	TGGCCGTATG	CCATCAGCAG	TGGGCTACCA	GCCGACCTTG	GCAGATKAAA	800
	TGGGCGCATT	GCAGG				815

25 2) INFORMATION FOR SEQ ID NO: 1846

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--------------------------|
| | (A) LENGTH: 1073 bases |
| | (B) TYPE: Nucleic acid |
| 30 | (C) STRANDEDNESS: Double |
| | (D) TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- | | |
|--|---|
| | (A) ORGANISM: <i>Basidiobolus ranarum</i> |
| | (B) STRAIN: ATCC 24670 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846

40	ACCTTCCTCC	TATCTTGA	AH GCCCTGGAGG	TCCAAAACCA	CAGCTCTCGY	50
	TTAGTTTTAG	AGGTGTCCCA	GCATTTGGGT	GAAAACACCG	TTCGTACTAT	100
	TGCTATGGAC	GGTACTGAAG	GATTGGTTTCG	TGGTCAAAAT	GTCGTAGATA	150
	CCGGATATCC	TATTAGAGTT	CCTGTCGGTC	CTGAATGTTT	GGGTCGTATC	200
45	ATGAACGTTA	TTGGCGAGCC	TGTTGATGAG	CGCGGYCCTA	TCAAGACCAA	250
	GAAGCTTGCA	CCCATCCACG	CTTCTCCCCC	CGAGTTCGTY	GACCAATCCA	300
	CCACCCCCGA	AATCTTGGAG	ACTGGTATTA	AGGTTGTCGA	TTTGTGCGCC	350
	CCTTACGCTC	GTGGTGGTAA	GATCGGTCTT	TTCGGTGGTG	CCGGTGTGCG	400
	TAAGACTGTG	TTTATCCAGG	AGTTGATYAA	CAACGTTGCC	AAGGCCACG	450
50	GTGGTTACTC	CGTGTTCGCT	GGTGTGTTGGT	AGCGTACTCG	TGAGGGTAAC	500
	GATTTGTACC	ACGAGATGAT	TCAAACCTGGT	GTCATCAAGC	TTGATGGCCA	550
	ATCCAAGGCT	GCCCTTGTCT	ACGGMCAAAT	GAACGAGCCC	CCAGGTGCTC	600
	GTGCCCGMGT	CGCTTTGACC	GGTCTTACCG	TTGCTGAATA	CTTCCGTGAT	650

GAGGAAGGHC AAGATGTGTT GCTCTTCATT GACAACATTT TCCGTTTCAC 700
 CCAAGCTGGT TCTGAAGTGT CYGCCTTGTT GGGTCGTATC CCCTCCGCTG 750
 TCGGTTACCA ACCCACCTTG GCCACCGATA TGGGTGTCAT GCAAGAGCGT 800
 ATTACCACCA CCAAGAAGGG TTCCATTACC TCTGTCCAGG CCATTTACGT 850
 5 CCCTGCTGAT GATTTGACCG ATCCCGCTCC TGCCACTACT TTTGCCCATC 900
 TTGACGCCAC CACCGTGTTG TCTCGTTCCA TCTCTGAGTT GGGTATTTAC 950
 CCCGCTGTCG ATCCCCTCGA CTCCAAGTCT CGTATGTTGG ATCCYCGTAT 1000
 TGTCGGTGAA GAGCACTACG ACATCGCCAC TGGTGTTCAG AAGATTCTCC 1050
 ARTCTTACAA GTCTCTCCAG GAT 1073
 10

2) INFORMATION FOR SEQ ID NO: 1847

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Blastomyces dermatitidis*
 25 (B) STRAIN: ATCC 56220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847

TGTCTTTATC CAGGAGTTGA TTGTACGTCT TGCCTCACCC TTTGGGTATT 50
 30 TTGCGAATAC TAATTATAGT AGAACAACAT TGCCAAGGCT CACGGTGGTT 100
 ACTCTGTCTT CACTGGTGTC GGTGAACGTA CTCGTGAGGG TAACGATTTG 150
 TACCACGAAA TGCAGGAAAC TGGTGTCAAT CAGCTCGAGG GTGAATCCAA 200
 GGTCGCCCTC GTGTTCGGTC AGATGAACGA GCCCCCTGGT GCCCGTGCCC 250
 GTGTGCTCTT TACTGGTTTG ACCATTGCCG AGTACTTCCG TGACGAGGAG 300
 35 GGTCAAGATG TGCTTCTCTT CATTGACAAC ATTTTCCGTT TCACTCAGGC 350
 CGGTTCTGAG GTGTCTGCCC TTTTGGGTCTG TATCCCCTCT GCCGTCGGTT 400
 ACCAGCCCAC TCTCGCCGTC GACATGGGTG TCATGCAGGA GCGTATTACC 450
 ACCACCACCA AGGTTCCAT CACCTCCGTC 480

40

2) INFORMATION FOR SEQ ID NO: 1848

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 50
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Blastomyces dermatitidis*

(B) STRAIN: ATCC 14112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848

5	TGTCTTCATT	CAGGAGTTGA	TTGTACGTCC	CTTCCTCTCT	ACAAATGACG	50
	GGCGAGGAAA	ATTTTGGCT	TTTTCTAATA	GCTCGTTATA	GAACAACATT	100
	GCCAAAGCCC	ACGGTGGTTA	CTCCGTTTTT	ACTGGTGTCG	GCGAGCGGAC	150
	CCGTGAAGGA	AACGATTTGT	ACCACGAGAT	GCAGGAAACC	CGTGTTATCC	200
	AGCTCGATGG	CGAGTCTAAG	GTCGCACTCG	TCTTCGGTCA	GATGAACGAG	250
10	CCCCCGGAG	CCCGTGCCCG	TGTTGCCCTC	ACTGGCCTGA	CCATTGCTGA	300
	ATATTTCCGT	GACGAGGAAG	GTCAAGACGG	TATGTATTCA	TATAAATTAC	350
	TCCGGGCAAA	TTGACTCAGA	ACCGCACTCA	CTCACACATA	TATTAGTGCT	400
	TCTCTTTATC	GACAACATTT	TCCGCTTCAC	CCAGGCCGGT	TCCGAAGTGT	450
	CCGCCCTGCT	TGGTCGTATT	CCCTCCGCCG	TCGGTTACCA	ACCCACTCTC	500
15	GCCGTCGACA	TGGGTGGTAT	GCAGGAACGT	ATCACAACCA	CCACCAAGGG	550
	CTCCATTACC	TYCGTG				566

20 2) INFORMATION FOR SEQ ID NO: 1849

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 817 bases
	(B) TYPE: Nucleic acid
25	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Campylobacter coli</i>
(B)	STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849

35	AATGAAGCCA	TTGTTGTAAA	TTTTGAAAGT	GAAGGCAAAA	AACAAAAACT	50
	TGTTTTAGAA	GTAGCAGCAC	ACTTGGGCGA	TAATAGAGTT	AGAACTATTG	100
	CTATGGATAT	GACAGATGGC	TTGGTAAGAG	GACTTAAAGC	AGAAGCTTTG	150
	GGTGCTCCTA	TTAGCGTTCC	TGTGGGTGAA	AAAGTTTTAG	GAAGAATTTT	200
40	TAATGTTACG	GGAGATTTGA	TCGATGAAGG	TGAAGAAATT	TCTTTTGATA	250
	AAAAATGGGC	AATTCATAGA	GATCCACCAG	CTTTTGAAGA	TCAAAGCACA	300
	AAAAGTGAGA	TTTTTGAAAC	AGGGATTAAA	GTTGTGGATT	TACTTGCTCC	350
	TTATGCAAAA	GGTGGTAAAG	TAGGTCTTTT	TGGTGGTGCA	GGTGTGGTA	400
	AAACTGTTAT	TATTATGGAG	CTTATTCACA	ATGTTGCATT	TAAACATAGC	450
45	GGCTATTCTG	TATTTGCAGG	TGTAGGTGAG	AGAACTCGTG	AAGGAAATGA	500
	CCTTTATAAT	GAAATGAAAG	AAAGTAATGT	TTTAGACAAA	GTTGCTCTAT	550
	GTTATGGACA	AATGAATGAA	CCACCAGGGG	CAAGAAATCG	TATTGCTTTA	600
	ACAGGTTTAA	CAATGGCTGA	GTATTTTAGA	GATGAAATGG	GTCTTGATGT	650
	GCTTATGTTT	ATTGATAATA	TCTTTAGATT	TTCACAATCA	GGTTCTGAAA	700
50	TGTCAGCACT	TTTAGGAAGA	ATTCCATCAG	CTGTGGGTTA	TCAACCAACC	750
	CTAGCAAGTG	AAATGGGTAA	ATTCCAAGAA	AGAATTACTT	CAACTAAAAA	800
	AGGATCAATT	ACTTCAG				817

2) INFORMATION FOR SEQ ID NO: 1850

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 775 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850

AAGGCAACAC GCATAAACTT ATTTTAGAGA CTGCTGCACA CCTTGGAGAT 50
 AATCGTGTAA GAACTATCGC TATGGATATG AGCGAAGGAC TTACAAGAGG 100
 GTTAGATGCT ATAGCGCTTG GGTCGCCTAT CAGTGTTCCCT GTTGGAGAAA 150
 20 AAGTTTTTAGG AAGAATATTC AACGTAATTG GTGATCTTAT AGACGAAGGC 200
 GAAGAAGAAA AATTTGATAA AAAATGGTCG ATTCATAGAG ATCCGCCGGC 250
 ATTTGAAGAT CAAAGCACAA AAAGTGAAAT TTTTGAAACA GGTATAAAAG 300
 TCGTAGATCT TTTGGCTCCT TATGCAAAAG GCGGTAAAGT TGGACTATTT 350
 GGCGGTGCCG GCGTTGGTAA AACAGTTATC ATTATGGAAC TTATCCACAA 400
 25 CGTTGCATTC AAACACAGCG GCTATTCGGT ATTTGCCGGT GTCGGTGAAA 450
 GAACAAGAGA GGTAACGAT CTTTATAATG AAATGAAAGA ATCCGGCGTT 500
 TTGGATAAAG TTGCCTTATG TTATGGACAA ATGAATGAAC CGCCGGGTGC 550
 AAGAAACCGT ATAGCGCTTA CTGGTCTTAC AATGGCTGAG TATTTTCGTG 600
 ACGAGATGGG ACTAGATGTT CTTATGTTTA TCGATAACAT CTTCCGTTTC 650
 30 TCACAATCAG GCTCAGAGAT GTCGGCTCTT CTTGGACGTA TCCCAAGTGC 700
 GGTGTTGTTAT CAACCAACGT TAGCTAGCGA AATGGGAAGA CTTCAAGAAA 750
 GAATCACATC AACTAAAAAA GTTTC 775

35

2) INFORMATION FOR SEQ ID NO: 1851

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 793 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851

CGAAGCTATT GAAGTAAATT TTACAGTAGA AGGCAACACG CATAAACTTA 50
 TTTTAGAGAC TGCTGCACAC CTTGGAGATA ATCGTGTAAG AACTATCGCT 100

	ATGGATATGA	GCGAAGGACT	TACAAGAGGG	TTAGATGCTA	TAGCGCTTGG	150
	GTCGCCTATC	AGTGTTCTCTG	TTGGAGAAAA	AGTTTTAGGA	AGAATATTCA	200
	ACGTAATTGG	TGATCTTATA	GACGAAGGCG	AAGAAGAAAA	ATTTGATAAA	250
	AAATGGTCGA	TTCATAGAGA	TCCGCCGGCA	TTTGAAGATC	AAAGCACAAA	300
5	AAGTGA AATT	TTTGAAACAG	GTATAAAAGT	CGTAGATCTT	TTGGCTCCTT	350
	ATGCAA AAGG	CGGTAAAGTT	GGACTATTTG	GCGGTGCCGG	CGTTGGTAAA	400
	ACAGTTATCA	TTATGGA ACT	TATCCACAAC	GTTGCATTCA	AACACAGCGG	450
	CTATTCGGTA	TTTGCCGGTG	TCGGTGAAAAG	AACAAGAGAG	GGTAACGATC	500
	TTTATAATGA	AATGAAAGAA	TCCGGCGTTT	TGGATAAAGT	TGCCTTATGT	550
10	TATGGACAAA	TGAATGAACC	GCCGGGTGCA	AGAAACCGTA	TAGCGCTTAC	600
	TGGTCTTACA	ATGGCTGAGT	ATTTTCGTGA	CGAGATGGGA	CTAGATGTTC	650
	TTATGTTTAT	CGATAACATC	TTCCGTTTCT	CACAATCAGG	CTCAGAGATG	700
	TCGGCTCTTC	TTGGACGTAT	CCCAAGTGCG	GTTGGTTATC	AACCAACGTT	750
	AGCTAGCGAA	ATGGGAAGAC	TTCAAGAAAG	AATCACATCA	ACT	793

2) INFORMATION FOR SEQ ID NO: 1852

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Campylobacter gracilis*

30 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852

	GGACTATTTA	CCGAAGATTA	ACGAAGCTAT	CGAGGTAAAA	TTTGACGTCG	50
35	AGGGCGCTCA	TCGCAGGCTG	ATCCTAGAGG	TAGCCGCGCA	CCTTGGAGAC	100
	AATCGCGTCC	GCACGATCGC	TATGGATATG	AGCGATGGAC	TTAGGCGAGG	150
	GCTTGAGGCC	GTCGCTTTGG	GCGCGCCTAT	TACGGTGCCT	GTGGGCGAGA	200
	AAGTTTTGGG	TAGAATTTTT	AATGTTACGG	GCGATCTGAT	CGACGAAGGC	250
	GAGGATGAAA	AATTTGAAAC	CCGCTGGTCG	ATCCACAGAG	ATCCGCCTAG	300
40	CTTTGAAAAT	CAAAGCACGA	AGAGTGAAAT	TTTTGAAACC	GGCATTAAAG	350
	TAGTCGATCT	GCTCGCCCCT	TATGCAAAGG	GCGGTAAGGT	AGGACTATTC	400
	GGCGGTGCTG	GCGTCGGTAA	GACCGTCATC	ATCATGGAAC	TGATTCACAA	450
	CGTCGCTTTC	AAACACAGCG	GCTACTCCGT	ATTTGCGGGT	GTCGGCGAGC	500
	GAACGAGAGA	GGGAAACGAC	CTTTATAACG	AGATGAAAGA	ATCGGGCGTT	550
45	TTGGATAAAG	TCGCCTTGAC	CTATGGTCAG	ATGAACGAAC	CGCCGGGAGC	600
	GAGAAACCGT	ATCGCGCTAA	CCGGTCTTAC	GATGGCCGAG	TATTTCCGCG	650
	ACGAGCTAGG	GCTTGACGTT	TTGATGTTTA	TTGATAATAT	CTTCCGCTTC	700
	TCGCAGTCGG	GTTCGGAGAT	GTCCGCGCTT	TTAGGACGAA	TTCCGTCCGC	750
	GGTCGGTTAT	CAGCCTACGC	TTGCCAGCGA	AATGGGTAAA	TTACAGGAGC	800
50	GCATTACTTC	TACTAAGAAG	GGCTC			825

2) INFORMATION FOR SEQ ID NO: 1853

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853

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TTTACCTCAA ATTAATGAAG CAATTGTTGT AAATTTTGAA AGCGAAGGAA      50
AAAAACATAA ACTTGTTTTA GAAGTAGCAG CTCATTTAGG AGATAATAGA      100
GTTAGAACTA TTGCTATGGA TATGACAGAT GGTTTGGTAA GGGGCTTAAA      150
20 AGCTGAGGCT TTAGGTGCTC CTATTAGTGT TCCTGTTGGT GAGAAAGTTT      200
TAGGAAGAAT TTTCAATGTT ACTGGAGATT TGATCGATGA AGGTGAAGAA      250
ATTTCTTTTG ATAAAAAATG GGCAATTCAT AGAGATCCGC CAGCTTTTGA      300
AGATCAAAGC ACAAAAAGTG AGATTTTGA AACAGGGATT AAAGTTGTAG      350
ATTTGCTTGC TCCTTATGCA AAAGGTGGTA AAGTAGGTCT TTTTGGTGGT      400
25 GCAGGTGTTG GTAAAACTGT TATTATTATG GAGCTTATTC ACAATGTTGC      450
ATTTAAGCAT AGCGGCTATT CTGTATTGTC AGGTGTGGGT GAGAGAACTC      500
GTGAAGGAAA TGACCTTTAT AATGAAATGA AAGAAAGTAA TGTTTTAGAC      550
AAAGTTGCTC TATGTTATGG ACAAATGAAT GAACCACCAG GAGCAAGAAA      600
TCGTATTGCT TTAACAGGTT TAACAATGGC TGAGTATTTT AGAGATGAAA      650
30 TGGGTCTTGA TGTGCTTATG TTTATTGATA ATATCTTTAG ATTTTCACAA      700
TCAGGTTCTG AAATGTCAGC ACTTTTAGGA AGAATTCCAT CAGCTGTGGG      750
TTATCAACCA ACCCTAGCAA GTGAAATGGG TAAATTCCAA GAAAGAATTA      800
CTTCAACTAA AAAAGGCT                                     818

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35

2) INFORMATION FOR SEQ ID NO: 1854

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus cecorum*
- (B) STRAIN: ATCC 43198

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854

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ATTACCTGAT ATCAACAACG CCTTATTGGT CTATAAAAAT GATGAACAAA      50

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	AAAGTAAAT	TGTGCTAGAA	GCTGCCTTAG	AATTAGGTGA	TGGCATCATT	100
	CGTACAATTG	CCATGGAATC	AACGGATGGT	TTACAACGTG	GGATGGAAGT	150
	TGTCGATACT	GGTAAACCAA	TTTCAGTTCC	AGTTGGTAAA	GAAACGCTAG	200
	GACGTGTCTT	TAACGTTTTA	GGGGATACGA	TTGATATGCA	AGAACCATTT	250
5	GCACAAGATG	CAGATCGTTC	TGCAATTCAT	AAAGCTGCAC	CAAAATTTGA	300
	AGACTTAAGT	ACAAGTACTG	AAATTTTAGA	AACAGGGATT	AAAGTTATCG	350
	ACTTATTAGC	ACCATATTTA	AAAGGTGGTA	AAGTCGGTCT	ATTCGGGGGT	400
	GCCGGAGTAG	GTAAAACCGT	TTTAATCCAA	GAATTAATCC	ATAATATTGC	450
	ACAAGAACAT	GGTGGGATTT	CTGTATTTAC	CGGTGTTGGT	GAACGTACAC	500
10	GTGAAGGAAA	TGACTTGTAT	CATGAAATGC	GTGATTGAGG	AGTTATTGAA	550
	AAAAGTCCA	TGGTGTGTTG	TCAAATGAAC	GAACCACTG	GAGCTCGTAT	600
	GCGTGTGCT	TTAACTGGGT	TAACGATTGC	TGAATATTTT	CGTGATGTAG	650
	AAGGACAAGA	TGTGTTGCTA	TTTATTGATA	ACATCTTCCG	TTTCACTCAA	700
	GCGGGTTCTG	AAGTATCAGC	CTTGCTTGGT	CGTATGCCAT	CTGCCGTGGG	750
15	TTATCAACCT	ACATTGGCTA	CAGAAATGGG	TCAATTACAA	GAACGTATCA	800
	CTTCAACTAA	GAAGGGCTCT	ATCACTTCTA			830

20 2) INFORMATION FOR SEQ ID NO: 1855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus columbae*
 (B) STRAIN: ATCC 51263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855

35	TCTTTACCAG	ATATCAATAA	TGCGCTTATT	GTCTATAAAA	ATGATGAACA	50
	AAAAAGTAAA	ATCGTGCTTG	AAGCTGCTTT	AGAGCTAGGA	GATGGCATTG	100
	TTCGTACGAT	TGCAATGGAA	TCAACTGATG	GATTGCAACG	TGGAATGGAA	150
	GTTTTTCGATA	CAGGTAAGCC	AATTTTCAGTA	CCAGTAGGTC	GTGAAACATT	200
40	AGGTCGTGTA	TTTAATGTTT	TAGGTGATAC	CATTGATACG	CAAGAAGCTT	250
	TTCCTGCTGA	TGCGAATCGT	GATGCGATTG	ATAAATCAGC	TCCAGCTTTT	300
	GAAGAATTAA	GTACAAGTAC	TGAAATCCTA	GAAACAGGGA	TTAAAGTTAT	350
	CGACTTACTA	GCACCATACT	TAAAAGGTGG	GAAAGTTGGT	CTATTCGGTG	400
	GTGCCGGTGT	AGGTAAAACC	GTATTAATTC	AAGAATTAAT	TCATAATATC	450
45	GCCCAAGAAC	ATGGGGGTAT	TTCAGTATTT	ACCGGTGTTG	GTGAACGTAC	500
	ACGTGAAGGA	AATGACTTGT	ATCACGAAAT	GCGTGATTCA	GGCGTTATCG	550
	AAAAAACTGC	TATGGTGTTT	GGGCAATGA	ACGAACCACC	TGGAGCACGT	600
	ATGCGTGTTG	CGCTAACTGG	ACTAACTATT	GCGGAATACT	TCCGTGATGT	650
	TGAAGGCCAA	GACGTATTGC	TATTTATTGA	TAATATCTTC	CGTTTTACTC	700
50	AAGCAGGTTT	TGAAGTTTCT	GCCTTACTTG	GTCGTATGCC	TTCTGCGGTA	750
	GGTTATCAAC	CTACTTTGGC	TACTGAAATG	GGTCAATTGC	AAGAACGGAT	800
	TACATCAACG	AAGAAAGGTT	CGA			823

2) INFORMATION FOR SEQ ID NO: 1856

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus dispar*
 (B) STRAIN: ATCC 51266

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856

TTACCAGACA TTAATAATGC CTTGGTTGTC TATAAAAATG ACGAACAAAA 50
 AACCAAGATT GTATTAGAAG CTGCCTTAGA ACTAGGAGAT GGTGTGATTC 100
 GAACTATCGC CATGGAATCT ACTGATGGCT TACAACGGGG AATGGAAGTT 150
 20 GTCGATACTG GCAGTTCCAT TTCTGTACCG GTAGGAAAAG AAACATTGGG 200
 TCGTGTATTT AACGTTTTAG GAAATACAAT TGACTTAGAA GAACCTTTTC 250
 CAGCGGATGC TAAACGTAGT GGTATCCATA AAAAAGCGCC TGATTTTGAT 300
 GAATTAAGCA CTAGTACAGA AATTTTAGAA ACAGGGATTA AAGTTATTGA 350
 CCTATTAGCC CCTTATTTAA AAGGTGGTAA AGTCGGATTA TTCGGTGGTG 400
 25 CCGGAGTTGG TAAAACCGTT TTAATTCAAG AATTAATTCA TAATATTGCC 450
 CAAGAACATG GTGGGATTTT TGTTTTTACT GGTGTTGGTG AAAGAACACG 500
 TGAAGGTAAT GACTTGTATT ATGAAATGAA AGAATCTGGC GTTATCGAAA 550
 AAAGTCCAT GGTATTTGGT CAAATGAATG AGCCACCTGG TGCCCGGATG 600
 CGGGTTGCTT TAACCGGACT TACCATTGCG GAATACTTCC GGGACGTTGA 650
 30 AGGACAAGAT GTATTGCTCT TTATCGATAA TATTTTCCGT TTTACCCAAG 700
 CTGGTTCAGA AGTATCTGCC TTATTAGGAC GGATGCCCTC TGCCGTTGGT 750
 TATCAACCAA CTTTGGCTAC TGAAATGGGA CAACTTCAAG AACGGATTAC 800
 CTCAACGAAA AAAGGTTCTA TTACAT 826

35

2) INFORMATION FOR SEQ ID NO: 1857

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857

TCCTTACCAG ACATCAACAA TGCGTTGATT GTTTACAAAA AAAATAAAAC 50

	AAAAGTTGTT	CTTGAAGCTG	CTTTGGAAC	TGGTGATGGT	GTTATCCGCA	100
	CGATCTCTAT	GGAATCAACA	GATGGCTTGC	AACGTGGAAT	GGAAGTTGTC	150
	GATACAGGCA	AACCAATCTC	AGTTCCCGTT	GGTAAAGAAA	CTTTAGGTCTG	200
	TGTGTTTAAC	GTATTAGGTG	AAACAATCGA	CAAAGAAGCG	CCTTTTCCAG	250
5	AAGATGCAGT	AAAAAGCGGT	ATTCTATAAA	AAGCGCCGGC	TTTTGAAGAA	300
	CTTAGTACCA	GTAATGAAAT	TTTAGAAACA	GGGATCAAAG	TTATCGACTT	350
	ATTAGCTCCT	TACTTAAAGG	GTGGTAAAGT	CGGACTATTT	GGTGGTGCCG	400
	GTGTTGGTAA	AACCGTCTTG	ATCCAAGAAT	TGATTCATAA	TATCGCCCAA	450
	GAACACGGTG	GTATTTTCACT	GTTTACGGGT	GTTGGTGAAC	GTAATCGTGA	500
10	AGGGAACGAC	CTTTATTATG	AAATGAAGGA	ATCAGGCGTT	ATTGAGAAAA	550
	CTGCCATGGT	GTTTGGACAA	ATGAACGAGC	CGCCAGGTGC	GCGTATGCGT	600
	GTTGCCTTGA	CTGGTTTGAC	ATTGGCTGAA	TATTTCCGAG	ATGAAGAAGG	650
	ACAAGATGTG	CTGTTGTTTA	TCGACAACAT	CTTCCGTTTC	ACTCAAGCCG	700
	GTTCTGAAGT	TTCTGCCTTG	CTTGGCCGGA	TGCCTTCAGC	CGTTGGCTAC	750
15	CAACCAACTT	TGGCAACTGA	AATGGGTCAA	TTGCAAGAAC	GAATCACTTC	800
	AACGAAGAAG	GGCT				814

20 2) INFORMATION FOR SEQ ID NO: 1858

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858

35	CGCATTAGTT	GTTTATAAAA	ATGATGAGCA	AAAATCAAAA	GTTGTTCTTG	50
	AAGCAGCATT	AGAATTAGGT	GACGGTGTGA	TCCGTACGAT	CGCAATGGAA	100
	TCGACGGATG	GACTACAACG	TGGAATGGAA	GTCATCGACA	CAAGCAAAGC	150
	GATCTCTGTA	CCAGTTGGAA	CAGAAACATT	AGGTCGTGTG	TTCAACGTGT	200
40	TAGGTGAAAC	AATCGATTTG	GAAGCACCAT	TTCCAGAGGA	TGCCCCAAGA	250
	AGCGAGATCC	ACAAGAAAGC	ACCAAATTTT	GATGAATTAA	GCACAAGTAC	300
	AGAGATTCTT	GAAACTGGGA	TCAAAGTCAT	TGACTTATTA	GCACCTTATT	350
	TAAAAGGTGG	GAAAGTTGGA	TTGTTTGGGG	GTGCCGGTGT	TGGTAAAACC	400
	GTACTGATCC	AAGAATTGAT	CCATAATATC	GCCCAAGAAC	ATGGGGGAAT	450
45	CTCAGTGTTT	ACCGGTGTAG	GGGAACGTAC	CCGTGAAGGA	AACGATCTGT	500
	ATTACGAAAT	GAAAGATTCA	GGCGTAATCG	AAAAAACAGC	GATGGTGTTT	550
	GGACAAATGA	ATGAGCCACC	AGGTGCTCGT	ATGCGTGTCG	CACTAACTGG	600
	ATTGACGATT	GCGGAATATT	TCCGTGATGT	CGAAGGACAA	GACGTGCTCT	650
	TATTTATTGA	TAATATTTTC	CGTTTCACCC	AAGCAGGTTT	AGAAGTATCT	700
50	GCCTTACTAG	GACGTATGCC	ATCAGCGGTT	GGTTATCAAC	CAACCTTAGC	750
	GACTGAAATG	GGACAACTCC	AAGAACGGAT	CACTTCAACG	A	791

2) INFORMATION FOR SEQ ID NO: 1859

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859

TCCTTACCAG ACATCAACAA TGC GTTGATT GTTTATAAAA AAGATAAAAC 50
 AAAAGTTGTT CTTGAAGCTG CTTTGGAAC TGGTGATGGT GTTATTCGCA 100
 CAATCGCCAT GGAATCAACG GATGGATTAC AACGTGGAAT GGAAGTTGTC 150
 20 GATACTGGCA AGCCTATTTT TGTTCCAGTA GGAAAAGAAA CTCTAGGTCTG 200
 TGTATTTAAT GTATTAGGTG AAACAATCGA CAAGGAAGCG CCTTTTCCAG 250
 AAGATGCAGA AAAAAGTGGT ATTCACAAGA AAGCACCAAC TTTCGAAGAA 300
 CTTAGCACAA GTAATGAGAT CTTAGAAACA GGAATCAAAG TTATTGACTT 350
 GTTAGCTCCT TACTTAAAAG GTGGTAAAGT TGGATTATTT GGTGGTGCCG 400
 25 GTGTTGGTAA AACAGTCTTG ATTCAAGAGC TAATTCATAA TATCGCTCAA 450
 GAACATGGTG GTATTTCTGT GTTTACTGGT GTTGGTGAAC GTACTCGTGA 500
 AGGGAACGAC CTTTATTATG AAATGAAAGA TTCTGGTGTT ATTGAGAAAA 550
 CTGCTATGGT GTTCGGTCAA ATGAACGAGC CGCCAGGTGC ACGTATGCGT 600
 GTTGCCTTAA CTGGTTTAA CTTAGCCGAA TACTTCCGTG ATGAAGAAGG 650
 30 ACAAGATGTG TTGCTATTTA TTGACAACAT TTTCCGTTTC ACTCAAGCCG 700
 GATCAGAAGT TTCTGCCTTA CTTGGCCGTA TGCCGTCAGC AGTTGGTTAC 750
 CAACCGACTT TAGCAACTGA AATGGGTCAA TTACAAGAAC GTATTACGTC 800
 GACGAAAAAA GGTTCAA 817

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2) INFORMATION FOR SEQ ID NO: 1860

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 852 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Globicatella sanguis*
 (B) STRAIN: ATCC 51173

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860

CCTGACATTC ATAATGCATT AATTGTAACG AACGCTGATA TGGCGGATGT 50

	AATGCAAGAA	AATATTTTCGG	ATGAAGAAAA	ATTATTAACC	TTAGAAGTTG	100
	CACTGGATTT	AGGTCATGGA	ATGGTCCGGA	CAATTGCGAT	GGAATCAACC	150
	GATGGTTTGG	AACGCGGCAT	GACAGTTGTG	GATTATTTAA	CACCGATTAA	200
	AGTGCCAGTA	GGCGAAGCCA	CTTTAGGTAG	AGTATTCAAT	GTTTTAGGTG	250
5	AGACAATTGA	TGAACTAGAA	CCGGTTGGCG	ACGATGTTGA	ACTCAAAAGT	300
	ATTCATCGTG	AAGCCCCTAA	ATATGAGGAC	TTAGATAATA	GTTTTTCATGT	350
	TTTAGAAACC	GGAATTAAGG	TCATCGATTT	ATTAGCTCCT	TATATTAAAG	400
	GGGGAAAAAT	CGGTTTATTC	GGTGGTGCCG	GAGTGGGTAA	AACGGTCTTA	450
	ATTCAGAAT	TAATTCATAA	TATTGCAGAA	CAATTAGGAG	GTATCTCAGT	500
10	TTTCACTGGG	GTTGGAGAAC	GTACCCGTGA	AGGGAATGAC	CTCGTTTTTG	550
	AAATGCGAGA	GTCAGGTGTA	AGCAAGAAGA	CGGCCATGGT	TTTCGGTCAA	600
	ATGAATGAAC	CACCTGGAGC	ACGTATGCGT	GTTGTCTTAA	CAGGACTTAC	650
	AATGGCGGAA	TATTTCCGTG	ACGAATTGAA	ACAAGACGTC	TTATTATTTA	700
	TTGATAATAT	TTATCGTTTT	ACTCAAGCAG	GTTCCGAAGT	GTCAGCCTTA	750
15	TTAGGTCGTA	TGCCTTCAGC	AGTAGGGTAT	CAACCAACTT	TAGCAAGTGA	800
	AATGGGACAA	ATGCAAGAAC	GTATTACGTC	WACGAAGCRC	GGTTCCATTA	850
	CA					852

20

2) INFORMATION FOR SEQ ID NO: 1861

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Lactococcus garvieae*
- (B) STRAIN: ATCC 49156
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861

	GCGCGACTCT	TCCTGAGATT	AATAACGCAC	TCATCGTTTA	CAAAGATGTA	50
	GACGGCGTTA	AACTAAAAT	CGTCCTTGAA	GTGGCGTTGG	AACTTGGTGA	100
	TGGTGCCGTA	CGTACCATCG	CTATGGAATC	AACTGATGGC	TTGACACGTG	150
40	GACTTGAAGT	TCTCGATACA	GGTAAAGCAA	TCAGCGTACC	TGTTGGTCAA	200
	GAAACACTTG	GACGTGTCTT	CAATGTACTT	GGAGATGCTA	TTGATGGAGG	250
	GGAAGCATT	GCTGAAAATG	CAGAACGCAG	CCCTATCCAT	AAAAAAGCCC	300
	CATCTTTTGA	TGAACTTTCA	ACAGCAAATG	AAATTCTGGT	GACAGGGATT	350
	AAAGTTATTG	ACTTGCTTGC	CCCATACCTT	AAAGGTGGTA	AGATTGGGTT	400
45	GTTCGGTGGT	GCCGGAGTTG	GTAAAACCGT	CCTTATCCAA	GAGTTGATTC	450
	ACAATATTGC	CCAAGAACAC	GGTGGTATTT	CCGTATTTAC	TGGTGTTGGG	500
	GAACGTACAC	GTGAAGGGAA	TGACCTTTAC	TGGGAAATGA	AAGAATCAGG	550
	CGTTATCGAA	AAAACAGCCA	TGGTCTTCGG	TCAAATGAAT	GAACCACCTG	600
	GAGCACGTAT	GCGTGTTGCT	CTTACTGGTT	TGACAATTGC	TGAATATTTT	650
50	CGTGATGTAG	AAAAACAAGA	CGTTTTGCTT	TTCATTGATA	ATATCTTCCG	700
	TTTCACCCAA	GCCGGTTCAG	AAGTATCTGC	CCTCTTAGGA	CGTATGCCAT	750
	CAGCCGTTGG	TTACCAACCT	ACGCTTGCAA	CTGAAATGGG	TCAACTTCAA	800
	GAACGTATCA	CTTCAACAAA	ACAAGGTT			828

2) INFORMATION FOR SEQ ID NO: 1862

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Lactococcus lactis*
 (B) STRAIN: ATCC 11454
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862

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AATTGCCTGA RATTAACAAT GCCTTGATTG TCTACAAAGA TGTCAATGGC      50
CTAAAAACAA AAATTACTCT TGAAGTTGCT TTGGAACCTG GTGATGGTGC      100
AGTTCGTACA ATCGCTATGG AATCTACTGA TGGCTTGACT CGTGGACTTG      150
AAGTCCTTGA TACAGGTAAA GCAGTCAGCG TTCCTGTTGG GGAAGCCACT      200
CTTGGTCGTG TTTTTAACGT TCTTGGTGAT GTTATTGACG GTGGGGAAGA      250
ATTTGCTGCT GATGCAGAAC GTAATCCTAT CCATAAAAAA GCTCCAACAT      300
TTGACGAATT GTCAACTGCA AACGAAGTTC TCGTAACTGG GATTAAAGTT      350
GTCGATTTGC TTGCACCTTA CCTTAAAGGT GGTAAAGTTG GACTTTTCGG      400
TGGTGCCGGA GTTGGTAAAA CCGTCCTTAT TCAAGAATTG ATTCACAACA      450
TCGCCCCAAGA ACACGGAGGT ATTTCTGTGT TTACCGGTGT TGGGGAACGT      500
ACTCGTGAAG GGAATGACCT TTACTGGGAA ATGAAAGAAT CAGGCGTTAT      550
TGAAAAAACT GCCATGGTCT TTGGTCAAAT GAATGAACCA CCAGGAGCAC      600
GTATGCGTGT TGCCCTTACT GGTTTGACAA TTGCTGAATA TTTCCGTGAT      650
GTTCAAGGTC AAGACGTACT GCTTTTCATT GACAACATCT TCCGTTTCAC      700
ACAAGCTGGT TCAGAAGTTT CTGCCCTTTT GGGACGTATG CCTTCTGCCG      750
TTGGTTACCA ACCAACACTT GCTACTGAAA TGGGGCAATT GCAAGAACGT      800
ATCACTTCTA CTAAGAAGGG TTCTGTTA                                828

```

35

2) INFORMATION FOR SEQ ID NO: 1863

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria ivanovii*
 (B) STRAIN: ATCC 19119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863

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CTTACCTGAA ATCTACAACG CCCTAGTTAT TGAATATAAA TCTGATGCAG      50

```

	AAGAAGCACC	AACTAGCCAA	CTTACTTTAG	AAGTAGCCAT	TCAATTAGGT	100
	GATGACGTTG	TTCGTACAAT	TGCAATGGCA	TCAACTGATG	GTGTTCAAAG	150
	AGGTATGGAA	GTTATTGATA	CTGGGAGCCC	AATCACAGTT	CCAGTTGGTA	200
	CAGTAACACT	TGGTCGTGTA	TTTAACGTAT	TAGGAAACAC	TATCGATTTG	250
5	GATGAGCCAC	TTCCAAGCGA	TATCAAGCGT	AATAAAATTC	ACCGTGAAGC	300
	ACCAACATTT	GACCAATTAG	CAACAAC TAC	TGAAATTCTT	GAAACAGGAA	350
	TAAAAGTTGT	AGACTTGCTA	GCCCCATATT	TAAAAGGTGG	TAAAATTGGT	400
	TTGTTCCGGC	GAGCGGGTGT	TGGTAAAACC	GTTTTAATCC	AAGAACTTAT	450
	TCATAATATC	GCTCAAGAAC	ATGGTGGTAT	TTCTGTGTTT	GCTGGTGTTG	500
10	GAGAACGTAC	TCGTGAAGGG	AACGATCTTT	ACTTTGAAAT	GAAAGACTCT	550
	GGTGTAATTG	AAAAAACTGC	CATGGTATTC	GGTCAAATGA	ACGAACCACC	600
	AGGTGCTCGT	ATGCGTGTAG	CTTTAACAGG	TCTTACAATC	GCTGAATATT	650
	TCCGTGATGA	AGAACACCAA	GATGTACTTC	TATTCAATGA	TAATATTTTC	700
	CGCTTTACTC	AAGCTGGTTC	AGAGGTTTCG	GCTTTACTAG	GTCGTATGCC	750
15	ATCTGCAGTA	GGTTATCAAC	CAACTCTAGC	TACCGAAATG	GGACAATTAC	800
	AAGAACGTAT	TACTTCTACT	AATGT			825

20 2) INFORMATION FOR SEQ ID NO: 1864

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864

35	GTCATATTCC	AGAGCTTTAT	GACGCTCTGG	AGGTTAAGGG	CGATGGTAAG	50
	CATCGTTCAG	ACCTAGTTCT	TGAGGTTCAA	CAGCAGATTG	GCGGTGGTGT	100
	GGTACGCTGC	ATTGCCATGG	GTTCTTCTGA	CGGTTTGAGC	AGAGGAATTG	150
	AGGCTGTAAA	TACTGGTGCC	GGTGTTAAGG	TTCCAGTTGG	TCGTGAGACC	200
40	CTAGGACGTA	TTATGAACGT	TTTAGGTCAG	CCTGTAGATG	AGAGAGGTCC	250
	TATCGGACAG	AAAGAGGATT	GGGAAATTCA	CCGTCCAGCT	CCTACCTATG	300
	CTGAGCAGTC	ATCAACTACA	GAAATTCTAG	AAACCGGTAT	TAAGGTTATG	350
	GACCTTATCT	GCCCATTTGC	TAAGGGTGGT	AAAGTTGGTC	TGTTCCGGTG	400
	TGCCGGTGTG	GGTAAGACAG	TTAACATGAT	GGAGCTTATC	AATAACATTG	450
45	CTAAGGCTCA	CTCAGGTCTA	TCTGTATTTA	CCGGTGTGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	CAGGAATCAA	AGGTTATCGA	550
	TAAGGTATCA	ATGATTTACG	GTCAGATGAA	CGAGCCTCCA	GGGAACCGTC	600
	TACGTGTTGC	TCTGACAGGT	CTGACTGTTG	CTGAGAAGTT	CCGTGACGAA	650
	GGTCTGGATG	TGCTTCTGTT	CATCGATAAC	ATCTATCGTT	ATACACTGGC	700
50	TGGTACAGAG	GTATCTGCTC	TGTTAGGCCG	TATGCCTTCA	GCTGTGGGTT	750
	ACCAGCTTAC	ACTGGCTGAG	GAAATGGGTG	TATTACAGGA	GCGTATTGCT	800
	TCAACTAAGA	AAGGTTCTAT	T			821

2) INFORMATION FOR SEQ ID NO: 1865

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865

```

TGATACTTTA CCAGATATCA ATAATGCATT AGCCGTATAT AAAAATGATG      50
AGAACAAGAC GCGTGTTGTA TTGGAAGCTA CTTTAGAACT TGGAGATGGG      100
GTAATTCGTG CCATTTCTAT GGGGTCTACT GACGGCTTGC AACGTGGCAT      150
20  GGAAGTTGTG GATACACAAG AACCTATTTT TGTTCCGGTA GGAAATGATA      200
CTTTAGGTCG TGTATTTAAT GTGTTAGGAG AAACAATAGA TAATCAGGAG      250
CCATTTCTTG AAGATGCTGA AAAAAGTGGT ATTCACAAAA AAGCCCCCTAG      300
TTTTGATGAA TTAAGTACTA GTTCGGAAAT ATTAGAAACA GGGATCAAAG      350
TGATTGATTT ATTAGAACCT TATCTAAGAG GCGGTAAAGT CGGATTGTTT      400
25  GGAGGCGCCG GTGTTGGAAA AACGGTGCTA ATTCAAGAAT TGATCAATAA      450
TGTTGCCCAA GAACACGGGG GTATTTCCGT GTTTAATGGT GTAGGTGAAC      500
GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGCAGGA TTCAGGCGTT      550
ATCGAAAAAA CAGCCATGGT GTTTGGTCAA ATGAACGAAC CACCAGGTGC      600
TCGTATGCGT GTTGCTTTAA CTGGCCTAAC ACTGGCAGAA TATTTTCGAG      650
30  ATGTTGAAGG TCAAGACGTA TTATTATTTA TTGATAATAT TTTCCGTTTT      700
ACACAAGCAG GTACCGAAGT TTCCGCTTTA CTTGGTAGAA TGCCATCTGC      750
TGTTGGCTAT CAACCCACAC TAGCAACTGA AATGGGGCAA CTGCAAGAAC      800
GGATTACGTC AACGGATAAG GG                                     822

```

35

2) INFORMATION FOR SEQ ID NO: 1866

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter fetus* subsp. *fetus*
 (B) STRAIN: ATCC 25936
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866

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ATCTCCTCAG GATCKATAGG ACTTGATATA GCTCTTGGTA TAGGCGGCGT      50

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	ACCAAAAGGA	AGAATAGTCG	AAATTTATGG	GCCAGAAAGC	TCTGGTAAAA	100
	CAACTCTTAC	TTTGCATTTA	ATAGCAGAAT	CTCAAAAAGT	CGGCGGAGTT	150
	TGCGCGTTTG	TAGATGCAGA	GCATGCACTT	GATGTTAAAT	ATGCTAAAAA	200
	TTTAGGCGTT	GATACGGATA	ACTTATATAT	TTCTCAACCG	GACTTCGGAG	250
5	AGCAAGCTCT	TGATATAGTA	GAAACTCTAG	CTAGAAGCGG	CGCCGTTGAT	300
	CTTATAGTAA	TAGATAGCGT	AGCAGCTYTA	ACACCAAAAA	GCGAAATAGA	350
	AGGCGATATG	GGAGATCAGC	ACGTAGGGCT	GCAAGCAAGA	CTCATGAGTC	400
	AAGCACTTAG	AAAATTAACC	GGAGTTGTCC	ATAAAATGGG	AACTACAGTT	450
	GTATTTATAA	ACCAAATTCG	TATGAAAATC	GGCGCTATGG	GCTATGGCAC	500
10	TCCTGAAACT	ACTACTGGCG	GAAATGCGCT	TAAATTTTAC	GCTTCAGTTA	550
	GACTTGACGT	ACGTAAAATA	GCTACTTTAA	AACAGAGCGA	TGAGCCAATC	600
	GGAAACCGCG	TAAAAGTAAA	AGTAGTAAAA	AACAAAGTCG	CTCCTCCTTT	650
	TAGACAAGCC	GAATTTGATA	TCATGTTTGG	AGAAGGTATC	AGCAAAGAAG	700
	GAGAGATAAT	AGATTACGGC	GTAAACTTTG	ATATTATCGA	TAAAAGCGGC	750
15	GCTTGTTTAA	GCTATGATAA	TTCAAATTA	GGTCAAGGCA	GAGAAAACCTC	800
	AAAAGCGTTT	TTAAAAGA				818

20 2) INFORMATION FOR SEQ ID NO: 1867

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter fetus* subsp. *venerealis*
 (B) STRAIN: ATCC 33561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867

35	TCTCCTCAGG	ATCKATAGGA	CTTGATATAG	CTCTTGGTAT	AGGCGGCGTA	50
	CCAAAAGGAA	GAATAGTCGA	AATTTATGGG	CCAGAAAGCT	CTGGTAAAAC	100
	AACTCTTACT	TTGCATTTAA	TAGCAGAATC	TCAAAAAGTC	GGCGGAGTTT	150
	GCGCGTTTGT	AGATGCAGAG	CATGCACTTG	ATGTTAAATA	TGCTAAAAAT	200
40	TTAGGCGTTG	ATACGGATAA	CTTATATATT	TCTCAACCGG	ACTTCGGAGA	250
	GCAAGCTCTT	GATATAGTAG	AAACTCTAGC	TAGAAGCGGC	GCCGTTGATC	300
	TTATAGTAAT	AGATAGCGTA	GCAGCTYTAA	CACCAAAAAG	CGAAATAGAA	350
	GGCGATATGG	GAGATCAGCA	CGTAGGGCTG	CAAGCAAGAC	TCATGAGTCA	400
	AGCACTTAGA	AAATTAACCG	GAGTTGTCCA	TAAAATGGGA	ACTACAGTTG	450
45	TATTTATAAA	CCAAATTCGT	ATGAAAATCG	GCGCTATGGG	CTATGGCACT	500
	CCTGAAACTA	CTACTGGCGG	AAATGCGCTT	AAATTTTACG	CTTCAGTTAG	550
	ACTTGACGTA	CGTAAAATAG	CTACTTTAAA	ACAGAGCGAT	GAGCCAATCG	600
	GAAACCGCGT	AAAAGTAAAA	GTAGTAAAAA	ACAAAGTCGC	TCCTCCTTTT	650
	AGACAAGCCG	AATTTGATAT	CATGTTTGGG	GAAGGTATCA	GCAAAGAAGG	700
50	AGAGATAATA	GATTACGGCG	TAAAACTTGA	TATTATCGAT	AAAAGCGGCG	750
	CTTGTTTTAG	CTATGATAAT	TCAAAATTAG	GTCAAGGCAG	AGAAAACCTCA	800
	AAAGCGTTTT	TAAA				814

2) INFORMATION FOR SEQ ID NO: 1868

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33560
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868

```

GATAGCATAG GCWCAGGTTC AGTTGGACTT GATCTTGCTT TAGGTATAGG      50
CGGTGTTCCA AAAGGAAGAA TTATAGAAAT TTATGGGCCCT GAAAGTTCAG      100
GTAAAACTAC TCTAACTCTA CACATTATCG CAGAATGCCA AAAAGCAGGT      150
GGGGTTTGTG CTTTTATCGA TGCAGAACAT GCACTTGATG TGAAATATGC      200
TAAAAATTTA GGTGTAAATA CAGATGATTT GTATGTTTCT CAACCTGATT      250
TTGGAGAGCA AGCCTTAGAA ATTGTAGAAA CTATAGCWAG AAGTGGTGCA      300
GTAGATCTTA TWGTAGTAGA TAGCGTTGCA GCWCTTACCC CAAAAGCAGA      350
AATTGAAGGC GATATGGGCG ATCARCATGT AGGACTTCAA GCAAGACTTA      400
TGTCTCAAGC TCTAAGAAAA CTTACAGGTA TAGTTCATAA AATGAATACC      450
ACAGTAATTT TCATCAACCA AATTTCGTATG AAAATCGGTG CTATGGGTTA      500
TGGTACTCCT GAAACCACAA CAGGTGGAAA TGCATTAAAA TTTTATGCTT      550
CTGTGCGTTT AGATGTTAGA AAAGTAGCAA CCTTAAAMCA AAACGWAGAM      600
CCTATAGGAA ACCGCGTTAA AGTAAAAGTA GTTAAAAATA AAGTTGCTCC      650
TCCATTCAAG CAAGCTGAAT TTGATGTGAT GTTTGGAGAG GGTTTAAGCC      700
GTGAAGGTGA ATTGATCGAT TATGGTGTA AACTTGATAT CGTAGATAAA      750
AGTGGTGCGT GGTTTTCTTA TAAAGATAAA AAAGTTGGAC AAGGTAGAGA      800
AAATTCAAAA GCTTTCTTAA AAGA                                     824

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35

2) INFORMATION FOR SEQ ID NO: 1869

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869

```

AGAAAGTTCT GGTAACAA CAGTTGCACT GCATGCGATT GCAGAAGTTC      50

```

AAAAACATGG CGGGACGGCA GCCTTTATTG ATGCCGAGCA CGCGTTGGAC 100
 CCTCAATACG CACAACGTCT AGGTGTAAAC ATTGATGAAT TGCTGCTATC 150
 ACAACCAGAT ACTGGGGAAC AAGGCTTAGA AATTGCAGAT GCTTTAGTTT 200
 CAAGTGGCGC AGTCGATATT ATCGTTATTG ACTCGGTGGC CGCGCTAGTC 250
 5 CCCCCTGCTG AAATCGATGG CGAGATGGGT GATGCGCACG TTGGTCTGCA 300
 GGCTCGTTTG ATGTCACAAG CATTGCGCAA GCTGTCAGGC TCTATCAACA 350
 AAACAAAGAC TATCGCCGTC TTTATTAACC AAATTCGT 388

10

2) INFORMATION FOR SEQ ID NO: 1870

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA
 20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870

TGAAAGTTCA GGTAACAA CAGTTGCACT ACACGCTATT GCAGAAGTAC 50
 AAAAAAATGG CGGAACGGCC GCTTTCATTG ATGCTGAGCA TGCCTTAGAT 100
 CCGCAATATG CACAAAATT AGGTGTGAAT ATCGATGAAC TACTTCTTTC 150
 30 ACAGCCTGAC ACAGGAGAAC AAGGTCTAGA GATCGCTGAT GCTTTAGTAT 200
 CAAGTGGGGC TGTAATATC GTAGTAGTCG ATTCAGTTGC TGCTTTAGTT 250
 CCACGAGCAG AAATCGACGG CGAAATGGGT GACTCACATG TCGGGTTACA 300
 AGCACGTTTG ATGTCTCAAG CATTGCGTAA ACTCTCTGGT TCGATCAACA 350
 AAACAAAAC AATCGCTATT TTCATCAACC AAATCCGT 388
 35

2) INFORMATION FOR SEQ ID NO: 1871

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria monocytogenes*
 30 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871

```

AGAGAGTTCC GGTAAAACAA CTGTTGCGCT TCATGCAATT GCGGAAGTAC      50
AAGCACAAGG CGGAACAGCA GCATTTATCG ATGCTGAGCA TGCCTTGGAT      100
CCGGCTTATG CTAAAAACCT AGGTGTAAAT ATTGATGAAT TATTACTATC      150
TCAACCAGAT ACAGGAGAAC AAGCTTTAGA GATTGCTGAA GCTTTAGTTA      200
5  GAAGTGGTGC AGTTGATATG TTAGTAATTG ACTCCGTTGC AGCACTTGTA      250
CCACGTGCTG AAATCGAAGG CGAGATGGGC GATGCTCATG TTGGATTACA      300
AGCACGTTTA ATGTCCCAAG CATTGCGTAA ACTTTCTGGT GTTATTAATA      350
AATCAAAAAC CATTGCTATT TTCATTAACC AAATTCGT      388

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10

2) INFORMATION FOR SEQ ID NO: 1872

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15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 388 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

20 (ii) MOLECULE TYPE: Genomic DNA

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      (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Streptococcus mitis
            (B) STRAIN: ATCC 49456

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25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872

```

AGAGTCATCT GGTAAGACAA CGGTTGCCCT TCATGCAGTT GCGCAAGCAC      50
AAAAAGAAGG TGGTATTGCT GCCTTTATCG ATGCGGAACA TGCCCTTGAT      100
30  CCAGCTTATG CTGCGGCCCT TGGTGTCAAC ATTGACGAAT TGCTCTTGTC      150
ACAACCAGAC TCAGGAGAGC AAGGTCTTGA GATTGCAGGA AAATTGATTG      200
ACTCAGGAGC CGTGGATCTT GTCGTAGTCG ACTCAGTTGC GGCCCTTGTC      250
CCTCGTGCGG AAATTGATGG AGATATCGGT GATAGCCACG TTGGTTTGCA      300
GGCTCGTATG ATGAGCCAGG CTATGCGTAA ACTTGGTGCT TCTATCAATA      350
35  AAACCAAAAAC AATTGCCATC TTTATCAACC AATTGCGT      388

```

2) INFORMATION FOR SEQ ID NO: 1873

40

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      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 430 bases
            (B) TYPE: Nucleic acid
            (C) STRANDEDNESS: Double
45  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

```

      (vi) ORIGINAL SOURCE:
50  (A) ORGANISM: Streptococcus oralis
      (B) STRAIN: ATCC 35037

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873

	GAACATGACG	CCGACTTTTT	CACGCAATTG	GTTGATAAAG	ATGGCAATTG	50
	TTTTGGTTTT	ATTGATAGAA	GCTCCGAGTT	TACGCATGGC	CTGGCTCATC	100
	ATTTCGAGCCT	GCAAACCAAC	GTGACTGTCT	CCAATATCCC	CATCAATTTT	150
5	CGCACGAGGT	ACAAGGGCCG	CAACTGAGTC	GATAACGACA	AGGTCAACTG	200
	CACCTGAGTC	AATCAATTTT	CCAGCAATTT	CAAGACCTTG	TTCACCTGAG	250
	TCTGGTTGTG	ACAAGAGCAA	TTCGTCAATA	TTCACACCAA	GGGCTGCAGC	300
	ATAGGCTGGG	TCAAGAGCAT	GTTCCGCATC	GATAAAGGCT	GCAATACCAC	350
	CTTCTTTCTG	TGCTTGCGCA	ACAGCGTGAA	GGGCAACCGT	TGTCTTACCA	400
10	GATGATTCTG	GCGCRTACAY	TTCGATGATA			430

2) INFORMATION FOR SEQ ID NO: 1874

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: ATCC 64746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874

30	TTGTCGTTGT	TGCTGCCTCC	GACGGTCAGA	TGTAGGTGGA	ACATCTTGGG	50
	AAATACGTCG	TAAAACACGT	CGCTTACGTT	TTCGCGAATA	GGCCCCAGAC	100
	TCGTGAGCAT	TTGCTGCTCG	CCCGCCAGGT	TGGTGTCCAG	AAGATCGTTG	150
	TCTTCGTCAA	CAAAATCGAT	GCTATTGATG	ATCCGGAGAT	GCTGGAAGTG	200
	GTCGAACTCG	AGATGCGTGA	GCTGCTGAAC	AGCTACGGTT	TCGAGGGTGA	250
35	AGAGACTCCG	ATCATTTTTCG	GTTCCGCTCT	CTGTGCTCTC	GAAGGACGCC	300
	GTGACGACAT	CGGTAAAGAC	AGAATTGAGC	AGCTTATGAA	CGCTGTGCAC	350
	ACCTGGATCC	CCACTCCTCA	GCGTGACCTC	GACAAACCTT	TCTTGATGTC	400
	TGTCGAGGAA	GTGTTCTCTA	TCGCCGGCCG	TGGTACCGTG	GCTTCTGGTC	450
	GTGTCGAGCG	TGGTATCTTG	AAGAAGGACT	CTGAGGTTGA	GATTGTTGGA	500
40	GGCTCCTTCG	AACCCAAGAA	GACCAAAGTC	ACCGACATTG	AAACCTTCAA	550
	GAAGAGCTGT	GATGAATCGC	GTGCTGGTGA	CAACTCTGGT	CTCCTCCTGC	600
	GTGGTATCCG	ACGTGAAGAC	GTCAAGCGTG	GTATGGTCAT	TGCTGTTCCC	650
	GGCAGACCA	AGGCTCACGA	CAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	700
	CGAGGCGGAG	GGTGGTCGTC	GTAAGGCTT	CGGTGCCAAC	TACCGTCCCC	750
45	AAGTCTTCAT	CCGTACTGCA	GGTAAGTTCC	CGCACACCGT	GTCCAGATCT	800
	TCCGAGAGAT	TAGCGATATA	TGCTAATGAT	TCATCAGACG	AGGCTGCTGA	850
	CCTCAGCTTC	CCTGACGGCG	ACCAATCTCG	CAGAGTTATG	CCTGGTGACA	900
	ACGTCGAGAT	GATCCTGAAG	ACCCACCACC	CTGTTGCTGC	TGAGGCT	947

50

2) INFORMATION FOR SEQ ID NO: 1875

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus versicolor*
 (B) STRAIN: WSA-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875

```

15 GCTGCTTCCG ATGGTCAAAT GTACGTCAAC CTTATATACA CCCTCTGATA      50
   TGACAGAATG TCGCCTAACA GCACGCGTGA ACTAGGCCCC AAACCCGTGA      100
   GCACTTGCTG CTTGCCCCGCC AGGTCGGTGT CCAGAAGATT GTTGTGTTCG      150
   TCAACAAGGT TGATGCCGTC GATGACCCTG AGATGTTGGA ACTTGTTGAG      200
   CTGGAAATGC GTGAGCTTCT CAGCACTTAC GGCTTCGAAG GCGAGGAGAC      250
20 CCCTATCATC TTCGGTTCCG CCCTATGCGC CCTCGAGGGT CGCCGCCCCG      300
   ATATCGGTAC TGAGCGAATT GACAGCCTTC TTGAGGCCGT TGACACCTGG      350
   ATCCCTACCC CTCAGCGTGA CCTGGACAAG CCTTTCCTGA TGTCTGTCTGA      400
   GGAGGTCTTC TCCATTGCCG GTCGTGGTAC CGTTGCCTCT GGCCGTGTTG      450
   AGCGTGGTCT CCTTAAGAAG GACAGCGAGG TCGAGATTCT CGGAGGTGGT      500
25 CAGGTCATGA AGACCAAGGT CACTGACATT GAGACATTCA AGAAGCACTG      550
   TGACGAATCC CGTGCTGGTG ACAACTCCGG TCTTCTTCTC CGTGGTATCC      600
   GCCGTGAGGA TGTCAAGCGC GGTATGGTTA TTGCTGCTCC CGCCTCTATC      650
   AAGGCCCAACA AGAAGTTCAT GGTCTCCATG TACGTCCTCA CTGAGGCAGA      700
   AGGTGGCCGT CGCAGTGGCT TCGGTGTCAA CTATCGTCCC CAGGCTTACA      750
30 TTCGCACTGC TGGTAAGTTT TCAAAACATT CGACCTCTCG CCTTAGAAGA      800
   AGAATACCTC TAACTTGTAT TTAGACGAGG CTTGCGACCT TTCTTTCCCC      850
   GATGGCGACA TGAGCCGCCG TGTCATGCCT GGTGACAACG TGGAAATGAT      900
   CCTCAACCTC AACAACCCTG TCG                                923

```

2) INFORMATION FOR SEQ ID NO: 1876

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Basidiobolus ranarum*
 (B) STRAIN: ATCC 24670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876

```

CATCATTGTT GTGTCCGCCA CTGATGGTCA AATGCCTCAA ACTCGTGAGC      50

```

	ATTTGTTGTT	GGCTCGCCAA	GTTGGTGTCC	AACACTTGGT	TGTCTTCATC	100
	AACAAGGTTG	ATGCCGTTGA	TGATCCTGAA	ATGTTGGAGT	TGGTCGAGAT	150
	GGAAATGCGT	GATTTGCTTT	CCCAATACGG	TTCCCCCGGA	GACAACGTCC	200
	CCATTATCCA	GGGTTCGCT	CTCTGCGCTC	TTGAGGACCG	CAACCCCGAG	250
5	ATCGGCCGTA	ACGCCATCAT	GAAGTTGATG	GAGGCTGTTG	ATAGCAGCAT	300
	CCCCACCCCT	GCCCCGTGATT	TGGACAAACC	TTTCCTCATG	CCCGTTGAAG	350
	ATGTGTTCTC	CATCTCTGGC	CGTGGTACTG	TTGCCACTGG	ACGTGTTGAG	400
	CGTGGTATGG	TCACCAAGGG	TACTGAAGTT	GAAATCGTCG	GTATGGGCGA	450
	GCACTTCAAG	ACCACCTTGA	CCGGTATTGA	AATGTTCCAC	AAGGAATTGG	500
10	ACAAGGGTAT	GGCTGGTGAC	AACATGGGTT	GCTTGCTTCG	TGGTGTCAAG	550
	CGTGAGCAAG	TCCGTGCTGG	TATGGTTATC	TGTGCCCCCG	GATCCGTCAA	600
	GCCACATAAG	AAGTTCATGG	CTCAGCTCTA	CATTCTCACC	AAGGATGAGG	650
	GAGGCCGCCA	CACTCCCTTC	GTCAACAAC	ACCGCCCACA	AATGTTCTTC	700
	AGAAGTGTG	ATGTTACCGC	CATCCTTAAG	CACCCCCCTG	GTACCCCCGA	750
15	TGCTGATGAG	AAGATGGTCA	TGCCCGGAGA	CAACGTTCAA	CTCGAGTGCG	800
	AGCTCTT					807

20 2) INFORMATION FOR SEQ ID NO: 1877

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter gracilis*
 (B) STRAIN: ATCC 33236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877

35	AGTTGTTTCT	GCTGCGGATG	GTCCTATGCC	TCAAACCTCGC	GAGCATATCT	50
	TGCTTTCTCG	TCAAGTAGGC	GTTCCATACA	TCGTAGTTTT	CCTAAACAAA	100
	ACCGATATGG	TCGATGATCC	GGATCTTTTA	GAGTTAGTTG	AAGAGGAAGT	150
	TAGAGATCTT	TTAAAAGAGT	ATAAATTCCC	TGGCGACGAA	ACCCCAATCA	200
10	TTAAGGGTTC	TGCTCTTAAG	GCTCTTGAGG	AAGCTAAGGC	CGGACAAGAC	250
	GGCGAATGGT	CTGCAAAGAT	TATGGAGCTT	ATGGACGCGG	TTGATAGCTA	300
	TATTCCAAC	CCTGTTTCGG	ATACTGATAA	AGATTTTCCTT	CTTCCGATCG	350
	AAGATATTTT	CTCGATTTCC	GGTCGCGGTA	CCGTTGTAAC	CGGTAGAATC	400
	GAAAAAGGTA	TCGTAAAGT	TGGTGATACT	ATCGAGATCG	TAGGTATTAA	450
15	ACCTACTCAG	ACTACTACCG	TCCTGGCGT	TGAGATGTTT	AGAAAAGAGA	500
	TGGATCAAGG	TGAAGCCGGC	GATAATGTAG	GTGTTTTATT	GCGCGGTACT	550
	AAGAAAGAGG	AAGTAGAGCG	CGGTATGGTT	TTATGCAAAC	CAAAATCGAT	600
	CACTCCTCAT	ACTAAATTTG	AGGGCGAGGT	TTATATCCTA	ACTAAAGAAG	650
	AAGGCGGACG	CCATACTCCA	TTCTTTAATA	ATTATAGACC	GCAGTTTTAC	700
50	GTTCGTACGA	CAGATGTTAC	CGGTTGATT	ACTCTTCCTG	AAGGAACCGA	750
	GATGGTTATG	CCGGGCGACA	ACGTTAAAT	CACCGTTGAG	CTAATCGCTC	800
	CGATCG					806

2) INFORMATION FOR SEQ ID NO: 1878

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni jejuni*
 (B) STRAIN: ATCC 33292

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878

GCTGCAGATG GCCCTATGCC ACAAAC TAGA GAGCACATTC TTCTTTCTCG 50
 TCAAGTAGGC GTTCCATATA TTGTTGTTTT TATGAATAAA GCAGATATGG 100
 TTGATGATGC TGAAC TTTTA GAGTTAGTTG AAATGGAAAT TAGAGAATTA 150
 20 TTAAGCTCTT ATGATTTCCC AGGCGATGAT ACACCTATTA TTTCTGGTTC 200
 TGCTTTAAAA GCTCTTGAAG AAGCTAAAGC TGGACAAGAT GGTGAATGGT 250
 CAGCAAAAAT TATGGATCTT ATGGCTGCAG TTGATAGCTA TATTCCAAC T 300
 CCAACTCGTG ATACTGAAAA AGACTTCTTG ATGCCAATTG AAGATGTTTT 350
 CTCAATTTCA GGTCGTGGTA CTGTTGTTAC AGGTAGAATT GAAAAAGGTG 400
 25 TTGTAAAAGT AGGTGATACT ATCGAAATCG TTGGTATTAA AGATACTCAA 450
 ACAACAAC TG TAACAGGTGT TGAAATGTTT AGAAAAGAAA TGGATCAAGG 500
 CGAAGCAGGA GATAACGTAG GTGTTCTTCT TCGTGGTACT AAAAAAGAAG 550
 AAGTTATCCG TGGTATGGTT CTTGCTAAAC CAAAATCAAT TACTCCACAC 600
 ACTGACTTCG AAGCTGAAGT TTATATCTTA AATAAAGATG AAGGTGGTAG 650
 30 ACATACTCCA TTCTTTAACA ACTATAGACC ACAGTTTTAT GTAAGAACAA 700
 CTGATGTTAC AGGTTTCGATT AAATTAGCTG ATGGTGTTGA AATGGTTATG 750
 CCAGGTGAAA ATGTGAGAAT TACTGTAAGC TTGATCGCTC CAGTAGCACT 800
 TGAAGA 806

35

2) INFORMATION FOR SEQ ID NO: 1879

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: WSA-222

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879

ATGTATGCAA CCGAGAGCAC TCCCGGATCT TGGTTTAAAT GGCACTAATA 50

	TAAGACAGGC	CTCAAACCTCG	AGAGCATTTA	CTTCTCGCCC	GTCAGATCGG	100
	TATCCAAAAA	ATCGTCGTCT	TCGTGAACAA	GGTTGATGCC	ATCGAGGACA	150
	AAGAGATGTT	GGAGCTTGTT	GAATTGGAGA	TGCGTGAAC	CCTAACCAGC	200
	TACGGTTTCS	AGGGTGAAGA	AACTCCCATC	ATTTTGGCT	CTGCTCTCTG	250
5	TGCCCTCSAA	GGAAGACAAC	CCGAGATCGG	TGTTACCAAG	ATTGATGAGC	300
	TCTTGCAGGC	CGTCGACACC	TGGATTCCCA	CTCCTCAGCG	TGAGACTGAC	350
	AAGCCCTTCT	TGATGTCCAT	TGAGGAAGTG	TTCTCTATTT	CCGGACGAGG	400
	AACCGTTGTC	TCCGGCCGTG	TGGAGCGTGG	TATCCTCAAG	AAGGACTCCG	450
	AAGTTGAAAT	TGTCGGCGGT	TCGCCCAGAG	CAATCAAAAC	CAAGGTTACC	500
10	GATATCGAAA	CCTTTAAGAA	GTCTTGCGAC	GAGTCTCGCG	CTGGTGATAA	550
	CTCCGGCTTG	CTCCTACGAG	GCGTTAAGCG	TGAAGATATT	AGCCGTGGCA	600
	TGGTCGTCGC	TGTACCAGGA	AGTGTCAAGG	CCCATACTGA	ATTCTTAGTT	650
	TCGCTTTACG	TCCTCACCGA	AGCTGAGGGT	GGGCGCAAAT	CTGGATTGAG	700
	CAGCAAGTAC	CGCCACAGAA	TGTTCAATCG	CACTGCCGGT	ATGTAATACT	750
15	GTGATAATTT	CGTTGACATG	GTACTGATTG	AATTCTATAG	ACGAAGCGGC	800
	TCAGCTCAGC	TGGCCCGGAG	AAGATCAAGA	CAAGATGGCT	ATGCCAGGAG	850
	ACAATATCGA	AATGATTTGC	ACCACCTTGC	ACCCAGTTGC	CGCCGA	896

20

2) INFORMATION FOR SEQ ID NO: 1880

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Erwinia amylovora*
 (B) STRAIN: ATCC 14976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880

	CTGGTAGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACYC	GTGAGCACAT	50
	CCTGCTGGGT	CGCCAGGTTG	GCGTGCCATA	CATCATCGTG	TTCCTGAACA	100
	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAGCTGGT	TGAAATGGAA	150
40	GTMCGTGACC	TGCTGTCACA	GTACGACTTC	CCAGGCGACG	ACACGCCAAT	200
	CGTGCRYGGT	TCTGCGCTGA	AAGCGCTGGA	RGGCGAAGCA	GAGTGGGAAG	250
	CGAAGATCAT	CGAACTGGCT	GGCCATCTGG	ATAACTACAT	CCCGGAACCA	300
	GAGCGTGCGA	TTGACAAACC	GTTCCTGCTG	CCAATTGAAG	ACGTGTTCTC	350
	CATCTCTGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	CGCGGTRTSG	400
15	TTAAAGTGGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	TACCGTGAAA	450
	TCAACCTGTA	CCGGCGTTGA	GATGTTCCGT	AAGCTGCTGG	ACGAAGGCCG	500
	TGCGGGTGAG	AACTGTGGTA	TCCTGCTGCG	CGGTATCAAG	CGCGAAGATA	550
	TCCAGCGTGG	TCAGGTTCTG	GCGAAGCCAG	GCACCATCAA	GCCACACACC	600
	AAGTTCGAGT	CAGAAGTTTA	TATTCTGTCT	AAAGACGAAG	GCGGCCGTCA	650
30	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	CGTACTACTG	700
	ACGTGACCGG	GACTATCGAA	CTGCCAGAAG	GCGTTGAGAT	GGTGATGCCA	750
	GGCGACAACA	TTCAGATGGT	TGTGACCCTG	ATCCACCCGA	TCGCCATG	798

2) INFORMATION FOR SEQ ID NO: 1881

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881

```

ATCCTGGTTG TTGCTGCGAC TGACGGYCCG ATGCCGCAGA CCCGTGAGCA      50
CATCCTGCTG GGTTCGTCAGG TAGGCGTTCC GTACATCATC GTGTTCTCTGA    100
ACAAATGCGA CATGGTTGAT GACGAAGAGC TGCTGGAAC TGGTTGAAATG      150
GAAGTTCGYG AACTGCTGTC TCAGTACGAC TTCCCGGGCG ACGACACTCC      200
GATCGTTCGT GGTTCCTGCTC TGAAAGCGCT GGAAGGCGAC GCAGAGTGGG      250
AAGCGAAAT CATCGAACTG GCTGGCTTCC TGGATTCTTA CATYCCGGAA      300
CCAGAGCGTG CGATTGACAA GCCGTTCTCTG CTGCCGATCG AAGACGTATT      350
CTCCATCTCC GGTTCGTGGTA CCGTTGTTAC CGGTCGTGTA GARCGCGGTA      400
TCATCAAAGT GGGCGAAGAA GTTGAAATCG TTGGTATCAA AGAGACTCAG      450
AAGTCTACCT GTACTGGCGT TGAAATGTTT CGCAAAC TGC TGGACGAAGG      500
CCGTGCCGGT GAGAACGTAG GTGTTCTGCT GCGTGGTATC AAACGTGAAG      550
AAATCGAACG TGGTCAGGTA CTGGCTAAGC CGGGCACCAT CAAGCCGCAC      600
ACCAAGTTCG AATCTGAAGT GTACATTCTG TCCAAAGATG AAGGCGGCCG      650
TCATACTCCG TTCTTCAAAG GCTACCGTCC GCAGTTCTAC TTCCGTACTA      700
CTGACGTGAC TGGCACCATC GAACTGCCGG AAGGCGTAGA GATGGTAATG      750
CCGGGCGACA ACATCAAAAT GGTGTTTACC CTGATCCACC CGATCGCGAT      800
GGACGACGGT                                     810

```

2) INFORMATION FOR SEQ ID NO: 1882

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 888 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: BM10711
 (C) ACCESSION NUMBER : AF015628
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882

```

ATGAATTTT ATTTAGAGGA GTTAACTTG TCTATTCCCG ATTCAGGTCC 50
ATACGGTATA ACTTCATCAG AAGACGGAAA GGTATGGTTC ACACAACATA 100
AGGCAAACAA AATCAGCAGT CTAGATCAGA GTGGTAGGAT AAAAGAATTC 150
5 GAAGTTCCTA CCCCTGATGC TAAAGTGATG TGTTTAATTG TATCTTCACT 200
TGGAGACATA TGGTTTACAG AGAATGGTGC AAATAAAATC GGAAAGCTCT 250
CAAAAAAAGG TGGCTTTACA GAATATCCAT TGCCACAGCC GGATTCTGGT 300
CCTTACGGAA TAACGGAAGG TCTAAATGGC GATATATGGT TTACCCAATT 350
GAATGGAGAT CGTATAGGAA AGTTGACAGC TGATGGGACT ATTTATGAAT 400
10 ATGATTTGCC AAATAAGGGA TCTTATCCTG CTTTTATTAC TTTAGGTTCG 450
GATAACGCAC TTTGGTTCAC GGAGAACCAA AATAATTCTA TTGGAAGGAT 500
TACAAATACA GGGAAATTAG AAGAATATCC TCTACCAACA AATGCAGCGG 550
CTCCAGTGGG TATCACTAGT GGTAACGATG GTGCACTCTG GTTTGTCTGAA 600
ATTATGGGCA ACAAATAGG TCGAATCACT ACAACTGGTG AGATTAGCGA 650
15 ATATGATATT CCAACTCCAA ACGCACGTCC ACACGCTATA ACCGCGGGGA 700
AAAATAGCGA AATATGGTTT ACTGAATGGG GGGCAAATCA AATCGGCAGA 750
ATTACAAACG ACAAACAAT TCAAGAATAT CAACTTCAAA CAGAAAATGC 800
GGAACCTCAT GGTATTACCT TTGGAAAAGA TGGATCCGTA TGGTTTGCAT 850
TAAATGTAA AATTGGGAAG CTGAATTGA ACGAATGA 888
20

```

2) INFORMATION FOR SEQ ID NO: 1883

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883

35 AGCCGCTTGA GCAAATTAAA CTA

23

2) INFORMATION FOR SEQ ID NO: 1884

40

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 23 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

```

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884

50

GTATCCCGCA GATAAATCAC CAC

23

2) INFORMATION FOR SEQ ID NO: 1885

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885

AGCGAAAAAC ACCTTGCCGA C 21

15

2) INFORMATION FOR SEQ ID NO: 1886

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886

GACGCCCCGCG CCACCACT 18

30

2) INFORMATION FOR SEQ ID NO: 1887

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887

GACGCCCCGCG ACACCACTA 19

45

2) INFORMATION FOR SEQ ID NO: 1888

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888

GACGCCCCGA ACACCACTA

19

10

2) INFORMATION FOR SEQ ID NO: 1889

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889

GTTCGCAACT GCAGCTGCTG

20

25

2) INFORMATION FOR SEQ ID NO: 1890

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890

40

TTCGCAACGG CAGCTGCTG

19

2) INFORMATION FOR SEQ ID NO: 1891

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891

CCGGAGCTGC CGAICGGG

18

5

2) INFORMATION FOR SEQ ID NO: 1892

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892

CGGAGCTGCC AARCGGGG

18

20

2) INFORMATION FOR SEQ ID NO: 1893

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893

35 GGAGCTGGCG ARCGGGGT

18

2) INFORMATION FOR SEQ ID NO: 1894

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894

50

GACCGGAGCT AGCGARCG

18

2) INFORMATION FOR SEQ ID NO: 1895

- (i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895

15 CGGAGCTAGC AARCGGGT 19

2) INFORMATION FOR SEQ ID NO: 1896

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896

30 GAAACGGAAC TGAATGAGGC G 21

2) INFORMATION FOR SEQ ID NO: 1897

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897

45 CATTACCATG GGCGATAACA G 21

50 2) INFORMATION FOR SEQ ID NO: 1898

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898

CCATTACCAT GAGCGATAAC AG

22

10

2) INFORMATION FOR SEQ ID NO: 1899

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: 15571
- (C) ACCESSION NUMBER: AF124984

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899

30	ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT	50
	GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA	100
	GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC	150
	CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC	200
	CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG	250
35	ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC	300
	TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA	350
	ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC	400
	TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG	450
	ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA	500
40	GGCGCTTCCC GGCGACGCC GCGACACCAC TACCCCGGCC AGCATGGCCG	550
	CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA	600
	CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT	650
	CCGCTCCGTG CTGCCGCGCG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG	700
	GCGAGCGGGG TGCGCGCGGG ATTGTGCGCC TGCTTGGCC GAATAACAAA	750
45	GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC	800
	CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT	850
	GGCAACGCTA A	861

50

2) INFORMATION FOR SEQ ID NO: 1900

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
- (B) STRAIN: SLK-47
- (C) ACCESSION NUMBER: Y11069

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900

```

15  CTGTTAGCCA CCCTGCCGCT GGC GG TACAC GCCAGCCCGC AGCCGCTTGA      50
    GCAAATTAAA CTAAGCGAAA GCCAGCTGTC GGGCCGCGTA GGCATGATAG      100
    AAATGGATCT GGCCAGCGGC CGCACGCTGA CCGCCTGGCG CGCCGATGAA      150
    CGCTTTCCCA TGATGAGCAC CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT      200
    GGCGCGGGTG GATGCCGGTG ACGAACAGCT GGAGCGAAAG ATCCACTATC      250
20  GCCAGCAGGA TCTGGTGGAC TACTCGCCGG TCAGCGAAAA ACACCTTGCC      300
    GACGGCATGA CGGTCGGCGA ACTCTGCGCC GCCGCCATTA CCATGAGCGA      350
    TAACAGCGCC GCCAATCTGC TACTGGCCAC CGTCGGCGGC CCCGCAGGAT      400
    TGACTGCCTT TTTGCGCCAG ATCGGCGACA ACGTCACCCG CCTTGACCGC      450
    TGGGAAACGG AACTGAATGA GGCGCTTCCC GGCGACGCCG GCGCCACCAC      500
25  TACCCCGGCC AGCATGGCCG CGACCCTGCG CAAGCTGCTG ACCAGCCAGC      550
    GTCTGAGCGC CCGTTCGCAA CGGCAGCTGC TGCAGTGGAT GGTGGACGAT      600
    CGGGTCGCCG GACCGTTGAT CCGCTCCGTG CTGCCGCGCG GCTGGTTTAT      650
    CGCCGATAAG ACCGGAGCTG GCGAGCGGGG TGCGCGCGGG ATTGTGCCCC      700
    TGCTTGGCCG GAATAACAAA GCAGAGCGCA TTGTGGTGAT TTATCTGCGG      750
30  GATACCCCGG CGAGCATGGC CGAGCGAAAT      780

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2) INFORMATION FOR SEQ ID NO: 1901

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: U92041

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901

```

50  ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT      50
    GGC GG TACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA      100
    GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC      150
    CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC      200

```

```

CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTGCGCGA 350
ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
5 TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGACTGCCTT TTTGCGCCAG 450
ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
GGCGCTTCCC GCGGACGCCC GCAACACCAC TACCCCGGCC AGCATGGCCG 550
CGACCTTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
10 CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG 700
GCGAGCGGGG TGCGCGCGGG ATTGTCGCCC TGCTTGGCCC GAATAACAAA 750
GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC 800
CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
GGCAACGCTA A 861
15

```

2) INFORMATION FOR SEQ ID NO: 1902

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 861 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Klebsiella pneumoniae*
 - 30 (B) STRAIN: 803
 - (C) ACCESSION NUMBER: AF164577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902

```

35 ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT 50
GGCGGTACAC GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CAAAGCGAAA 100
GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC 150
CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC 200
CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG 250
40 ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC 300
TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTGCGCGA 350
ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC 400
TGCTGGCCAC CGTCGGCGGC CCCGCAGGAT TGACTGCCTT TTTGCGCCAG 450
ATCGGCGACA ACGTCACCCG CCTTGACCGC TGGGAAACGG AACTGAATGA 500
45 GGCGCTTCCC GCGGACGCCC GCGACACCAC TACCCCGGCC AGCATGGCCG 550
CGACCTTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA 600
CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT 650
CCGCTCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTG 700
CCGAGCGGGG TGCGCGCGGG ATTGTCGCCC TGCTTGGCCC GAATAACAAA 750
50 GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACGCCGG CGAGCATGGC 800
CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT 850
GGCAACGCTA A 861

```

2) INFORMATION FOR SEQ ID NO: 1903

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: ATCC 700603
 (C) ACCESSION NUMBER: AF132290
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903

	ATGCGTTATT	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
	GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
20	GCCAGCTGTC	GGGCAGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150
	CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
	CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
	ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
	TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGGCATGA	CGGTCGGCGA	350
25	ACTCTGTGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
	TGCTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
	ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
	GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
	CGACCCTGCG	CAAGCTGCTG	ACCAGCCAGC	GTCTGAGCGC	CCGTTCGCAA	600
30	CGGCAGCTGC	TGCAGTGGAT	GGTGGACGAT	CGGGTCGCCG	GACCGTTGAT	650
	CCGCTCCGTG	CTGCCGGCGG	GCTGGTTTAT	CGCCGATAAG	ACCGGAGCTG	700
	CCAAACGGGG	TGCGCGCGGG	ATTGTCGCC	TGCTTGGCCC	GAATAACAAA	750
	GCAGAGCGGA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
	CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
35	GGCAACGCTA	ACCCGGCGGT	GGCCGCGCGC	GTTATCCGGC	TCGTAG	896

2) INFORMATION FOR SEQ ID NO: 1904

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: JC2926
 (C) ACCESSION NUMBER: AF148851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904

```

      ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT      50
      GCGGTACAC  GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA      100
5     GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC      150
      CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC      200
      CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG      250
      ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC      300
      TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA      350
10    ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTGC      400
      TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG      450
      ATCGGCGACA ACGTCACCCG CTTTGACCGC TGGGAAACGG AACTGAATGA      500
      GCGCTTCCC  GCGGACGCCC GCGACACCAC TACCCCGGCC AGCATGGCCG      550
      CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA      600
15    CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT      650
      CCGTCCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTA      700
      GCGAGCGGGG TGCGCGCGGG ATTGTCGCCC TGCTTGGCCC GAATAACAAA      750
      GCAGAGCGCA TTGTGGTGAT TTATCTGCGG GATACCCCGG CGAGCATGGC      800
      CGAGCGAAAT CAGCAAATCG CCGGGATCGG CGCGGCGCTG ATCGAGCACT      850
20    GGCAACGCTA A                                     861

```

2) INFORMATION FOR SEQ ID NO: 1905

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (C) ACCESSION NUMBER: AF096930

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905

```

40    ATGCGTTATA TTCGCCTGTG TATTATCTCC CTGTTAGCCA CCCTGCCGCT      50
      GCGGTACAC  GCCAGCCCGC AGCCGCTTGA GCAAATTAAA CTAAGCGAAA      100
      GCCAGCTGTC GGGCCGCGTA GGCATGATAG AAATGGATCT GGCCAGCGGC      150
      CGCACGCTGA CCGCCTGGCG CGCCGATGAA CGCTTTCCCA TGATGAGCAC      200
      CTTTAAAGTA GTGCTCTGCG GCGCAGTGCT GGCGCGGGTG GATGCCGGTG      250
45    ACGAACAGCT GGAGCGAAAG ATCCACTATC GCCAGCAGGA TCTGGTGGAC      300
      TACTCGCCGG TCAGCGAAAA ACACCTTGCC GACGGCATGA CGGTCGGCGA      350
      ACTCTGCGCC GCCGCCATTA CCATGAGCGA TAACAGCGCC GCCAATCTAC      400
      TACTGGCCAC CGTCGGCGGC CCCGCAGGAT TGA CTGCCTT TTTGCGCCAG      450
      ATCGGCGACA ACGTCACCCG CTTTGACCGC TGGGAAACGG AACTGAATGA      500
50    GCGCTTCCC  GCGGACGCCC GCGACACCAC TACCCCGGCC AGCATGGCCG      550
      CGACCCTGCG CAAGCTGCTG ACCAGCCAGC GTCTGAGCGC CCGTTCGCAA      600
      CGGCAGCTGC TGCAGTGGAT GGTGGACGAT CGGGTCGCCG GACCGTTGAT      650
      CCGTCCCGTG CTGCCGGCGG GCTGGTTTAT CGCCGATAAG ACCGGAGCTA      700

```

GCAAACGGGG	TGCGCGCGGG	ATTGTCGCCC	TGCTTGCCCC	GAATAACAAA	750
GCAGAGCGCA	TTGTGGTGAT	TTATCTGCGG	GATACGCCGG	CGAGCATGGC	800
CGAGCGAAAT	CAGCAAATCG	CCGGGATCGG	CGCGGCGCTG	ATCGAGCACT	850
GGCAACGCTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1906

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906

20 CCTTATTCCC TTTTTTGCGG

20

2) INFORMATION FOR SEQ ID NO: 1907

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907

35

CACCTATCTC AGCGATCTGT CT

22

40 2) INFORMATION FOR SEQ ID NO: 1908

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908

AACAGCGGTA AGATCCTTGA GAG

23

2) INFORMATION FOR SEQ ID NO: 1909

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909

ATGACTTGGT TAAGTACTCA CC

22

2) INFORMATION FOR SEQ ID NO: 1910

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910

ATGACTTGGT TGAGTACTCA CC

22

2) INFORMATION FOR SEQ ID NO: 1911

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911

CCATAACCAT GGGTGATAAC AC

22

2) INFORMATION FOR SEQ ID NO: 1912

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid

1000

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912

CCATAACCAT GAGTGATAAC AC

22

10

2) INFORMATION FOR SEQ ID NO: 1913

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913

CGCCTTGATC ATTGGGAACC

20

25

2) INFORMATION FOR SEQ ID NO: 1914

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914

CGCCTTGATC GTTGGGAACC

20

40

2) INFORMATION FOR SEQ ID NO: 1915

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915

CGCCTTGATA GTTGGGAACC

20

5

2) INFORMATION FOR SEQ ID NO: 1916

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916

CGTGGGTCTT GCGGTATCAT

20

20

2) INFORMATION FOR SEQ ID NO: 1917

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917

CGTGGGTCTG GCGGTATCAT

20

35

2) INFORMATION FOR SEQ ID NO: 1918

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918

GTGGGTCTCA CCGTATCATT G

21

50

2) INFORMATION FOR SEQ ID NO: 1919

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919

CGTGGGTCTC TCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1920

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920

CGTGGNTCTC GCGGTATCAT

20

2) INFORMATION FOR SEQ ID NO: 1921

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1921

CGTGGGTCTA GCGGTATCAT T

21

2) INFORMATION FOR SEQ ID NO: 1922

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid

1003

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922

GTTTTCCAAT GATTAGCACT TTTA

24

10

2) INFORMATION FOR SEQ ID NO: 1923

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923

GTTTTCCAAT GATAAGCACT TTTA

24

25

2) INFORMATION FOR SEQ ID NO: 1924

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924

40 GTTTTCCAAT GCTGAGCACT TTT

23

2) INFORMATION FOR SEQ ID NO: 1925

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925

CGTTTTCCAA TGATGAGCAC TTT

23

5

2) INFORMATION FOR SEQ ID NO: 1926

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926

GTTTTCCAAT GGTGAGCACT TTT

23

20

2) INFORMATION FOR SEQ ID NO: 1927

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 35 (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: MC9690-129
 (C) ACCESSION NUMBER: AF126482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1927

40	ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT	50
	TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG	100
	CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC	150
	AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT	200
	GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG	250
45	CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG	300
	GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT	350
	AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA	400
	ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG	450
	CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT	500
50	GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA	550
	TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT	600
	TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC	650
	ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG	700

GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

5

2) INFORMATION FOR SEQ ID NO: 1928

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: HB251
 (C) ACCESSION NUMBER: X57972

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928

25	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
30	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTAAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCATTGGG	AACCGGAGCT	500
35	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
40	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

45

2) INFORMATION FOR SEQ ID NO: 1929

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Klebsiella oxytoca*
(B) STRAIN: 26W
(C) ACCESSION NUMBER: U09188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929

```
10 ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
   GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
15 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
   ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
   CACAACATGG GGGATCATGT AACCCGCCTT GATAGTTGGG AACCGGAGCT      500
20 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
   TGGCAACAAC GTTGCGCAAA CTATTAAGTG GCGAACTACT TACTCTAGCT      600
   TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
   ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
   GAGCCGGTAA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
25 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
   TATGGATG                                     808
```

30 2) INFORMATION FOR SEQ ID NO: 1930

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AF190692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930

```
45 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
   TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
   CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC      150
   AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
50 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTTGACG      250
   CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
   GTTGAAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
   AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
```


	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
5	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
	GAGCCGGTGA	GCGTGGGTCT	GGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
10	AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 1931

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

25

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: BM2728
- (C) ACCESSION NUMBER: AF104442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1931

30

	ATGAGTATTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
	TTGCCTTCCT	GTTTTTGCTC	ACCCAGAAAC	GCTGGTGAAA	GTAAAAGATG	100
	CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
	AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
35	GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTTGACG	250
	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
	ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTTG	450
40	CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
	GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
	TGGCAACAAC	GTTGCGCAAA	CTATTAAGT	GCGAACTACT	TACTCTAGCT	600
	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
45	GAGCCGGTGA	GCGTGGGTCT	CTCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
	GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
	TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
	AGCATTGGTA	A				861

50

2) INFORMATION FOR SEQ ID NO: 1932

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 10 (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AF190695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932

15 ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 50
TTGCCTTCCT GTTTTGTCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 100
CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC 150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGCT 200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG 250
20 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG 300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT 350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA 400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG 450
CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT 500
25 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA 550
TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT 600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC 650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG 700
GAGCCGGTGA GCGTGGGTCT AGCGGTATCA TTGCAGCACT GGGGCCAGAT 750
30 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC 800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA 850
AGCATTGGTA A 861

35

2) INFORMATION FOR SEQ ID NO: 1933

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 861 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
(C) ACCESSION NUMBER: AF190693

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT 50
TTGCCTTCCT GTTTTGTCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG 100

```

CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAGCT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGGT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
5 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG      450
CACAACATGG GGGATCATGT AACCCGCCTT GATCGTCGGG AACC GGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
10 TGGCAACAAC GTTGCGCAAA CTATTAAGT GCGAACTACT TACTCTAGCT      600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
GAGCCGGTGA GCGTGGATCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
15 TATGGATGAA CGAGATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
AGCATTGGTA A      861

```

20 2) INFORMATION FOR SEQ ID NO: 1934

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - 25 (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934

GAACGCCAGC GCGAAATTCA AAAAG

25

35

2) INFORMATION FOR SEQ ID NO: 1935

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - 40 (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935

AGCTCGGCAT ACTTCGACAG G

21

50

2) INFORMATION FOR SEQ ID NO: 1936

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
5 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936
10 TACCACCCGC ACGGC 15

15 2) INFORMATION FOR SEQ ID NO: 1937

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937
CGGAGTCGCC GTCGATG 17

30 2) INFORMATION FOR SEQ ID NO: 1938

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938
CCGCGCACCA TTGCTTCGTA CACTGAGGAG TCTCCGCGCG G 41

45 2) INFORMATION FOR SEQ ID NO: 1939

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939

5

CGACCCGGAT GGTAGTATCG ATAATGATCC GCCAGCGGCC GGGTCG

46

10 2) INFORMATION FOR SEQ ID NO: 1940

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940

GTATCGTTGG TGACGTAAT

19

25

2) INFORMATION FOR SEQ ID NO: 1941

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941

GCAATGGTCC GTTTAAGT

18

40

2) INFORMATION FOR SEQ ID NO: 1942

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

45 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942

GACTGGAACA AAGCCTATAA AAAATCA

27

5 2) INFORMATION FOR SEQ ID NO: 1943

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- 10 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943

GCTGGTGGAC GGCCAG

16

20

2) INFORMATION FOR SEQ ID NO: 1944

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944

TTTCGCCGCC ATGCGTTAC

19

35

2) INFORMATION FOR SEQ ID NO: 1945

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945

CGGCGACTAC GCGGTAT

17

50

2) INFORMATION FOR SEQ ID NO: 1946

1013

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 bases
(B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946

CGGCGACTTC GCGGTAT

17

15

2) INFORMATION FOR SEQ ID NO: 1947

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
20 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947

CGGTATACGG CACCATCGT

19

30

2) INFORMATION FOR SEQ ID NO: 1948

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
35 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948

GCGGTATACA ACACCATCG

19

45

2) INFORMATION FOR SEQ ID NO: 1949

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949

CGGTATACGC CACCATCGT

19

10

2) INFORMATION FOR SEQ ID NO: 1950

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 15 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950

GGCGACATCG CCTGC

15

25

2) INFORMATION FOR SEQ ID NO: 1951

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 17 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951

GGCGACAGAG CCTGCTA

17

40

2) INFORMATION FOR SEQ ID NO: 1952

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952

1015

CCTGCTATGG AGCGATGGT

19

5

2) INFORMATION FOR SEQ ID NO: 1953

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953

CGCCTGCTAT AAAGCGATGG T

21

20

2) INFORMATION FOR SEQ ID NO: 1954

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 589 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883
 35 (C) ACCESSION NUMBER: AF052258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954

	ACACCGGTCA ACATTGAGGA AGAGCTTAAG AACTCTTATC TGGATTATGC	50
10	GATGTCGGTC ATTGTTGGCC GTGCGCTGCC GGATGTCCGA GATGGCCTGA	100
	AGCCCGGTACA CCGTCGCGTA CTTTACGCCA TGAACGTATT GGGCAATGAC	150
	TGGAACAAAG CCTATAAAAA ATCAGCCCGT GTCGTTGGTG ACGTAATCGG	200
	TAAATACCAC CCGCACGGCG ACTCCGCGGT ATACGACACC ATCGTGCCTA	250
	TGGCGCAGCC GTTCTCGCTG CGTTACATGC TGGTGGACGG CCAGGGTAAC	300
15	TTTGGTTCCA TCGACGGCGA CTCCGCCGCG GCGATGCGTT ATACCGAAAT	350
	TCGTCTGGCG AAAATCGCTC ATGAGCTGAT GGCCGATCTT GAAAAAGAGA	400
	CGGTCGATTT CGTCGACAA TATGACGGTA CGGAGCGTAT TCCGGACGTC	450
	ATGCCGACCA AAATTCCTAA CCTGCTGGTG AACGGCGCCT CCGGGATCGC	500
	CGTAGGGATG GCCACCAACA TACCGCCACA TAACCTGACG GAAGTGATTA	550
20	ACGGCTGTCT GCGGTATGTT GACGATGAAG ACATCAGCA	589

2) INFORMATION FOR SEQ ID NO: 1955

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955

CGCGCAACCA TTGCTTCGTA CACTGAGGAG TCTGCGCG

38

2) INFORMATION FOR SEQ ID NO: 1956

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956

	CGGTAAAACC	ACTTTAACTG	CTGCAATCAC	CAAAGTTT	TCTGAAGAAG	50
	GTGGTGCAGA	TTTCTTAGAT	TATTCATCTA	TTGATAAAGC	ACCAGAAGAG	100
35	AGAGCTAGAG	GTATTACCAT	TTCTACTGCT	CATGTTGAAT	ATGAAACTCC	150
	AAACAGACAT	TATTCACATG	TTGATTGTCC	AGGTCATCAA	GATTATATTA	200
	AGAACATGAT	TACTGGTGCA	GCTCAAATGG	ATGGTGCTAT	TATTGTTGTT	250
	GCAGCTACTG	ATGGTCAAAT	GCCACAAACT	AAGGAACATT	TATTATTAGC	300
	TAGACAAGTT	GGTGTTCAAC	ATTTAGTTGT	TTTTGTTAAC	AAGTGTGATA	350
40	CCGTTGATGA	TCCAGAAATG	TTRGAATTAG	TTGAAATGGA	AATGAGAGAA	400
	TTATTGACCG	AATATGGATT	YGATGGTGAT	AACACACCAG	TTATTATGGG	450
	TTCTGCATTA	ATGGCATTAG	AAGGTAAGAG	ACCAGAAGTT	GGTAAAGAAT	500
	CTATTGTAA	GTTAATGGAA	GCTGTTGATA	CTTGGATTCC	AACTCCACAA	550
	AGAGACTTAG	AAAAACCATT	CTTATTACCA	ATTGATGAAG	TTTTCTCTAT	600
45	TTCTGGTAGA	GGTACTGTTG	TTTCTGGTAC	TGTTGATAGA	GGTACATTAA	650
	AGAAGGGTGA	AGAAGTTGAA	ATTGTTGGTG	GTAAGAAGG	TGTTATTAAG	700
	ACTACTGTTA	CCGGTATTGA	AATGTATCAC	AAGGAATTAG	ATCAAGCACA	750
	AGCTGGTGAT	ACTCCAGGTA	TTTTGTAAAG	AGGTGTAAAG	AGAGATCAAA	800
	TTGCAAGAGG	TCAAATTCTT	GCAAAGCCAG	GWTCTGTAA	GGCATACAAG	850
50	AAGTTCCTTAT	CATCATTATA	CATTTTAAAC	AAGGAAGAAG	GTGGTAGACA	900
	TACTCCATTT	TCTGAAAATT	ACAGACCTCA	AATGTACATT	AGAAGTTCCA	950
	ATGTTAATGT	TACTTTGAAG	TTCCAGAAA	CTGAAGAAG		989

2) INFORMATION FOR SEQ ID NO: 1957

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 991 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida utilis*
 (B) STRAIN: ATCC 22023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957

GGTAAGACCA	CCCTTACTGC	CGCCATCACC	AAGTGCCTTG	CTGAGAAGGG	50
AGGTGCCTCG	TTCTTGGACT	ACAGTGCCAT	CGACAAGGCG	CCAGAGGAGA	100
GAGCAAGAGG	TATCACCATC	TCCACTGCGC	ACGTTGAGTA	TGAAACTGCC	150
AACAGACACT	ACTCGCACGT	TGACTGTCCA	GGTCACGCTG	ATTACATCAA	200
GAACATGATT	ACCGGTGCTG	CGCAGATGGA	CGGTGCTATC	ATTGTCGTTG	250
CAGCCACTGA	CGGTCAGATG	CCACAGACCA	GAGAACACTT	GTTGCTTGCC	300
AGACAAGTTG	GTGTCCAGCA	CATTGTTGTC	TTCGTCAACA	AGGTTGACAC	350
CATCGACGAC	CCTGAGATGC	TTGAGCTTGT	TGAAATGGAG	ATGAGAGAGT	400
TGCTTACTTC	GTATGGATTT	GACGGTGATA	ACACCCCAGT	TATCATGGGT	450
TCTGCTTTGT	GTGCTTTGGA	AGGCCGTGAG	CCAGAGATTG	GTGCTAAGGC	500
CATTGACAAG	TTGATGGAGG	CCATTGATGA	GTACATCCCA	ACTCCTCAGA	550
GAGACCTGGA	AAAGCCATTC	YTGATGGGTG	TTGAAGACGT	GTTCTCGATC	600
TCTGGTAGAG	GTACCGTTGT	CACRGGCCGT	GTTGAGCGTG	GTAACCTGAA	650
GAAAGGTGAT	GAAATTGAAC	TTGTTGGCTA	CAACAAGAAC	CCAATCAAGA	700
CCACCGTCAC	CGGTATCGAA	ATGTTCAAGA	AGGAGTTGGA	ATCTGCCATG	750
GCTGGTGACA	ACTGTGGTAT	CTTGTTGCGT	GGTATCAAGA	GAGATGACGT	800
CAAGAGAGGT	ATGGTTGCTG	CTAAGCCAGG	CTCCGTCTCT	GCACACACCA	850
AGTTCCTCGC	TTCCTTGTA	ATCCTGACRA	AGGAGGAAGG	TGGTCGTCAC	900
AGTGCCTTTG	CTGAGAACTA	CAGACCACAG	ATGTTTATCA	GAACCGGAGA	950
TGTCACCACC	ATCTTGACAT	GGCCAGAGGA	GCACGCTGAC	C	991

2) INFORMATION FOR SEQ ID NO: 1958

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 985 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958

	CGGTAAGACC	ACTTTGACCG	CCGCCATCAC	CAAGGTGTTG	AGCGCCAAAG	50
	GTGGTGCTTC	CTTCTTGGAC	TACGGGTCCA	TCGACAGAGC	CCCTGAGGAG	100
5	AGAGCCAGAG	GTATTACTAT	CTCGACTGCC	CACGTTGAGT	ACGAGACCGA	150
	TAAGAGACAC	TACGCCCACG	TTGATTGCCC	TGGTCACGCT	GATTACATCA	200
	AGAACATGAT	CACTGGTGCC	GCCCAAATGG	ACGGTGCCAT	TATTGTCGTT	250
	GCTGCTTCTG	ATGGCCAAAT	GCCGCAGACC	AGAGAGCACT	TGTTGCTTGC	300
	CAGACAGGTT	GGTGTGCAGA	ACTTGTTTGT	GTTTGTTAAC	AAGGTGGACA	350
10	CCATCGACGA	CCCCGAAATG	TTGGAGTTGG	TGGAGATGGA	AATGAGAGAA	400
	TTGTTGACCC	ACTACGGCTT	TGACGGTGAC	AACACCCCTG	TCATCATGGG	450
	TTCGGCGTTG	TGTGCCTTGG	AAGACAGGCA	GCCTGAGATT	GGCGAGCAAG	500
	CCATCATGAA	GTTGTTGGAC	GCTGTCGACG	AGTACATTCC	CACTCCTCAG	550
	AGAGACTTGG	AGCAACCATT	TTTGATGCCC	GTTGAGGATG	TTTTCTCCAT	600
15	CTCTGGCAGA	GGTACTGTTG	TCACCGGTCG	TGTTGAGAGA	GGCTCATTGA	650
	AGAAGGGTGA	GGAGATTGAG	ATTGTTGGCG	ACTTCCCCAA	GCCCTTCAAG	700
	ACTACCGTCA	CCGGCATTGA	GATGTTCAAG	AAGGAGTTGG	ATGCCGCGAT	750
	GGCGGGCGAC	AACGCCGGGA	TCTTGTTGAG	AGGTGTCAAG	AGAGACGAGG	800
	TCTCGAGAGG	TATGGTTTTG	GCCAAGCCCG	GTACTGTCAC	TTCGCACACC	850
20	AAGGTGTTGG	CGTCGCTTTA	CATCTTGACC	AAAGAGGAAG	GTGGCCGCCA	900
	CTCGCCCTTT	GGTGAGAACT	ACAAGCCACA	GTTATTTCATC	AGAACCTCCG	950
	ATGTCACTGG	TACTTTGAGG	TTCCCCGCCG	GTGAG		985

25

2) INFORMATION FOR SEQ ID NO: 1959

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|--------------------------|
| | (A) LENGTH: 973 bases |
| 30 | (B) TYPE: Nucleic acid |
| | (C) STRANDEDNESS: Double |
| | (D) TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

- | | |
|----|---|
| | (A) ORGANISM: <i>Candida catenulata</i> |
| | (B) STRAIN: ATCC 10565 |
| 40 | (C) ACCESSION NUMBER: |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959

	CGGTAAGACC	ACCTTGACTG	CCGCCATCAC	CAAGGTTCTC	TCCGAGAAGG	50
	GTGGTGCCGA	CTTCTTGGAC	TACGGTGCCA	TTGACAGAGC	CCCCGAGGAG	100
45	CGTGCCCGTG	GTATCACCAT	CTCCACTGCC	CACGTTGAGT	ACGAGACTGA	150
	CAACCGTCAC	TACGCCCACA	TTGACTGTCC	CGGTCACGCT	GATTACATCA	200
	AGAACATGAT	TACCGGTGCC	GCCCAGATGG	ACGGTGCCAT	TATTGTCCTT	250
	GCTGCTACTG	ACGGTGCCAT	GCCCCAGACC	CGCGAGCACT	TGCTTCTCGC	300
	CCGTCAGGTT	GGTATCCAGG	AATTGGTTGT	GTTTGTGAAC	AAGGTTGACA	350
50	CCATCGACGA	CCCCGAGATG	TTGGAGCTCG	TTGAGATGGA	GATCCGCGAG	400
	TTGTTGTCTG	AGTTCGGTTT	TGACGGTGAC	AACACCCCCG	TCATCATGGG	450
	TTCCGCTTTG	TGCGCTTTGG	AGGGCAAGCA	GCCCGAGATT	GGTGAGCAGG	500
	CTATCACCAA	GTTGATGGCC	GCCGTTGACG	AGCACATCCC	CACCCCCCAG	550

CGTGACTTGG AGCAGCCTTT CTTGATGCCT GTTGAGGGTG TTTTCTCTAT 600
 CTCTGGCCGT GGTACCGTGG TGACTGGTAA GGTGCCCCGT GGTGTCCCTCA 650
 AGAAGGGTGA GGAGATTGAG ATTGTTGGCA ACTTTGACAA GCCCTACAAG 700
 GTGACTGTGA CTGGTATTGA GATGTTCAAG AAGGAGTTGG ACCAGGCCAT 750
 5 GGCTGGTGAC AACGCCGGTA TCTTGTTGCG TGGTGTCAAG CGTGACGAGG 800
 TGTCTCGTGG TATGGTTTTG GCCAAGCCCCG GCACTGTTGT CTCGCACAAG 850
 AAGGTTTTGG CTTTCGCTTTA CATCTTGACC CAGGAGGAGG GTGGCCGTAA 900
 GACCGGCTTC GGCTCCAACCT ACAAGCCCCA GTTGTTCCTG CGCACTACCG 950
 ACGTCACTGG TACCCTCACC TTC 973
 10

2) INFORMATION FOR SEQ ID NO: 1960

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 985 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Candida krusei*
 25 (B) STRAIN: ATCC 28870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960

AAGACTACCT TGACTGCTGC AATCACCAAG GTCTTAGCTG ATCAAGGTGG 50
 30 TGCTGATTTT TTAGATTATG CATCTATTGA CAAGGCTCCT GAAGAAAGAG 100
 CAAGAGGTAT TACTATCTCT ACTGCTCACG TTGAGTATGA AACCCCAAAC 150
 AGACATTATT CTCATGTCGA TTGTCCTGGC CATCAAGATT ATATTAAGAA 200
 TATGATTACT GGTGCTGCAC AAATGGATGG TGCTATTATT GTTGTGCTG 250
 CTACTGATGG TCAAATGCCA CAACTAAGG AACATTTATT ATTAGCAAGA 300
 35 CAAGTTGGTG TTCAACATTT AGTTGTCTTT GTTAATAAAT GTGACACCAT 350
 TGATGACCCA GAAATGTTGG AATTAGTTGA AATGGAAATG AGAGAACTAT 400
 TGTCTGAATA TGGTTTTGAT GGTGATAACA CTCCAGTTAT TATGGGTTCT 450
 GCATTGATGG CTTTAGAAGA CAAGAGACCT GAAGTTGGTA AGGAATCTAT 500
 TTTAAAGTTA ATGGAAGCYG TTGACACATG GATTCCAACC CCAGAGAGAG 550
 40 ATTTAGAAAA ACCATTTTGG TTACCTATTG ATGAAGTTTT CTCAATCTCT 600
 GGTAGAGGTA CTGTCGTTTC TGGTACTGTC GAAAGAGGTA CTTTGAAGAA 650
 GGGTGAAGAA GTTGAAATTG TTGGTGGTAA GGATGGTTCT ATTAAACTA 700
 CTGTCACAGG TATTGAAATG TATCACAAGG AATTAGACCA AGCGCAAGCA 750
 GGTGATACTC CAGGTATTTT ATTAAGAGGT GTCAAGAGAG ACCAAATCAA 800
 45 GAGAGGTCAA ATTTTAGCAA AGCCAGATTC CGTTAAGGCA TACAAGAAGT 850
 TCTTGGCTTC CCTTTATATC TTAACCAAGG AAGAAGGTGG TAGACATACA 900
 CCATTCTCTG AAAACTACAG ACCACAAATG TACATCAGAA CTACCAATGT 950
 TAACGTTACT TTGAAGTTCC CAGACACTGA AGAAG 985

50

2) INFORMATION FOR SEQ ID NO: 1961

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961

10

GCTCAAGGCA GATGGCATTC CC

22

15 2) INFORMATION FOR SEQ ID NO: 1962

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962

GGACAAGGCG GTTGCGTTTG AT

22

30

2) INFORMATION FOR SEQ ID NO: 1963

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963

CATTCCTGTC TCGCTCGACA GT

22

45

2) INFORMATION FOR SEQ ID NO: 1964

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964

5

ATCTGCCTGC CCGTCTTGC

19

10 2) INFORMATION FOR SEQ ID NO: 1965

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
(B) TYPE: Nucleic acid
15 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmid pGS05
(C) ACCESSION NUMBER: M36657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965

25

ATGAATAAAT CGCTCATCAT TTTCGGCATC GTCAACATAA CCTCGGACAG 50
TTTCTCCGAT GGAGGCCGGT ATCTGGCGCC AGACGCAGCC ATTGCGCAGG 100
CGCGTAAGCT GATGGCCGAG GGGGCAGATG TGATCGACCT CCGTCCGGCA 150
TCCAGCAATC CCGACGCCGC GCCTGTTTCG TCCGACACAG AAATCGCGCG 200
30 TATCGCGCCG GTGCTGGACG CGCTCAAGGC AGATGGCATT CCCGTCTCGC 250
TCGACAGTTA TCAACCCGCG ACGCAAGCCT ATGCCTTGTC GCGTGGTGTG 300
GCCTATCTCA ATGATATTCG CGGTTTTCCA GACGCTGCGT TCTATCCGCA 350
ATTGGCGAAA TCATCTGCCA AACTCGTCGT TATGCATTCTG GTGCAAGACG 400
GGCAGGCAGA TCGGCGCGAG GCACCCGCTG GCGACATCAT GGATCACATT 450
35 GCGGCGTTCT TTGACGCGCG CATCGCGGCG CTGACGGGTG CCGGTATCAA 500
ACGCAACCGC CTTGTCCTTG ATCCCGGCAT GGGGTTTTTT CTGGGGGCTG 550
CTCCCGAAAC CTCGCTCTCG GTGCTGGCGC GGTTTCGATGA ATTGCGGCTG 600
CGCTTCGATT TGCCGGTGCT TCTGTCTGTT TCGCGCAAAT CCTTTCTGCG 650
CGCGCTCACA GGCCGTGGTC CGGGGGATGT CGGGGCCGCG AACTCGCTG 700
10 CAGAGCTTGC CGCCGCCGCA GGTGGAGCTG ACTTCATCCG CACACACGAG 750
CCGCGCCCTT TGCGCGACGG GCTGGCGGTA TTGGCGGCGC TGAAAGAAAC 800
CGCAAGAATT CGTTAA 816

15

2) INFORMATION FOR SEQ ID NO: 1966

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
50 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966

5 CATGCCAGTC TTGCCAACG 19

2) INFORMATION FOR SEQ ID NO: 1967

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967

20

CAGCAATAAG TAATCCAGCG ATG 23

25 2) INFORMATION FOR SEQ ID NO: 1968

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

30

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968

GGAGAGATTT CACCGCATAG 20

40

2) INFORMATION FOR SEQ ID NO: 1969

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969

AGCCAACCAT CATGCTATTC CA 22

2) INFORMATION FOR SEQ ID NO: 1970

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1206 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Transposon Tn10
 (C) ACCESSION NUMBER: J01830

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970

ATGAATAGTT CGACAAAGAT CGCATTGGTA ATTACGTTAC TCGATGCCAT 50
 GGGGATTGGC CTTATCATGC CAGTCTTGCC AACGTTATTA CGTGAATTTA 100
 TTGCTTCGGA AGATATCGCT AACCACCTTG GCGTATTGCT TGCACCTTTAT 150
 20 GCGTTAATGC AGGTTATCTT TGCTCCTTGG CTTGGAAAAA TGTCTGACCG 200
 ATTTGGTCGG CGCCAGTGC TGTGTGTGTC ATTAATAGGC GCATCGCTGG 250
 ATTACTTATT GCTGGCTTTT TCAAGTGC GC TTTGGATGCT GTATTTAGGC 300
 CGTTTGCTTT CAGGGATCAC AGGAGCTACT GGGGCTGTCT CGGCATCGGT 350
 CATTGCCGAT ACCACCTCAG CTTCTCAACG CGTGAAGTGG TTCGGTTGGT 400
 25 TAGGGGCAAG TTTTGGGCTT GGTTTAATAG CGGGGCCTAT TATTGGTGGT 450
 TTTGCAGGAG AGATTTCACC GCATAGTCCC TTTTTTATCG CTGCGTTGCT 500
 AAATATTGTC ACTTTCCTTG TGGTTATGTT TTGGTTCCGT GAAACCAAAA 550
 ATACACGTGA TAATACAGAT ACCGAAGTAG GGGTTGAGAC GCAATCGAAT 600
 TCGGTATACA TCACTTTATT TAAAACGATG CCCATTTTGT TGATTATTTA 650
 30 TTTTTCAGCG CAATTGATAG GCCAAATTCC CGCAACGGTG TGGGTGCTAT 700
 TTACCGAAAA TCGTTTTGGA TGGAAATAGCA TGATGGTTGG CTTTTCATTA 750
 GCGGGTCTTG GTCTTTTACA CTCAGTATTC CAAGCCTTTG TGGCAGGAAG 800
 AATAGCCACT AAATGGGGCG AAAAAACGGC AGTACTGCTC GAATTTATTG 850
 CAGATAGTAG TGCATTTGCC TTTTLAGCGT TTATATCTGA AGGTTGGTTA 900
 35 GATTTCCCTG TTTTAATTTT ATTGGCTGGT GGTGGGATCG CTTTACCTGC 950
 ATTACAGGGA GTGATGTCTA TCCAAACAAA GAGTCATGAG CAAGGTGCTT 1000
 TACAGGGATT ATTGGTGAGC CTTACCAATG CAACCGGTGT TATTGGCCCA 1050
 TTAAGTTTAA CTGTTATTTA TAATCATTCA CTACCAATTT GGGATGGCTG 1100
 GATTTGGATT ATTGGTTTAG CGTTTTACTG TATTATTATC CTGCTATCGA 1150
 40 TGACCTTCAT GTTAACCCCT CAAGCTCAGG GGAGTAAACA GGAGACAAGT 1200
 GCTTAG 1206

15 2) INFORMATION FOR SEQ ID NO: 1971

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971

5 CYGACTGYGC CATCCTYATC A

21

2) INFORMATION FOR SEQ ID NO: 1972

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972

20 MGICAGCTCA TYITTGCWKS C

21

2) INFORMATION FOR SEQ ID NO: 1973

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973

35 RACACCRGIY TTGGWITCCT T

21

2) INFORMATION FOR SEQ ID NO: 1974

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974

50 ACAAGGGITG GRMSAAGGAG AC

22

2) INFORMATION FOR SEQ ID NO: 1975

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975

TGRCCRGGGT GGTRAGGAC G

21

2) INFORMATION FOR SEQ ID NO: 1976

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976

GATGGAYTCY GTYAAITGGG A

21

2) INFORMATION FOR SEQ ID NO: 1977

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977

GATGGAYTCY GTYAARTGGG A

21

2) INFORMATION FOR SEQ ID NO: 1978

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978

CATCITGYAA TGGYAATCTY AAT

23

10

2) INFORMATION FOR SEQ ID NO: 1979

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979

CATCYTGYAA TGGYAASCTY AAT

23

25

2) INFORMATION FOR SEQ ID NO: 1980

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980

40 TCRATGGCIT CIAIRAGRGY YT

22

2) INFORMATION FOR SEQ ID NO: 1981

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981

TGGACACCIS CAAGIGGKCY G

21

5

2) INFORMATION FOR SEQ ID NO: 1982

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982

TGGACACYIS CAAGIGGKCY G

21

20

2) INFORMATION FOR SEQ ID NO: 1983

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983

35 CYGAYTGCGC YATICTCATC A

21

2) INFORMATION FOR SEQ ID NO: 1984

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984

50

CYGAYTGYGC YATYCTSATC A

21

2) INFORMATION FOR SEQ ID NO: 1985

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: M1-106
 (C) ACCESSION NUMBER: U81804

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
20	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTCTT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCTA	250
	AGTACCAGGT	TACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTGC	350
25	CACCGGTATC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCTGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGT	TACAACCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
30	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCCGGTGTT	TCCAAGGGTA	AGACCCTTCT	CGAGGCCATC	GACGCCAGTA	700
	GGCCCCCTAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTCGCCCCC	ACCAACGTCA	850
35	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTCCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
40	TTGCAAGTTC	TCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTT	CCCAGAAGCC	TCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATTAA	GAGTGTGGAG	AAGTCCGATG	GGAAGAGCGG	CAAGGTTACC	1350
45	AAGGCCGCCG	AGAAGGCTGC	TAAGAAGAAG	TAA		1383

2) INFORMATION FOR SEQ ID NO: 1986

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus neoformans*

(B) STRAIN: B3501

(C) ACCESSION NUMBER: U81803

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986

	ATGGGTAAGG	ACAAGCTGCA	CGTCAACGTC	GTTGTTATCG	GTCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
15	TCGACAAGCG	AACCATTGAG	AAGTTCGAGA	AGGAGGCTCA	AGAGCTCGGA	150
	AAGTCTTCTT	TCAAGTACGC	TTGGGTTCCT	GACAAGCTTA	AGGCCGAGCG	200
	AGAGCGAGGT	ATCACCATCG	ACATTGCTCT	TTGGAAGTTC	GAGACCCCCA	250
	GGTACCAGGT	CACCGTCATT	GACGCCCCCG	GTCACCGAGA	CTTCATCAAG	300
	AACATGATCA	CCGGTACCTC	CCAGGCTGAC	TGTGCCATCC	TCATCATTCG	350
20	CACCGGTATC	GGTGAGTTCG	AGGCCGGTAT	CTCCAAGGAC	GGTCAGACCC	400
	GAGAGCACGC	CCTCCTCGCC	TTCACCCTCG	GTGTCAGGCA	GCTCATTGTT	450
	GCTTGCAACA	AGATGGACAC	CTGCAAGTGG	TCCGAGGACC	GATTCAACGA	500
	AATCGTCAAG	GAGACCAACG	GTTTCATCAA	GAAGGTTGGC	TACAACCCCCA	550
	AGGCTGTCCC	CTTCGTCCCC	ATCTCTGGTT	GGCACGGTGA	CAACATGTTG	600
25	GAGGAGACCA	CCAACATGCC	CTGGTACAAG	GGATGGACCA	AGGAGACCAA	650
	GTCTGGTGTT	TCCAGGGGTA	AGACCCTTCT	CGAGGCCATC	AGCGCCAGTA	700
	GGCCCCATAC	CCGACCCACC	GACAAGCCCC	TCCGTCTCCC	TCTCCAGGAC	750
	GTCTACAAGA	TCGGTGGTAT	CGGCACAGTC	CCTGTCGGCC	GAGTCGAGAC	800
	CGGTGTCATC	AAGGCCGGTA	TGGTCGTCAA	GTTCGCCCCC	ACCAACGTCA	850
30	CCACTGAAGT	CAAGTCCGTT	GAGATGCACC	ACGAGCAGAT	CCCCGAGGGT	900
	CTTCCCGGAG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCATCAAGGA	950
	CATCCGACGA	GGTAACGTCT	GTGGTGACTC	CAAGAACGAC	CCCCCTATGG	1000
	AGGCTGCTTC	TTTCAACGCC	CAGGTTATCG	TCCTTAACCA	CCCTGGTCAG	1050
	ATCGGTGCCG	GTTACACCCC	CGTTCTCGAC	TGTCACACTG	CCCACATTGC	1100
35	CTGCAAGTTT	GCTGAGTTGA	TCGAGAAGAT	TGACCGACGA	ACCGGTAAGG	1150
	TCATGGAGGC	CGCCCCCAAG	TTCGTCAAGT	CTGGTGACGC	CGCCATTGTC	1200
	AAGCTTGTTG	CCCAGAAGCC	CCTCTGTGTT	GAGACCTACG	CCGACTACCC	1250
	CCCTCTTGGT	CGATTGCGCG	TCCGAGACAT	GCGACAGACC	GTTGCCGTTG	1300
	GTGTTATCAA	GAGCGTGGAC	AAGACCGAGA	AGGGTGGCAA	GGTCACCAAG	1350
40	GCTGCTGAGA	AGGCTGCCAA	GAAGAAGTAA			1380

2) INFORMATION FOR SEQ ID NO: 1987

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

50

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: X01638

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987

```

ATGGGTAAAG AGAAGTCTCA CATTACGTT GTCGTTATCG GTCATGTCGA      50
TTCTGGTAAG TCTACCACTA CCGGTCATTT GATTTACAAG TGTGGTGGTA      100
TTGACAAGAG AACCATCGAA AAGTTCGAAA AGGAAGCCGC TGAATTAGGT      150
10 AAGGGTTCTT TCAAGTACGC TTGGGTTTTG GACAAGTTAA AGGCTGAAAG      200
AGAAAGAGGT ATCACTATCG ATATTGCTTT GTGGAAGTTC GAAACTCCAA      250
AGTACCAAGT TACCGTTATT GATGCTCCAG GTCACAGAGA TTTCATCAAG      300
AACATGATTA CTGGTACTTC TCAAGCTGAC TGTGCTATCT TGATTATTGC      350
TGGTGGTGTC GGTGAATTTC AAGCCGGTAT CTCTAAGGAT GGTCAAACCA      400
15 GAGAACACGC TTTGTTGGCT TTCACCTTGG GTGTTAGACA ATTGATTGTT      450
GCTGTCAACA AGATGGACTC CGTCAAATGG GACGAATCCA GATTCCAAGA      500
AATTGTCAAG GAAACCTCCA ACTTTATCAA GAAGGTTGGT TACAACCCAA      550
AGACTGTTCC ATTCGTCCCA ATCTCTGGTT GGAACGGTGA CAACATGATT      600
GAAGCTACCA CCAACGCTCC ATGGTACAAG GGTGGGGAAA AGGAAACCAA      650
20 GGCCGGTGTC GTCAAGGGTA AGACTTTGTT GGAAGCCATT GACGCCATTG      700
AACCAACCATC TAGACCAACT GACAAGCCAT TGAGATTGCC ATTGCAAGAT      750
GTTTACAAGA TCGGTGGTAT TGGTACTGTG CCAGTCGGTA GAGTTGAAAC      800
CGGTGTCATC AAGCCAGGTA TGGTTGTTAC TTTCGCCCCA GCTGGTGTTA      850
CCACTGAAGT CAAGTCCGTT GAAATGCATC ACGAACAATT GGAACAAGGT      900
25 GTTCCAGGTG ACAACGTTGG TTTCACGTC AAGAACGTTT CCGTTAAGGA      950
AATCAGAAGA GGTAACGTCT GTGGTGACGC TAAGAACGAT CCACCAAAGG      1000
GTTGCGCTTC TTTCACGCT ACCGTCATTG TTTTGAACCA TCCAGGTCAA      1050
ATCTCTGCTG GTTACTCTCC AGTTTTGGAT TGTCACACTG CTCACATTGC      1100
TTGTAGATTC GACGAATTGT TGGAAAAGAA CGACAGAAGA TCTGGTAAGA      1150
30 AGTTGGAAGA CCATCCAAAG TTCTTGAAGT CCGGTGACGC TGCTTTGGTC      1200
AAGTTCGTTT CATCTAAGCC AATGTGTGTT GAAGCTTTCA GTGAATACCC      1250
ACCATTAGGT AGATTCGCTG TCAGAGACAT GAGACAAACT GTCGCTGTCG      1300
GTGTTATCAA GTCTGTTGAC AAGACTGAAA AGGCCGCTAA GGTTACCAAG      1350
GCTGCTCAAA AGGCTGCTAA GAAATAA      1377
35

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2) INFORMATION FOR SEQ ID NO: 1988

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 50 (C) ACCESSION NUMBER: M10992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988

	ATGGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTG GTA	100
	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
5	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTACACAGAG	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
	TGGTGGTGTC	GGTGAATTTC	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTTGGCT	TTACCTTGG	GTGTTAGACA	ATTGATTGTT	450
10	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTCTGTCCT	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
15	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
	GTTTACAAGA	TTGGTGGTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
20	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTTGGAT	TGTCACACTG	CTCACATTGC	1100
	TTGTAGATTG	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
25	AAGTTCGTTT	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCT	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

30

2) INFORMATION FOR SEQ ID NO: 1989

- (i) SEQUENCE CHARACTERISTICS:
- 35 (A) LENGTH: 1377 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
(B) STRAIN: ATCC 10895
45 (C) ACCESSION NUMBER: X73978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
50	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTG GTA	100
	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250

	AGTACCACGT	CACTGTCATT	GACGCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
5	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550
	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
10	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
15	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
20	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
	ACCATTGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCTG	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCCAA	AGGCTGGTAA	GAAATAG			1377

25

2) INFORMATION FOR SEQ ID NO: 1990

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 1377 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 35 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eremothecium gossypii*
(C) ACCESSION NUMBER: A29820
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990

	ATGGGTAAGG	AAAAGACTCA	CGTTAACGTT	GTCGTCATCG	GTCACGTCGA	50
	CTCTGGTAAG	TCTACTACCA	CCGGTCACTT	GATCTACAAG	TGTGGTGGTA	100
45	TTGACAAGAG	AACCATCGAG	AAGTTCGAGA	AGGAGGCTGC	CGAGTTGGGT	150
	AAGGGTTCTT	TCAAGTACGC	CTGGGTTTTG	GACAAATTGA	AGGCTGAGAG	200
	AGAGAGAGGT	ATCACCATCG	ACATTGCGTT	GTGGAAGTTC	GAGACTCCAA	250
	AGTACCACGT	CACTGTCATT	GACCCCCCAG	GCCACAGAGA	CTTCATCAAG	300
	AACATGATTA	CCGGTACTTC	TCAAGCTGAC	TGTGCCATCT	TGATCATTGC	350
50	TGGTGGTGTC	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAC	GGTCAGACCA	400
	GAGAGCACGC	TTTGTGGCT	TACACCTTGG	GTGTCAAGCA	GTTGATCGTT	450
	GCCATCAACA	AGATGGACTC	CGTCAAGTGG	GACGAGTCCA	GATACCAGGA	500
	GATTGTCAAG	GAGACCTCCA	ACTTCATCAA	GAAGGTCGGT	TACAACCCTA	550

	AGACTGTTCC	ATTCGTTCCA	ATCTCCGGCT	GGAACGGTGA	CAACATGATT	600
	GAGGCCACCA	CCAACGCCCC	ATGGTACAAG	GGCTGGGAGA	AGGAGACCAA	650
	GGCTGGTGCC	GTCAAGGGTA	AGACCTTGTT	GGAGGCCATT	GACGCCATTG	700
	AGCCACCTGT	CAGACCAACT	GACAAGGCAT	TGAGATTGCC	ATTGCAGGAT	750
5	GTCTACAAGA	TCGGTGGTAT	TGGTACGGTT	CCAGTCGGCA	GAGTCGAGAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	CTTCGCCCCA	TCCGGTGTCA	850
	CCACTGAAGT	CAAGTCCGTC	GAGATGCACC	ACGAGCAATT	GGAGGAGGGT	900
	GTCCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	950
	GATCAGAAGA	GGTAACGTTT	GCGGTGACTC	CAAGAACGAC	CCACCAAAGG	1000
10	CTGCTGAGTC	CTTCAACGCT	ACCGTCATTG	TCTTGAACCA	CCCAGGTCAA	1050
	ATCTCTGCCG	GTTACTCTCC	AGTCTTGAC	TGTCACACTG	CCCACATTGC	1100
	TTGTAAGTTC	GACGAGTTGT	TGGAGAAGAA	CGACAGAAGA	ACCGGTAAGA	1150
	AGTTGGAAGA	CTCTCCAAAG	TTCCTAAAGG	CCGGTGACGC	TGCCATGGTC	1200
	AAGTTTGTCC	CATCCAAGCC	AATGTGTGTT	GAGGCTTTCA	CCGACTACCC	1250
15	ACCATGGGGT	AGATTGCTG	TCAGAGACAT	GAGACAGACC	GTTGCTGTCC	1300
	GTGTCATCAA	GTCTGTTGTC	AAGTCCGACA	AGGCTGGTAA	GGTCACCAAG	1350
	GCCGCCCAAA	AGGCTGGTAA	GAAATAG			1377

20

2) INFORMATION FOR SEQ ID NO: 1991

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus oryzae*
 (B) STRAIN: KBN616
 (C) ACCESSION NUMBER: AB007770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1991

	TGGGGTAAGT	TTATCAACCC	GTCGAGTTGT	GTTGCATCTC	AGATCATGGC	50
	TGACAAGTAC	TTTCTCCTT	ACAGTAAGGA	AGACAAGCAG	CACATCAACA	100
40	TCGTCGTTAT	CGGCCACGTC	GATTCCGGCA	AGTCCACCAC	CACTGGTCAC	150
	TTGATCTACA	AGTGTGGTGG	TATCGACCAG	CGTACCATCG	AGAAGTTCGA	200
	GAAGGAAGCC	GCTGAGCTCG	GTAAGGGTTC	CTTCAAGTAC	GCCTGGGGTTC	250
	TTGACAAGCT	CAAGTCCGAG	CGTGAGCGTG	GTATCACCAT	CGATATCGCC	300
	CTCTGGAAGT	TCCAGACCTC	CAAGTATGAG	GTCACCGTCA	TTGGTAAGCA	350
45	TTTGAGTTCC	AACCTACGTT	GCCCAACATT	TACAGTCATC	TAACAAAGTT	400
	CAATAGATGC	CCCCGGTCAC	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	450
	ACTTCCCAGG	CTGACTGCGC	TATCCTCATC	ATTGCCTCCG	GTAAGTGGTGA	500
	ATTCGAGGCT	GGTATCTCCA	AGGATGGTCA	GACCCGTGAG	CACGCTCTGC	550
	TCGCTTTTAC	CCTCGGTGTC	CGTCAGCTCA	TCGTTGCCCT	CAACAAGATG	600
50	GACACCTGCA	AGTGGTCTCA	GGATCGTTAC	AACGAAATCG	TTAAGGAGAC	650
	TTCCAACCTT	ATCAAGAAGG	TCGGATACAA	CCCCAAGAGC	GTTCTTTTCG	700
	TCCCCATCTC	CGGTTTCAAC	GGTGACAACA	TGATTGAGGC	CTCCACCAAC	750
	TGCCCTGGT	ACAAGGGCTG	GGAGAAGGAG	ACCAAGGCTG	GCAAGTCCAC	800

	CGGTAAGACC	CTTCTCGAGG	CCATCGATGC	CATCGAGCCC	CCCGTCCGTC	850
	CCACCGACAA	GCCTCTCCGT	CTTCCCCTCC	AGGATGTCTA	CAAGATCTCT	900
	GGTATCGGTA	CTGTGCCCCG	CGGTCGTGTC	GAGACTGGTG	TCATCAAGCC	950
	TGGTATGGTC	GTTACTTTTCG	CTCCTGCCAA	CGTGACCACT	GAAGTCAAGT	1000
5	CCGTTGAAAT	GCACCACCAG	CAGCTCCAGG	CCGGTAACCC	CGGTGACAAC	1050
	GTTGGTTTCA	ACGTCAAGAA	CGTCTCCGTC	AAGGAAGTCC	GCCGTGGTAA	1100
	CGTTGCCGGT	GACTCCAAGA	ACGACCCCCC	TGCTGGCTGC	GATTCCCTCA	1150
	ACGCCCAGGT	CATCGTCCTT	AACCACCCCC	GTCAGGTCGG	CAACGGTTAC	1200
	GCTCCCGTCC	TGGACTGCCA	CACCGCTCAC	ATTGCTTGCA	AGTTCGCTGA	1250
10	GCTCCTTGAG	AAGATTGACC	GCCGTACCGG	TAAATCTGTT	GAGGACAAGC	1300
	CCAAGTTCAT	CAAGTCTGGT	GATGCTGCCA	TCGTCAAGAT	GATTCCCTCC	1350
	AAGCCCATGT	GTGTGGAGTC	TTTCACTGAC	TTCCCCCCTC	TTGGTCGTTT	1400
	CGCTGTCCGT	GACGTAAGTT	TTTCCCTCTT	GACTATCTTC	ACAATTTTTT	1450
	ACATATTTTC	ACGCCTCGTC	CCACTCTTTT	TCCTCCCTTC	CTCTTTGGTT	1500
15	CCCCTTTTTG	CCTGCAAGTT	CTCTATAGCT	AACATGATGT	CTAGATGCGT	1550
	CAAAGTGTG	CCGTCGGAGT	TATCAAGTCG	GTTGAGAAGA	AACTGGCGG	1600
	TTCTGGCAAG	GTCACCAAGG	CCGCCAGAA	GGCTGGCAAG	AAATAA	1646

20

2) INFORMATION FOR SEQ ID NO: 1992

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: R106
- (C) ACCESSION NUMBER: U19723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992

	ATGGGTAAGG	AAAAGTCCCA	CATCAACGTC	GTCGTTATCG	GCCACGTCGA	50
	CTCCGGTAAG	TCGACCACCA	CCGGTCACTT	GATCTACAAG	TGCGGTGGTA	100
40	TCGACAAGCG	TACCATCGAG	AAGTTCGAGA	AGGAAGCCGC	CGAACTCGGC	150
	AAGGGTTCCT	TCAAGTACGC	CTGGGTCCCTC	GACAAGCTGA	AGTCTGAGCG	200
	TGAGCGTGGT	ATCACTATCG	ATATCGCTCT	GTGGAAGTTC	GAGACCCCCA	250
	AGTACATGGT	CACCGTCATC	GATGCCCCCG	GTCACCGTGA	TTTCATCAAG	300
	AACATGATCA	CTGGTACCTC	CCAGGCTGAC	TGCGCCATTC	TCATCATTGC	350
45	CGCCGGTACT	GGTGAGTTCG	AGGCTGGTAT	CTCCAAGGAT	GGCCAGACTC	400
	GTGAGCACGC	CCTTCTCGCC	TACACCCCTG	GTGTCAAGCA	GCTCATCGTC	450
	GCTATCAACA	AGATGGACAC	CACCAAGTGG	TCTGAGGCCC	GTTACCAGGA	500
	GATCATCAAG	GAGACCTCCG	GTTTCATCAA	GAAGGTCGGC	TACAACCCCA	550
	AGCACGTTCC	CTTTGTCCCC	ATCTCGGGTT	TCAACGGTGA	CAACATGATT	600
50	GAGGTTTCTT	CCAAGTGCCC	CTGGTACAAG	GGTTGGGAGA	AGGAGACCAA	650
	GGCCAAGGCC	ACTGGTAAGA	CTCTCCTCGA	GGCCATTGAC	GCCATCGACC	700
	CTCCTTCGCG	CCCCACCGAC	AAGCCCCCTC	GTCTTCCCCT	CCAGGATGTC	750
	TACAAGATCG	GTGGTATTGG	CACGGTGCCC	GTCGGCCGTG	TCGAGACCGG	800

TACCATCAAG GGTGGTATGG TCGTCACCTT CGCCCCCGCT GGTGTCACCA 850
 CTGAGGTCAA GTCCGTCGAG ATGCACCACG AGCAGCTCTC CGAGGGTCTC 900
 CCCGGTGACA ACGTCGGCTT CAACGTCAAAG AACGTCTCCG TCAAGGAGAT 950
 CCGTCGTGGT AACGTTGCCG GTGACTCCAA GAACGACCCC CCCAAGGGTT 1000
 5 GCGACTCCTT CAACGCCCAG GTCATCGTCC TCAACCACCC CGGTCAGGTC 1050
 GGTGCTGGTT ACGCACCCGT CCTCGATTGC CACACTGCC ACATCGCCTG 1100
 CAAGTTCTCC GAGCTTGTTG AGAAGATTGA CCGCCGTACC GGCAAGTCCG 1150
 TTGAGGCCGC CCCCAAGTTC ATCAAGTCTG GTGACGCCG CATCGTCAAG 1200
 ATGGTTCCCT CCAAGCCTAT GTGTGTTGAG GCCTTCACTG ACTACCCTCC 1250
 10 TCTCGGTCGT TTCGCCGTCC GTGACATGAG ACAGACCGTC GCTGTCGGTG 1300
 TCATCAAGTC CGTCGCCAAG TCCGACAAGC AGGGTGCCGG TAAGGTACC 1350
 AAGGCCGCTG TCAAGGCTGG CAAGAAGTAA 1380

15

2) INFORMATION FOR SEQ ID NO: 1993

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1383 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA
 25
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: 186AS
 (C) ACCESSION NUMBER: U14100
 30
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993

ATGGGTAAGG AAGACAAGAC TCACATTAAC CTCGTCGTCA TCGGCCACGT 50
 CGATTCGGGC AAATCTACCA CCACTGGTCA TTTGATCTAC AAATGCGGTG 100
 35 GTATTGACAG CCGTACCATT GAGAAGTTCG AAAAGGAAGC CGAAGAGTTG 150
 GGCAAGAAAT CTTCAAATA TGCGTGGGTC CTTGACAAAC TGAAGTCTGA 200
 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAA TTCGAGACTC 250
 CGAAGTACAG TGTCACTGTC ATTGATGCTC CCGGCCATCG TGACTTCATC 300
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GACTGCGCTA TCCTCATCAT 350
 40 TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CTCGTGAGCA CGCTCTGCTT GCTTTACCCC TTGGTGTGAG GCAACTCATC 450
 GTTGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGT CCCGTTTCAA 500
 CGAAATCATC AAGGAGGTTT CCAACTTCAT CAAGAAGGTC GGATATAACC 550
 CCAAGGCTGT TCCCTTCGTG CCAATCTCTG GTTTCGAGGG TGACAACATG 600
 45 ATTGAACCTT CCCCCAACTG CACATGGTAC AAGGGCTGGA ACAAGGAGAC 650
 TGCCTCTGGC AAGTCTTCTG GTAAAACCTT TCTCGATGCC ATTGACGCCA 700
 TTGAACCCCC AACCCGTCCT ACCGATAAGC CCCTCCGTCT TCCCTCCAG 750
 GATGTGTACA AAATCTCTGG TATTGGCACT GTTCCCGTCG GACGTGTTGA 800
 GACTGGTGTC ATCAAGCCCG GTATGGTCGT GACTTTCGCT CCCTCCAACG 850
 50 TCACCACTGA AGTCAAGTCC GTCGAAATGC ACCACCAACA ACTCCAGGCT 900
 GGTTACCCTG GCGACAACGT CGGCTTCAAC GTCAAGAACG TTTCAGTCAA 950
 GGAAGTCCGC CGTGGCAACG TTGCTGGCGA CTCCAAAAAT GATCCCCCTA 1000
 AGGGCTGCGA ATCCTTCAAT GCCCAGGTCA TCGTCCTTAA CCACCCCGGC 1050

CAGGTTGGCG CTGGTTATGC CCCAGTCCTC GACTGCCACA CTGCCCACAT 1100
 TGCTTGCAAG TTCTCTGAGC TTATTGAGAA GATCGACCGC CGTACCGGAA 1150
 AGTCTGTTGA GAACAACCCC AAGTTCATCA AGTCTGGTGA TGCTGCTATC 1200
 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTGGAGCCCT TCACTGACTA 1250
 5 TCCCCCTCTT GGACGTTTCG CTGTCCGTGA CATGAGACAA ACCGTCGCTG 1300
 TCGGTGTCAT CAAGTCCGTC ATCAAGTCTG ACAAGACTGC TGGCAAGGTC 1350
 ACCAAGGCCG CGCAGAAGGC CACCAAGAAA TAA 1383

10

2) INFORMATION FOR SEQ ID NO: 1994

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 15 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neurospora crassa*
 (C) ACCESSION NUMBER: D45837

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994

ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCTACCA CTACCGGTCA CTTGATCTAC AAGTGCGGTG 100
 GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC 150
 30 GGTAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA 200
 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC 250
 CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGTCATCG TGATTTTCATC 300
 AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TCCTCATCAT 350
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 35 CCCGTGAGCA CGCCCTGCTC GCCTACACCC TCGGTGTCAA GCAGCTCATT 450
 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGA CTCGTTTCGA 500
 GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTT GGCTACAACC 550
 CCGCTGGTGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG 600
 CTTGAGCCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC 650
 10 CAAGGCCGGC AAGGCCACTG GCAAGACCTT CCTCGAGGCC ATCGACGCCA 700
 TTGAGCCCCC CAAGCGTCCT ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
 GATGTCTACA AGATCGGTGG TATCGGCACA GTGCCCCTCG GCCGTATCGA 800
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CTTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG 900
 15 GGTGTCCCGG GTGACAACGT CGGCTTCAAC GTGAAGAAGC TTTCCGTCAA 950
 GGATATCCGC CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG 1000
 CTGGCGCCGC CTCTTTCACC GCCCAGGTCA TCGTTCTCAA CCACCCCGGT 1050
 CAGGTCGGTG CCCGCTACGC CCCCGTCCTC GACTGCCACA CTGCCCACAT 1100
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACTGGTA 1150
 50 AGGCTGTTGA GGCCTCCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250
 CCCTCCCCTC GGCCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCCG 1300
 TCGGTGTCAT CAAGGCCGTC GACAAGTCCA CCGTGCCGC TGGCAAGGTC 1350

ACCAAGTCCG CTGCCAAGGC CGCCAAGAAG TAA

1383

5 2) INFORMATION FOR SEQ ID NO: 1995

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospira anserina*
 (C) ACCESSION NUMBER: X74799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995

20 ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT 50
 CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG 100
 GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC 150
 GGCAAGGGCT CTTTCAAGTA TGCTGGGTT CTTGACAAGT TGAAGGCCGA 200
 25 GCGTGAGCGT GGTATCACCA TCGATATTGC CCTCTGGAAG TTCGAGACCC 250
 CCAAGTACTA TGTACCGTC ATTGATGCC CCGGCCATCG TGATTTTCATC 300
 AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT 350
 TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CCEGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC 450
 30 GTCGCCATCA ACAAGATGGA CACCACCAAG TGGTCCGAGG CCCGCTTCAA 500
 CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC 550
 CCAAGACTGT TGCTTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG 600
 CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGGT 650
 CAAGGGTGGC AAGGCCACCG GCAAGACCTT CTTGAGGCC ATCGACTCCA 700
 35 TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTCCAG 750
 GATGTCTACA AGATCGGCGG TATCGGCACA GTCCCTGTCT GCGGTATCGA 800
 GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CTTTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
 GGTGTTCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA 950
 40 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCCA 1000
 TGGGCGCCGC CTCTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC 1050
 CAGGTCGGTG CTGGTTACGC CCCCCTCCTC GATTGCCACA CTGCCCACAT 1100
 CGCCTGCAAG TTCTCTGAGC TCCTGCAGAA GATCGACCGC CGTACTGGTA 1150
 AGGCCGTTGA GGAGAGCCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC 1200
 45 GTCAAGATGG TTCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACTGAGTA 1250
 CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTGCTG 1300
 TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTT 1350
 ACCAAGTCCG CTGCCAAGGC TGGCAAGAAA TAA 1383

50

2) INFORMATION FOR SEQ ID NO: 1996

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Podospora curvicolla*
 (B) STRAIN: VLV
 (C) ACCESSION NUMBER: X96614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996

```

15  ATGGGCAAGG AGGACAAGAC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
    CGATTCCGGC AAGTCGACCA CCACTGGTCA CTTGATCTAC AAGTGCGGTG      100
    GTATTGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC TGCTGAGCTC      150
    GGCAAGGGCT CTTTCAAGTA TGCCTGGGTT CTTGACAAGT TGAAGGCCGA      200
20  GCGTGAGCGT GGTATCACCA TTGATATCGC CCTCTGGAAG TTCGAGACCC      250
    CCAAGTACTA TGTCAACGTC ATCGATGCCC CCGGCCATCG TGATTTCATC      300
    AAGAACATGA TTACTGGTAC TTCCCAGGCC GATTGCGCCA TTCTCATCAT      350
    TGCCGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
    CCCGTGAGCA CGCTCTCCTC GCCTACACCC TCGGTGTGAA GCAGCTCATC      450
25  GTCGCCATCA ACAAGATGGA CACCACCAA TGGTCCGAGG CCCGCTTCAA      500
    CGAGATCATC AAGGAGACCT CCAACTTCAT CAAGAAGGTC GGCTACAACC      550
    CCAAGACTGT TGCTTTCGTC CCCATCTCCG GTTTCAACGG CGACAACATG      600
    CTTGAGGCTT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGGT      650
    CAAGGGTGGC AAGGCTACTG GCAAGACCCT CCTCGAGGCC ATCGACTCCA      700
30  TCGAGCCCCC CAAGCGTCCC ACCGACAAGC CCCTCCGTCT TCCCCTTCAG      750
    GACGTTTACA AGATCGGCGG TATCGGCACA GTCCCTGTCTG GCCGTATCGA      800
    GACTGGTATC CTCAAGCCCG GTATGGTCGT TACCTTCGCC CCTTCCAACG      850
    TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCTCTGAG      900
    GGTGTCCCCG GTGACAACGT TGGTTTCAAC GTGAAGAACG TCTCCGTCAA      950
35  GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTC      1000
    TTGGCGCCGC TTCTTTTCGAT GCCCAGGTCA TCGTCCTCAA CCACCCCGGC      1050
    CAGGTCGGTG CTGGTTACGC CCCCGTCCTC GATTGCCACA CTGCCCACAT      1100
    CGCCTGCAAG TTCGCTGAGC TCCTGCAGAA GATCGATCGC CGTACTGGTA      1150
    AGGCTGTTGA GGAGAGCCCT AAGTTCATCA AGTCTGGTGA TGCTGCCATC      1200
40  GTCAAGATGA TTCCCTCAA GGCATGTGC GTTGAGGCTT TCACTGAGTA      1250
    CCCTCCCCTC GGTCGTTTCG CTGTCCGTGA CATGCGTCAG ACCGTCGCTG      1300
    TCGGTGTCAT CAAGAAGGTC GAGAAGGCCG CTGCTGGTTC CGGCAAGGTC      1350
    ACCAAGTCCG CTGCCAAGGC TGGTGGCAAG AAATAA      1386
  
```

2) INFORMATION FOR SEQ ID NO: 1997

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Sordaria macrospora*
 (B) STRAIN: 000
 (C) ACCESSION NUMBER: X96615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997

```

10 ATGGGTAAGG AAGACAAGGC TCACATCAAC GTCGTCGTTA TCGGCCACGT      50
   CGATTCCGGC AAGTCCACCA CTACCGGTCA CCTGATCTAC AAGTGCGGTG      100
   GTATCGACAA GCGTACCATC GAGAAGTTCG AGAAGGAAGC CGCTGAGCTC      150
   GGCAAGGGTT CCTTCAAGTA TGCCTGGGTT CTTGACAAGC TCAAGGCCGA      200
15 GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG TTCGAGACTC      250
   CCAAGTACTA CGTCACCGTC ATCGATGCCC CCGGCCATCG TGATTTTCATC      300
   AAGAACATGA TCACTGGTAC CTCCCAGGCT GATTGCGCTA TTCTCATCAT      350
   TGCCGCTGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA      400
   CTCGTGAGCA CGCTCTTCTC GCCTACACCC TCGGTGTCAA GCAGCTCATC      450
20 GTTGCCATCA ACAAGATGGA CACCACCCAG TGGTCCCAGG CTCGTTTCGA      500
   GGAGATCATC AAGGAGACCA AGAACTTCAT CAAGAAGGTC GGCTACAACC      550
   CCGCCACCGT CGCTTTCGTC CCCATCTCCG GCTTCAACGG CGACAACATG      600
   CTTGAGGCCT CCACCAACTG CCCCTGGTAC AAGGGTTGGG AGAAGGAGAC      650
   CAAGGCCGGC AAGTCCACTG GCAAGACCCT CCTCGAGGCC ATCGACGCCA      700
25 TTGAGCAGCC CAAGCGCCCG ACCGACAAGC CCCTCCGTCT TCCCCTCCAG      750
   GATGTCTACA AGATCGGCGG TATCGGCACA GTGCCCCTCG GCCGTATCGA      800
   GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CTTTCCAACG      850
   TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTTGCTCAG      900
   GGTGTTCCCG GTGACAACGT CGGCTTCAAC GTGAAGAACG TTTCCGTCAA      950
30 GGATATCCGT CGTGGTAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCTG      1000
   TCGGCGCTGC CTCTTTCACC GCCCAGGTCA TCGTCCTTAA CCACCCCGGT      1050
   CAGGTCGGTG CCGGCTACGC TCCCGTCCTC GATTGCCACA CTGCCCACAT      1100
   TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGATCGC CGTACTGGTA      1150
   AGGCTGTTGA GACTTCTCCC AAGTTCATCA AGTCTGGTGA TGCTGCCATC      1200
35 GTCAAGATGA TTCCCTCCAA GCCCATGTGC GTCGAGGCTT TCACCGACTA      1250
   CCCTCCCCTC GGTCGTTTCG CCGTCCGTGA CATGCGTCAG ACCGTCGCTG      1300
   TCGGTGTCAT CAAGGCCGTC GACAAGACCC AGGCTGTGCG TGGCAAGGTC      1350
   ACCAAGTCTG CTGCCAAGGC TGCCAAGAAG TAA                        1383

```

10

2) INFORMATION FOR SEQ ID NO: 1998

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1383 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichoderma reesei*

(B) STRAIN: QM9414

(C) ACCESSION NUMBER: Z23012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998

5
 ATGGGTAAGG AGGACAAGAC TCACATCAAC GTGGTCGTCA TCGGCCACGT 50
 CGACTCCGGC AAGTCTACCA CCACTGGTCA CTTGATCTAC CAGTGCGGTG 100
 GTATCGACAA GCGTACCATT GAGAAGTTCG AGAAGGAAGC CGCCGAAGTC 150
 GGCAAGGGTT CTTCAAGTA CGCGTGGGTT CTTGACAAGC TCAAGGCCGA 200
 10 GCGTGAGCGT GGTATCACCA TCGACATTGC CCTCTGGAAG TTCGAGACTC 250
 CCAAGTACTA TGTCACCGTC ATTGACGCTC CCGGCCACCG TGACTTCATC 300
 AAGAACATGA TCACTGGTAC TTCCCAGGCC GACTGCGCTA TCCTCATCAT 350
 CGCTGCCGGT ACTGGTGAGT TCGAGGCTGG TATCTCCAAG GATGGCCAGA 400
 CCCGTGAGCA CGCTCTGCTC GCCTACACCC TGGGTGTCAA GCAGCTCATC 450
 15 GTCGCCATCA ACAAGATGGA CACTGCCAAC TGGGCCGAGG CTCGTTACCA 500
 GGAAATCATC AAGGAGACTT CCAACTTCAT CAAGAAGGTC GGCTTCAACC 550
 CCAAGGCCGT TGCTTTCGTC CCCATCTCCG GCTTCAACGG TGACAACATG 600
 CTCACCCCTT CCACCAACTG CCCCTGGTAC AAGGGCTGGG AGAAGGAGAC 650
 CAAGGCTGGC AAGTTCACCG GCAAGACCTT CCTTGAGGCC ATCGACTCCA 700
 20 TCGAGCCCCC CAAGCGTCCC ACGGACAAGC CCCTGCGTCT TCCCTCCAG 750
 GACGTCTACA AGATCGGTGG TATCGGAACA GTTCCCGTCG GCCGTATCGA 800
 GACTGGTGTC CTCAAGCCCG GTATGGTCGT TACCTTCGCT CCCTCCAACG 850
 TCACCACTGA AGTCAAGTCC GTCGAGATGC ACCACGAGCA GCTCGCTGAG 900
 GGCCAGCCTG GTGACAACGT TGGTTTCAAC GTGAAGAACG TTTCCGTCAA 950
 25 GGAAATCCGC CGTGGCAACG TTGCCGGTGA CTCCAAGAAC GACCCCCCA 1000
 TGGGCGCCGC TTCTTTCACC GCCCAGGTCA TCGTCATGAA CCACCCCGGC 1050
 CAGGTCGGTG CCGGTACGC CCCCGTCCTC GACTGCCACA CTGCCACAT 1100
 TGCCTGCAAG TTCGCCGAGC TCCTCGAGAA GATCGACCGC CGTACCGGTA 1150
 AGGCTACCGA GTCTGCCCCC AAGTTCATCA AGTCTGGTGA CTCCGCCATC 1200
 30 GTCAAGATGA TCCCTCCAA GCCCATGTGC GTTGAGGCTT TCACCGACTA 1250
 CCCTCCCCTG GGTCGTTTCG CCGTCCGTGA CATGCGCCAG ACCGTCGCTG 1300
 TCGGTGTCAT CAAGGCCGTC GAGAAGTCTT CTGCCGCCGC CGCCAAGGTC 1350
 ACCAAGTCCG CTGCCAAGGC CGCCAAGAAA TAA 1383

35

2) INFORMATION FOR SEQ ID NO: 1999

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999

CATGTCAAYA TTGGTACTAT TGGTCATGT

29

50

2) INFORMATION FOR SEQ ID NO: 2000

1041

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000

CCACCYTCIC TCAMGTTGAA RCGTT 25

15 2) INFORMATION FOR SEQ ID NO: 2001

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001

ACYACITTRA CIGCYGCIYAT YAC 23

30 2) INFORMATION FOR SEQ ID NO: 2002

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002

CCIGARGARA GAGCIMGWGG T 21

45 2) INFORMATION FOR SEQ ID NO: 2003

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003

CATYTCRAIR TTGTCACCTG G

21

2) INFORMATION FOR SEQ ID NO: 2004

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1360 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: SC5314
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004

GCTGCCTTCG	ACCGTTCTAA	ACCTCATGTC	AACATTGGTA	CTATTGGTCA	50
TGTTGATCAT	GGTAAACTA	CATTGACTGC	TGCTATCACC	AAAGTTT TAG	100
CCGAACAAGG	TGGTGCCAAC	TTCTTGGAAT	ATGGTTCTAT	TGATAGAGCT	150
CCAGAAGAAA	GAGCTAGAGG	TATCACTATT	TCCACTGCCC	ACGTTGAATA	200
CGAAACCAAG	AACAGACACT	ATGCCCACGT	TGATTGTCCA	GGACACGCTG	250
ATTATATCAA	AAATATGATT	ACTGGTGCCG	CTCAAATGGA	TGGTGCTATC	300
ATTGTTGTTG	CTGCCACTGA	TGGTCAAATG	CCTCAAACCA	GAGAACATTT	350
GTTATTGGCC	AGACAAGTTG	GTGTTCAAGA	CTTGGTTGTG	TTTGTCAACA	400
AAGTCGATAC	TATTGATGAC	CCTGAAATGT	TGGAATTAGT	CGAAATGGAA	450
ATGAGAGAAT	TGTTATCCAC	CTACGGTTTT	GATGGTGACA	ACACTCCAGT	500
TATTATGGGA	TCTGCTTTAA	TGGCTTTGGA	AGACAAGAAA	CCAGAAATTG	550
GTAAGGAAGC	TATCTTGAAA	TTGTTAGATG	CTGTGCGATG	ACACATTCCA	600
ACTCCATCAA	GAGACTTGGA	ACAACCATTT	TTGTTACCAG	TTGAAGACGT	650
GTTCTCCATC	TCCGGTAGAG	GAAGTGTGT	CACTGGTAGA	GTTGAAAGAG	700
GTGTTTTGAA	GAAGGGTGAA	GAAATCGAAA	TTGTTGGTGG	TTTTGACAAA	750
CCTTACAAGA	CTACTGTTAC	CGGTATTGAA	ATGTTCAAAA	AAGAATTAGA	800
CTCTGCTATG	GCTGGTGACA	ACTGTGGTGT	TTTGTTAAGA	GGTGTTAAAA	850
GAGATGAAAT	CAAGAGAGGT	ATGGTTTTGG	CCAAACCAGG	TACTGCTACT	900
TCTCACAAGA	AGTTCTTGGC	TTCCTTGAT	ATTTTGACTT	CCGAAGAAGG	950
TGGTCGTTCC	ACTCCATTTG	GTGAAGGTTA	CAAGCCTCAA	TGCTTCTTCA	1000
GAACTAACGA	TGTCACTACC	ACATTTTCAT	TCCCAGAAGG	AGAAGGTGTT	1050
GATCATTCTC	AAATGATCAT	GCCAGGTGAC	AACATTGAAA	TGGTTGGTGA	1100
ATTGATCAAA	TCTTGTCAT	TAGAAGTCAA	CCAACGTTTC	AACTTGAGAG	1150
AAGGTGGTAA	AACTGTTGGT	ACTGGTTTGA	TTACCAGAAT	CATCGAATAA	1200
ACAGAATGTG	CACTGTGAAT	AATAAAAAGA	AAAGAGGTAT	ATATAGGTGA	1250
CTTTGTATTT	TGTATTGAAC	AATAAAATTC	TGTAAATAGT	AAGGGCCTCA	1300
GAAGTTTTGA	TTTGATTTAT	GCCATGTGGA	CTTGTAGAGA	TATCCTTCTC	1350
AAACTTCTTG					1360

2) INFORMATION FOR SEQ ID NO: 2005

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Schizosaccharomyces pombe*

(C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005

AAGCCGCATG	TCAATATTGG	TACTATTGGT	CATGTTGACC	ACGGTAAAAC	50
GACGTTGACG	GCTGCTATTA	CTAAATGCCT	TTCTGATCTT	GGTCAAGCTA	100
GTTTTATGGA	TTATAGTCAA	ATTGACAAGG	CCCCCGAGGA	AAAGGCACGT	150
GGTATTACCA	TTTCATCTGC	CCATGTTGAA	TACGAAACTG	CTAATCGTCA	200
CTATGCCCAT	GTGGATTGTC	CTGGTCACGC	CGATTACATT	AAGAATATGA	250
TTACTGGTGC	TGCTACAATG	GATGGCGCTA	TCATTGTTGT	TTCTGCTACC	300
GATGGTCAAA	TGCCTCAAAC	TCGTGAACAT	TTGCTTCTGG	CTCGTCAAGT	350
CGGTGTAAAG	CAAATTGTTG	TATACATCAA	TAAAGTCGAT	ATGGTCGAGC	400
CTGATATGAT	CGAGCTTGTC	GAAATGGAAA	TGCGTGAGCT	ACTCTCCGAA	450
TACGGATTTG	ATGGTGACAA	TACTCCAATT	GTTAGCGGCA	GTGCTTTATG	500
TGCCTTAGAG	GGTCGTGAGC	CTGAGATTGG	TCTCAATAGT	ATTACTAAAT	550
TGATGGAAGC	TGTTGATAGT	TATATTACTC	TTCCTGAAAG	AAAAACGGAT	600
GTCCCTTTCT	TGATGGCCAT	CGAGGACGTT	TTTTCAATTT	CAGGTCGCGG	650
AACTGTAGTC	ACTGGCCGTG	TCGAGCGCGG	TACTTTAAAG	AAGGGTGCTG	700
AAATCGAAAT	CGTCGGTTAT	GGTAGCCATT	TAAAGACTAC	CGTTACTGGA	750
ATTGAAATGT	TCAAAAAGCA	GCTTGATGCC	GCCGTTGCCG	GTGACAATTG	800
TGGCCTTTTA	CTTCGTTCTA	TCAAGCGAGA	GCAATTAAAA	CGTGGAATGA	850
TTGTCGCTCA	ACCAGGAACC	GTTGCTCCTC	ATCAGAAATT	CAAGGCATCA	900
TTCTATATTT	TGACAAAAGA	GGAAGGAGGT	CGTCGTACCG	GTTTCGTTGA	950
CAAGTATCGT	CCCCAACTGT	ACAGTCGTAC	TTCCGACGTT	ACTGTCTGAAC	1000
TTACCCACCC	TGATCCTAAC	GACTCAGACA	AAATGGTTAT	GCCTGGAGAC	1050
AATGTCGAGA	TGATCTGTAC	GCTTATTCAC	CCCATTGTCA	TCGAAAAAGG	1100
ACAACGCTTC	ACAGTTCGTG	AGGGTGGAAG	CACTGTAGGC	ACAGCTTTGG	1150
TTACTGAACT	TTTGGATTAG	TGCATTTATG	AACTTATTGG	CTTTAAAAAT	1200
TTTGCAATGCT	GAATACCAAT	ATTATGTCCC	TTCTCAGAAAT	TCTATAACTA	1250
CAGTGTCAAT	ATTGTAATAA	GACTTTTGCA	TCCATTGACA	ATGGTATTTG	1300
ATACTTTTAT	AGTTTCTACT	ATTGTTAGCC	AAAGTTATAA	AA	1342

2) INFORMATION FOR SEQ ID NO: 2006

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006

TGGAGCCGGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2007

1045

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007

TGGAGCCAGT GAGCGTGG

18

2) INFORMATION FOR SEQ ID NO: 2008

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008

TCTGGAGCCG ATGAGCGTG

19

2) INFORMATION FOR SEQ ID NO: 2009

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009

CTGGAGCCAG TAAGCGTGG

19

2) INFORMATION FOR SEQ ID NO: 2010

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: KMK107
 (C) ACCESSION NUMBER: AF027199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010

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ATGAGTATTC AACATTTTCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTAAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCTGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGACG CCTGCAGCAA      550
TGGCAACAAC GTTGCGCAAA CTATTAAC TGCGAACTACT TACTCTAGCT      600
TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC      650
ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG      700
GAGCCAGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT      750
GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC      800
TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA      850
AGCATTGGTA A                                     861

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2) INFORMATION FOR SEQ ID NO: 2011

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*
 (B) STRAIN: CLSis L-491
 (C) ACCESSION NUMBER:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011

```

ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT      50
TTGCTTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG      100
CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAGCT GGATCTCAAC      150
AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT      200
GAGCACTTTT AAAGTTCTGC TATGTGGTGC GGTATTATCC CGTGTTGACG      250
CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG      300
GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT      350
AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA      400
ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTTG      450
CACAACATGG GGGATCATGT AACCCGCCTT GATCGTTGGG AACCGGAGCT      500
GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA      550
TGGCAACAAC GTTGCGCAAA CTATTAAC TGCGAACTACT TACTCTAGCT      600

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TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	700
GAGCCAGTAA	GCGTGGATCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ATGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

2) INFORMATION FOR SEQ ID NO: 2012

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012

CCGCGGATTA TTAAACCGCC CTTCCGCGG-MR-HEG-ATGTCAGAGG GATAGATCCA 49

2) INFORMATION FOR SEQ ID NO: 2013

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
- (B) STRAIN: ATCC 33433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013

AGCTTAAGAA	CTCTTATCTG	GATTACGCGA	TGTCGGTCAT	TGTTGGCCGT	50
GCGCTGCCGG	ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	100
TTACGCCATG	AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	150
CAGCCCGTGT	CGTGGGTGAC	GTGATCGGTA	AATATCACCC	GCATGGTGAT	200
ACTGCCGTCT	ATGACACTAT	CGTCCGTATG	GCACAGCCAT	TCTCACTGCG	250
ATACATGCTG	GATAGTGGTC	AAGGTAAGTT	CGGTTCTGTC	GATGGCGACT	300
CCGCCGCAGC	GATGCGTTAT	ACGGAAATCC	GTATGTCGAA	AATCGCCCAT	350
GAG					353

2) INFORMATION FOR SEQ ID NO: 2014

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 bases
- (B) TYPE: Nucleic acid

1048

- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
- (B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014

```

AGCTCCTATC TGGATTATGC GATGTCGGTC ATTGTTGGCC GTGCGCTGCC      50
AGATGTCCGA GATGGCCTGA AGCCGGTACA CCGTCGCGTA CTTTACGCCA      100
TGAACGTACT AGGCAATGAC TGGAAACAAAG CCTATAAAAA ATCTGCCCCGT      150
GTCGTTGGTG ACGTAATCGG TAAATACCAT CCCCATGGTG ACTCGGCGGT      200
CTATGACACG ATCGTCCGCA TGGCGCAGCC ATTCTCGCTG CGTTATATGC      250
TGGTAGACGG TCAGGGTAAC TTCGGTTCTA TCGACGGCGA CTCTGCGGCG      300
GCAATGCGTT ATACGGAAAT CCGTCTGGCG AAAATTGCCC ATGAACTGAT      350
GGCCG

```

2) INFORMATION FOR SEQ ID NO: 2015

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015

CCAAGAAGCT CAAAACATC TG

22

2) INFORMATION FOR SEQ ID NO: 2016

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016

TADCCTGTCC AWACAGCCAT

20

2) INFORMATION FOR SEQ ID NO: 2017

(i) SEQUENCE CHARACTERISTICS:

1049

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017

ACTTTGAATA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2018

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018

ACACTAAACA AGGTTGGTTT AG

22

2) INFORMATION FOR SEQ ID NO: 2019

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019

ACACTAAACA AGGTCGGTCT AG

22

2) INFORMATION FOR SEQ ID NO: 2020

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020

WO 01/23604
GTAGCTCCAG ATGAAATGTT TG

PCT/CA00/01150

22

2) INFORMATION FOR SEQ ID NO: 2021

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021

GTAGCTCCAG ACGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2022

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022

GTAGCTCCAG ATGAAACGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2023

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023

GTAAGTCCAG ATGAAATGTT TG

22

2) INFORMATION FOR SEQ ID NO: 2024

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid

1051

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024

AGTGAAAAGA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2025

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025

AGTGAGAAAA TGGCTGCTGC

20

2) INFORMATION FOR SEQ ID NO: 2026

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026

TCCAAGCATG CATTATGCAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2027

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027

TCGGTCTAGA TAGAGCTAAA ACG

23

2) INFORMATION FOR SEQ ID NO: 2028

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028

TATGCTCTTC AACATCACG

20

2) INFORMATION FOR SEQ ID NO: 2029

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029

AGCCGTTGAG ACTTTGAATA AG

22

2) INFORMATION FOR SEQ ID NO: 2030

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030

CTTAATGGTC TTGGTATCG

19

2) INFORMATION FOR SEQ ID NO: 2031

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1053

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031

CGTGACTGGG GTTCTGCTAT GA

22

2) INFORMATION FOR SEQ ID NO: 2032

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032

CGTGACTGGG GATCATCAAT GA

22

2) INFORMATION FOR SEQ ID NO: 2033

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033

CGTGACTGGG GTTCTGCCAT GA

22

2) INFORMATION FOR SEQ ID NO: 2034

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034

ATCAAGAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2035

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035

ATCAAGAACA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2036

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036

ATCAAGAACA CTGGTTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2037

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037

ATCAAAAATA CTGGTTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2038

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1055

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038

ATCAAGAATA CTGGCTACGT AG

22

2) INFORMATION FOR SEQ ID NO: 2039

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039

ATCAAAAACA CTGGCTATGT AG

22

2) INFORMATION FOR SEQ ID NO: 2040

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040

TGTGACCCCA GACAAACCC

19

2) INFORMATION FOR SEQ ID NO: 2041

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041

GTTGAGCGGC AGCACTATCT

20

2) INFORMATION FOR SEQ ID NO: 2042

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042

CACGGGGATT TCTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2043

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043

CACGGGGATT ACTCTATTTA

20

2) INFORMATION FOR SEQ ID NO: 2044

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044

ACCGTAAGTC GGCCAAGTCA

20

2) INFORMATION FOR SEQ ID NO: 2045

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045

1057

GTTCTTTCTC CGTATCGTC

19

2) INFORMATION FOR SEQ ID NO: 2046

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046

ACGGGGATTT TTCTATCTAT

20

2) INFORMATION FOR SEQ ID NO: 2047

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: CS109
- (C) ACCESSION NUMBER: Z49094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTATGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACCTCTAGTA	AAATCTACGA	CAATAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAATTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTAG	CGATTAGTT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900

1058

AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCAC	AACTTGGTGC	TCGTCATCAA	1050
GCAAGTAATG	TTTCATTTCG	TACCAACCAG	GCCGTAGAAA	CCAATCGTGA	1100
CTGGGGATCA	TCAATGAAAC	CAATCACTGA	CTATGCTCCC	GCTTTAGAAT	1150
ATGGAGTCTA	TGACTCTACT	GCTTCTATTG	TACATGATGT	CCCTTATAAC	1200
TATCCTGGCA	CTGATACTCC	ACTCTACAAC	TGGGATCATG	TCTACTTTGG	1250
AAACATTACA	ATCCAGTATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAACACAAC	GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTATCA	CAAACCAATG	1500
TATATCAATA	AAATCGTCTT	TAGTGATGGT	AGCGAAAAAG	AATTTTCTGA	1550
TGCTGGTACA	CGAGCTATGA	AAGAGACTAC	TGCCTATATG	ATGACTGAAA	1600
TGATGAAAAC	TGTTTTAACT	TACGGAACAG	GACGTGGAGC	CTACCTACCA	1650
TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	CTGACGAAGA	1700
AATTGAAAAG	TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GATGAAATGT	1750
TTGTAGGGTA	TACCCGTAAA	TATGCAATGG	CTGTTTGGAC	AGGATACTCA	1800
AATCGTCTAA	CTCCAATCAT	CGGAGATGGT	TTCTTGTGTT	CTGGTAAAGT	1850
CTATCGTTCA	ATGATAACTT	ACCTTTCTGA	AGATGACCAA	CCTGGAGATT	1900
GGACAATGCC	AGATGGCTTG	TATAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAACTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2048

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: R6
- (C) ACCESSION NUMBER: M90527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATACCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGCAA	350
TTCCCTCCAA	GGTGGATCAG	CTCTCACTCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	TTGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTAG	CGATTCA GTT	AGAACAAAAA	GCAACCAAGC	AAGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAA TGGAAC	TATGGAATGC	550

AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGC	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGGCTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAAGTCATC	AATCAAGTTG	850
AAGAAGAAAC	AGGCTATAAC	CTACTCACAA	CTGGGATGGA	TGTCTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATTT	ACAATACAGA	950
CGAATACGTT	GCCTATCCAG	ACGATGAATT	GCAAGTCGCT	TCTACCATTG	1000
TTGATGTTTC	TAACGGTAAA	GTCATTGCC	AGCTAGGAGC	ACGCCATCAG	1050
TCAAGTAATG	TTTCCTTCGG	AATTAACCAA	GCAGTAGAAA	CAAACCGCGA	1100
CTGGGGATCA	ACTATGAAAC	CGATCACAGA	CTATGCTCCT	GCCTTGGAGT	1150
ACGGTGTCTA	CGAGTCAACT	GCCACTATCG	TTCACGATGA	GCCCTATAAC	1200
TACCCTGGGA	CAAATACCCC	TGTTTATAAC	TGGGATAGGG	GCTACTTTGG	1250
CAACATCACC	TTGCAATACG	CCCTGCAACA	ATCGCGAAAC	GTCCCAGCCG	1300
TGGAAACTCT	AAACAAGGTC	GGACTCAACC	GCGCCAAGAC	TTTCCTAAAT	1350
GGTCTCGGAA	TCGACTACCC	AAGTATTCAC	TACTCAAATG	CCATTTCAAG	1400
TAACACAACC	GAATCAGACA	AAAAATATGG	AGCAAGTAGT	GAAAAGATGG	1450
CTGCTGCTTA	CGCTGCCTTT	GCAAATGGTG	GAACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	TAGTGATGGG	AGTGAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AAGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAAC	AGTCTTGAGT	TATGGAAC	GACGAAATGC	CTATCTTGCT	1650
TGGCTCCCTC	AGGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGACGAGGA	1700
AATTGAAAAC	CACATCAAGA	CCTCTCAATT	TGTAGCACCT	GATGAACTAT	1750
TTGCTGGCTA	TACGCGTAAA	TATTCAATGG	CTGTATGGAC	AGGCTATTCT	1800
AACCGTCTGA	CACCACTTGT	AGGCAATGGC	CTTACGGTCG	CTGCCAAAGT	1850
TTACCGCTCT	ATGATGACCT	ACCTGTCTGA	AGGAAGCAAT	CCAGAGGATT	1900
GGAATATACC	AGAGGGGCTC	TACAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2049

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: URU-E159
- (C) ACCESSION NUMBER: AF139890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAAT	CAACTCATTG	CTGACTTGGG	200

TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAA	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400
TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCAAATGGTG	GCACTTACTA	TAAACCAATG	1500
TATATCCATA	AAGTCGTCTT	CAGTGATGGA	AGTAAAAAAG	AGTTCTCTAA	1550
TGTCGGAAC	CGTGCCATGA	AGGAAACGAC	AGCCTATATG	ATGACCGACA	1600
TGATGAAAC	AGTCTTGACT	TATGGAAGTG	GGCGTGGAGC	CTATCTTCCT	1650
TGGCTTCCTC	AAGCTGGTAA	AACAGGAACC	TCTAACTATA	CAGATGAGGA	1700
AGTTGAAAC	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCTG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCTTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAATG	GAGAATTCGT	ATTTAAAAAT	1950
GGTGCTCGTT	CTACGTGGAA	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCAATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCATAA					2160

2) INFORMATION FOR SEQ ID NO: 2050

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 8303; 35193
- (C) ACCESSION NUMBER: AF046230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050

CTGTGGGATA	TCTACAACTC	CGATCAATAC	GTCTCTTACC	CTGACGATGA	50
TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	TTCAAATGGT	AAAGTCATCG	100
CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	ACGTTTCATT	TGGTACCAAC	150
CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	TCTGCTATGA	AACCAATCAC	200
CGATTATGCA	CCTGCCATAG	AATACGGTGT	TTATGATTCC	ACTGCAACTA	250
TGGTTAATGA	TATTCCTTAT	AACTATCCGG	GAACAAGCAC	ACCTGTCCTAC	300
AACTGGGATA	GAGCATATTT	CGGTAATATT	ACTCTGCAAT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AAGTAATACA	ACAGAATCTA	ATAAACAAATA	500
CGGAGCAAGT	AGTGAAAAAA	TGGCTGCTGC	TTATGCTGCC	TTTGCAAATG	550
GTGGCACTTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTCAGTGAT	600
GGAAGTAAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	700
CTGGGCGTGG	AGCCTATCTT	CCTTGGCTTC	CTCAAGCTGG	TAAAACAGGA	750
ACCTCTAACT	ATACAGATGA	GGAAGTTGAA	AACCACATCA	AGAACACTGG	800
CTATGTAGCT	CCAGATGAAA	TGTTTGTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAT	TCGAATCGTT	TAACCTCTAT	CGTTGGAGAT	900
GGTTTCCTAG	TTGCAGCTAA	AGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 63509; M11
- (C) ACCESSION NUMBER: AF046238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGATGATGA	50
CATGCAAGTA	GCTTCGACTA	TTGTAGATGT	ATCTAATGGT	AACGTTATTG	100
CACAACTTGG	TGCTCGTCAT	CAAGCAAGTA	ATGTTTCATT	CGGCACCAAC	150
CAGGCTGTGG	AGACCAATCG	TGACTGGGGT	TCTTCTATGA	AACCAATCAC	200
TGACTATGCT	CCCGCTTTAG	AATATGGAGT	CTATGACTCT	ACTGCTTCTA	250
TTGTACATGA	TGTTCTTAT	AACTATCCTG	GCACTGATAC	TCCAGTCTAC	300
AACTGGGATC	ATGTCTACTT	TGGAAACATT	ACAATCCAGT	ATGCTCTTCA	350
ACAATCACGA	AATGTCACAG	CCGTTGAGAC	TTTGAATAAG	GTCGGTCTAG	400
ATAGAGCTAA	AACCTTCCTT	AATGGTCTTG	GTATCGACTA	TCCAAGCATG	450
CATTATGCAA	ACGCCATTTT	AAGTAACACA	ACTGAATCCA	ACAAACAGTA	500
CGGTGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTATGCCGCC	TTTTCTAATG	550
GTGGTATTTA	CCACAAACCA	ATGTATATCA	ATAAAATCGT	CTTCAGTGAT	600
GGTAGTGAAA	AAGAATTTTC	TGATGCTGGT	ACACGAGCTA	TGAAAGAAAC	650
TACTGCCTAT	ATGATGACCG	AAATGATGAA	AACTGTTTAA	GCTTACGGAA	700
CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	CACAAGCAGG	TAAGACAGGT	750

ACTTCTAACT	ATACTGACGA	CGAAATTGAA	AAGTATATCA	AGAACACTGG	800
CTACGTAGCT	CCAGATGAAA	TGTTTGTTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	TAACTCCAAT	CGTAGGAGAT	900
GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC			930

2) INFORMATION FOR SEQ ID NO: 2052

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: #22/HA5
- (C) ACCESSION NUMBER: AB006877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052

GTCTCTTACC	CTGACGATGA	TTTGCAAGTC	GCATCTACGG	TCGTAGATGT	50
TTCCAATGGT	AAAGTCATCG	CCCAACTTGG	AGCTCGTCAC	CAAGCAAGTA	100
ACGTTTTCATT	TGGTACCAAC	CAAGCTGTGG	AAACCAATCG	TGACTGGGGT	150
TCAACAATGA	AACCAATCAC	CGATTATGCA	CCTGCCATAG	AATACGGTGT	200
ATATGATTCC	ACTGCAACTA	TGGTTAATGA	TATTCCTTAT	AACTATCCGG	250
GAACAAGCAC	ACCTGTCTAC	AACTGGGATC	GAGCATATTT	TGGTAATATT	300
ACTCTGCAAT	ATGCCCTTCA	ACAATCACGT	AATGTTACAG	CAGTTGAAAC	350
ATTAAACAAG	GTTGGTTTAG	ATCGAGCCAA	AACTTTCCTA	AATGGCTTAG	400
GTATCGATTA	CCCAAGCATA	CACTATGCTA	ACGCCATTTT	AAGTAATACA	450
ACAGAACTA	ACAAACATTA	CGGTGCAAGT	AGTGAAAAAA	TGGCTGCTGC	500
TTATGCCGCC	TTTGCTAATG	GTGGTATTTA	CCACAAACCA	ATGTATATCA	550
ATAAAATCGT	CTTTAGTGAT	GGTAGTGAGA	AAGAATTTTC	TGATGCTGGT	600
ACACGAGCTA	TGAAAGAAAC	TACTGCCTAT	ATGATGACCG	AAATGATGAA	650
AACTGTTTTA	GCTTACGGAA	CCGGACGTGG	TGCTTACCTA	CCATGGCTTC	700
CACAAGCAGG	TAAGACAGGT	ACTTCTAACT	ATACTGATGA	CGAAATCGAA	750
AAACATATCA	AGAATACTGG	CTACGTAGCT	CCAGATGAAA	TGTTTGTAGG	800
CTATACTCGT	AAGTATTCTA	TGGCTGTATG	GACTGGTTAC	TCAAATCGTT	850
TAACTCCAAT	TGTTGGAGAT	GGTTTCCTAG	TTGCTGCTAA	GGTTTATCGC	900
TCAATGATAT	CGTATCTATC	AGAAGATGAC	CAACCTGGAG	ATTGGACGAT	950
GCCAGACGGC	CTGTTCCGAA	ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	1000
GTTCTACGTG	GAACACACCT	GCTCCACAAC	AACCCCATC	AACTGAAAGT	1050
TCAAGCTCAT	CATCAGATAG	TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	1100
AAGCACAAAT	AATAGTACGA	CTACCAATCC	TAACAATAAT	ACGCAACAAT	1150
CAAATACAAC	CCCTGATCAA	CAAAATCAGA	ATCCTCAACC	AGCAC	1195

2) INFORMATION FOR SEQ ID NO: 2053

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: 17619

(C) ACCESSION NUMBER: AF046237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053

CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	50
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	100
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	150
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	200
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	250
TCGTTTCACGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	300
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	350
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	400
ACCGCGCCAA	GACTTTCCTA	AATGGTCTCG	GAATCGACTA	CCCAAGTATT	450
CACTACTCAA	ATGCCATTTT	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	500
TGGAGCAAGT	AGTGAAAAGA	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	550
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	600
GGGAGTGAAA	AAGAGTTCTC	TAATGTCGGA	ACTCGTGCCA	TGAAGGAAAC	650
GACAGCCTAT	ATGATGACCG	AAATGATGAA	AACAGTCTTG	AGTTATGGAA	700
CTGGACGAAA	TGCCTATCTT	GCTTGGCTTC	CTCAAGCTGG	TAAAACAGGT	750
ACCTCTAACT	ATACAGATGA	AGAAATTGAA	AAACACATCA	AAAACACTGG	800
CTATGTAGCT	CCAGATGAAA	CGTTTGTTGG	TTATACTCGT	AAGTATTCTA	850
TGGCTGTATG	GACAGGTTAC	ACAAACCGTC	TCACACCAAT	TGTGGGGGAT	900
GGCTTCACAG	TTGCTGCCAA	AGTTTACCGC			930

2) INFORMATION FOR SEQ ID NO: 2054

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: R6

(C) ACCESSION NUMBER: Y07845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054

CGTCGCATTC	TCTACGGAAT	GAATGAATTG	GGTGTGACCC	CAGACAAACC	50
CCATAAAAAA	TCTGCTCGTA	TTACAGGGGA	TGTCATGGGT	AAATACCACC	100
CACACGGGGA	TTCCTCTATT	TATGAAGCCA	TGGTCCGTAT	GGCTCAATGG	150
TGGAGCTACC	GTTACATGCT	TGTAGATGGT	CATGGGAATT	TTGGTTCCAT	200
GGATGGAGAT	AGTGCTGCCG	CTCAACGTTA	TACCGAGGCA	CGTATGAGCA	250
AGATTGCTCT	GGAAATGCTT	CGTGATATCA	ACAAAAATAC	AGTTGATTTC	300
GTTGAT					306

2) INFORMATION FOR SEQ ID NO: 2055

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2472 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 7785
- (C) ACCESSION NUMBER: Z67739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055

ATGTCTAACA	TTCAAAACAT	GTCCCTGGAG	GACATCATGG	GAGAGCGCTT	50
TGGTCGCTAC	TCCAAGTACA	TTATTCAAGA	CCGGGCTTTG	CCAGATATTC	100
GTGATGGGTT	GAAGCCGGTT	CAGCGCCGTA	TTCTTTATTC	TATGAATAAG	150
GATAGCAATA	CTTTTGACAA	GAGCTACCGT	AAGTCGGCCA	AGTCAGTCGG	200
GAACATCATG	GGGAATTTC	ACCCACACGG	GGATTCTTCT	ATCTATGATG	250
CCATGGTTTCG	TATGTCACAG	AACTGGAAAA	ATCGTGAGAT	TCTAGTTGAA	300
ATGCACGGTA	ATAACGGTTC	TATGGACGGA	GATCCTCCTG	CGGCTATGCG	350
TTATACTGAG	GCACGTTTGT	CTGAAATTGC	AGGCTACCTT	CTTCAGGATA	400
TCGAGAAAAA	GACAGTTCCT	TTTGCATGGA	ACTTTGACGA	TACGGAGAAA	450
GAACCAACGG	TCTTGCCAGC	AGCCTTTCCA	AACCTCTTGG	TCAATGGTTC	500
GACTGGGATT	TCGGCTGGTT	ATGCCACAGA	CATTCCCTCC	CATAATTTAG	550
CTGAGGTCAT	AGATGCTGCA	GTTTACATGA	TTGACCACCC	AACTGCAAAG	600
ATTGATAAAC	TCATGGAATT	CTTACCTGGA	CCAGACTTCC	CTACAGGGGC	650
TATTATTCAG	GGTCGTGATG	AAATCAAGAA	AGCTTATGAG	ACTGGGAAAG	700
GGCGCGTGGT	TGTTCGTTCC	AAGACTGAAA	TTGAAAAGCT	AAAAGGTGGT	750
AAGGAACAAA	TCGTTATTAC	TGAGATTCCT	TATGAAATCA	ATAAGGCCAA	800
TCTGTCAAG	AAAATCGATG	ATGTTCTGT	TAATAACAAG	GTAGCTGGGA	850
TTGCTGAGGT	TCGTGATGAG	TCTGACCGTG	ATGGTCTTCG	TATCGCTATC	900
GAACTTAAGA	AAGACGCTAA	TACTGAGCTT	GTTCTCAACT	ACTTATTTAA	950
GTACACCGAC	CTACAAATCA	ACTACAACTT	TAATATGGTG	GCGATTGACA	1000
ATTTACACAC	TCGTCAGGTT	GGGATTGTTC	CAATCCTGTC	TAGCTACATC	1050
GCTCACCGTC	GAGAAGTGAT	TTTGGCGCGT	TCACGCTTTG	ACAAAGAAAA	1100
GGCTGAGAAA	CGTCTCCATA	TCGTCGAAGG	TTTGATTTCG	GTGATTTCGA	1150
TTTTGGATGA	AGTCATTGCT	CTTATCCGTG	CTTCTGAGAA	TAAGGCGGAC	1200
GCCAAGGAAA	ACCTCAAAGT	TAGCTATGAT	TTTACGGAAG	AACAGGCTGA	1250
GGCTATCGTA	ACTTTGCAAC	TGTACCGTTT	GACCAATACC	GATGTGGTTG	1300
TCTTGCAGGA	AGAAGAAGCA	GAGCTTCGTG	AGAAGATTGC	TATGCTGGCG	1350
GCTATTATCG	GTGATGAAAG	GACTATGTAC	AATCTCATGA	AGAAAGAACT	1400
TCGTGAGGTC	AAGAAGAAAT	TTGCAACTCC	TCGTTTGAGT	TCTTTAGAAG	1450
ACACTGCGAA	AGCAATTGAG	ATTGATACAG	CTAGTCTTAT	CGCTGAGGAA	1500
GATACCTACG	TCAGCGTGAC	CAAGGCAGGT	TACATCAAGC	GTACCAGTCC	1550
ACGTTCTTT	GCGGCTTCCA	CCTTGGAAGA	AATTGGCAAG	CGTGATGATG	1600
ACCGTTTGAT	TTTTGTTC	TCTGCCAAGA	CAACCCAGCA	CCTCTTGATG	1650
TTCAACAAGTC	TTGGAAATGT	CATCTACAGA	CCAATCCATG	AGTTGGCAGA	1700
TATTTCGTTGG	AAGGACATCG	GAGAGCATCT	GAGCCAAACC	ATCACAAACT	1750
TTGAAACGAA	TGAAGAAATC	CTTTATGTGG	AAGTACTGGA	TCAGTTTGAC	1800
GATGCGACAA	CCTACTTTGC	AGTGACTCGC	CTTGGTCAAA	TCAAACGGGT	1850

AGAGCGAAAA	GAATTCACCTC	CATGGCGGAC	CTATAGATCT	AAGTCTGTCA	1900
AGTATGCTAA	GCTCAAAGAC	GATACAGATC	AGATTGTAGC	AGTGGCTCCG	1950
ATTAAACTAG	ATGATGTTGT	CTTGGTTAGT	CAAAATGGTT	ATGCCCTGCG	2000
TTTCAATATC	GAAGAGGTTT	CGGTTGTCGG	TGCTAAGGCA	GCAGGTGTCA	2050
AGGCTATGAA	TTTGAAAGAA	GATGATGTCC	TCCAATCTGG	CTTTATCTGT	2100
AATACTTCGT	CCTTCTACCT	CTTGACCCAG	CGTGGAAAGCT	TGAAACGTGT	2150
TTCTATTGAG	GAAATTCTAG	CAACCAGCCG	TGCCAAACGA	GGATTACAAG	2200
TCTTGCGTGA	GTTGAAAAAC	AAACCGCATC	GTGTCTTCTT	GGCAGGAGCA	2250
GTTGCAGAGC	AAGGATTTGT	TGGCGATTTT	TTCAGTACGG	AAGTGGATGT	2300
GAACGACCAA	ACTCTGCTTG	TCCAATCCAA	TAAAGGAACA	ATCTATGAAA	2350
GCCGATTGCA	AGACTTGAAC	TTGTCAGAAC	GCACTAGCAA	TGGAAGCTTC	2400
ATTTCTGACA	CGATTTTACA	TGAAGAAGTT	TTTGACGCTT	ATCTTCAGGA	2450
AGTAGTTACT	GAAGATAAAT	AA			2472

2) INFORMATION FOR SEQ ID NO: 2056

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATTGCCCAAC	TTGGAGCTCG	TCACCAAGCA	AGTAACGTTT	150
CATTTGGCAC	CAACCAAGCT	GTGGAAACCA	ATCGTGACTG	GGGTTCAACA	200
ATGAAACCAA	TCACAGACTA	TGCTCCTGCC	TTGGAATACG	GTGTCTACGA	250
TTCAACTGCT	ACTATCGTTC	ACGATGAGCC	CTATAACTAT	CCTGGGACAG	300
ATACCCCTGT	CTATAACTGG	GATAGGGGCT	ACTTTGGCAA	TATCACCTTG	350
CAATACGCCC	TGCAACAATC	GCGAAACGTC	CCAGCCGTGG	AAACACTAAA	400
CAAGGTCGGG	CTCAACCGCG	CCAAGACTTT	TCTAAATGGT	CTCGGAATCG	450
ACTACCCAAG	TATTCACTAC	TCAAATGCCA	TTTCAAGTAA	CACAACCGAG	500
TCAGACAAAA	AATATGGAGC	AAGTAGTGAA	AAGATGGCTG	CTGCTTACGC	550
TGCCTTTGCA	AATGGTGGAA	CTTACTATAA	ACCAATGTAT	ATCCATAAAG	600
TCGTCTTTAG	TGATGGAAGT	GAAAAAGAGT	TCTCTAATGT	CGGAACTCGC	650
GCCATGAAAG	AAACGACTGC	TTACATGATG	ACAGAAATGA	TGAAAACAGT	700
CTTGACGTAC	GGAATTGGTC	GTGGTGCCTA	CCTGCCTTGG	CTTCCTCAAG	750
CTGGTAAAAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AACTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TATGGACAGG	CTATTCTAAC	CGTCTGACAC	900
CACTTGTAGG	CGATGGCCTT	ACGGTCGCTG	CCAAGGTTTA	CCGCTCTATG	950
ATGACCTACC	TGTCTGAAGG	AAGCAATCCA	GAGGATTGGA	ATATACCAGA	1000
GGGGCTCTAC	AGAAATGGAG	AATTTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TC				1212

2) INFORMATION FOR SEQ ID NO: 2057

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057

ATGTAGACCA	AGAAGCTCAA	AAACATCTGT	GGGATATTTA	CAATACAGAC	50
GAATACGTTG	CCTATCCAGA	CGATGAATTG	CAAGTCGCTT	CTACCATTGT	100
TGATGTTTCT	AACGGGAAAG	TTATTGCTCA	GTTAGGTTCT	CGTCACCAAT	150
CAAGCAATGT	TTCCTTCGGA	ATCAACCAAG	CTGTTGAAAC	CAACCGTGAC	200
TGGGGTTCTG	CCATGAAGCC	AATCACAGAC	TATGCTCCTG	CCTTAGAGTA	250
TGACATCTAC	GACTCAACTG	CTTCGATTGT	ACATGATGTT	CCTTATAACT	300
ATCCAGGTAC	TGATACTCCC	CTCTACAAC	GGGATAAAGT	CTACTTTGGA	350
AATATTACAA	TCCAGTATGC	ACTTCAACAG	TCACGTAATG	TCACAGCCGT	400
TGAGACTTTG	AATAAGGTCG	GTCTAGATAG	AGCTAAAACC	TTTCTTAATG	450
GTCTTGGTAT	CGACTATCCA	AGCATGCATT	ATGCAAACGC	CATTTCAAGT	500
AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	AGAAAAATGGC	550
TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	AAACCAATGT	600
ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	ATACGCTGAT	650
CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	TGACAGAAAT	700
GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	TATCTCCCTT	750
GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATAC	AGATGATGAA	800
ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GATAGCTCCAG	ACGAAATGTT	850
TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	GGTATGGACA	GGTTACTCAA	900
ACCGCCTGAC	TCCTATCGTT	GGTGATGGCT	TCTATGTTGC	AGCTAAGGTT	950
TACCGTTCAA	TGATGACTTA	TCTGTCTGAG	GATAACAACC	CTGGCGACTG	1000
GACTATGCCA	GAAGGTCTCT	ATCGAAGTGG	TGAGTTCGTC	TTTAAAAAAG	1050
GTGCTCGTTC	TGCATGGACT	GCTCCTGCTC	CGCAACAGGC	CCCAACACCA	1100
GAAAGTTCGA	GCTCGACATC	AGAAAGTTCA	ACTTCACAGT	CAAGCTCAAC	1150
TACTCCAAGC	ACGAATAATA	GTGCAACAA	TAATACCAAT	AACCAGCAAC	1200
CAAATACAAC	GCCTGGTCAA	CAAAACCAGA	ACCAAAATCA	GA	1242

2) INFORMATION FOR SEQ ID NO: 2058

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058

GAAGCTCAAA	AACATCTGTG	GGATATTTAC	AATACAGACG	AATACGTTGC	50
CTATCCAGAC	GATGAATTGC	AAGTCGCTTC	TACCATTGTT	GATGTTTCTA	100
ACGGGAAAGT	TATTGCTCAG	TTAGGTTCTC	GTCACCAATC	AAGCAATGTT	150
TCCTTCGGAA	TCAACCAAGC	TGTTGAAACC	AACCGTGACT	GGGGTTCTGC	200
CATGAAGCCA	ATCACAGACT	ATGCTCCTGC	CTTAGAGTAT	GACATCTACG	250
ACTCAACTGC	TTCGATTGTA	CATGATGTTT	CTTATAACTA	TCCAGGTACT	300
GATACTCCCC	TCTACAACCT	GGATAAAGTC	TACTTTGGAA	ATATTACAAT	350
CCAGTATGCA	CTTCAACAGT	CACGTAATGT	CACAGCCGTT	GAGACTTTGA	400
ATAAGGTCGG	TCTAGATAGA	GCTAAAACCT	TTCTTAATGG	TCTTGGTATC	450
GACTATCCAA	GCATGCATTA	TGCAAACGCC	ATTTCAAGTA	ATACGACTGA	500
GTCAAACAAA	AAGTACGGAG	CAAGTAGTGA	GAAAATGGCT	GCTGCTTACG	550
CTGCTTTTGC	TAACGGTGGT	ATCTACCATA	AACCAATGTA	TATCAACAAA	600
ATCGTCTTTA	GCGATGGTAG	CTCAAAAGAA	TACGCTGATC	CTGGTACTCG	650
TGCCATGAAA	GAGACGACCG	CCTATATGAT	GACAGAAATG	ATGAAGACTG	700
TCTTGGCATA	CGGAACGGGT	CGTGGTGCTT	ATCTCCCTTG	GCTACCTCAA	750
GCTGGTAAGA	CTGGTACATC	AAACTATACA	GATGATGAAA	TTGAAAACTA	800
CATCAAAAAT	ACTGGTTATG	TAGCTCCAGA	CGAAATGTTT	GTTGGTTATA	850
CTCGCAAATA	TTCAATGGCG	GTATGGACAG	GTTACTCAAA	CCGCCTGACT	900
CCTATCGTTG	GTGATGGCTT	CTATGTTGCA	GCTAAGGTTT	ACCGTTCAAT	950
GATGACTTAT	CTGTCTGAGG	ATAACAACCC	TGGCGACTGG	ACTATGCCAG	1000
AAGGTCTCTA	TCGAAGTGGT	GAGTTCGTCT	TTAAAAAAGG	TGCTCGTTCT	1050
GCATGGACTG	CTCCTGCTCC	GCAACAGGCC	CCAACACCAG	AAAGTTCGAG	1100
CTCGACATCA	GAAAGTTCAA	CTTCACAGTC	AAGCTCAACT	ACTCCAAGCA	1150
CGAATAATAG	TGCAAACAAT	AATACCAATA	ACCAGCAACC	AAATACAACC	1200
CCTGGTCAAC	AAAACCAGAA	CCAAA			1225

2) INFORMATION FOR SEQ ID NO: 2059

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: StrR-38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059

TGGCTACTTT	GGAAACATTA	CAGTCCAGTA	TGCTCTTCAA	CAATCACGAA	50
ATGTCACAGC	CGTTGAGACT	TTGAATAAGG	TCGGTCTAGA	TAGAGCTAAA	100
ACCTTCCTCA	ATGGACTTGG	TATCGATTAT	CCAAGCATGC	TTTATGCAAA	150
CGCCATTTCA	AGTAACACAA	CTGAATCCAA	CAAAAAGTAC	GGAGCAAGTA	200
GTGAAAAAAT	GGCCGCTGCC	TACGCAGCTT	TTGCTAATGG	TGGTACTTAC	250
CACAAACCAA	TGTATATCAA	TAAAATCGTC	TTTAGTGATG	GTAGTGAAAA	300
AGAATTTTCT	GATGCCGGTA	CTCGGGCTAT	GAAAGAACT	ACTGCCTATA	350

TGATGACCGA	AATGATGAAA	ACTGTCTTAT	TATACGGAAC	CGGACGTGGA	400
GCCTACCTAC	CTTGGCTTCC	ACAAGCAGGT	AAGACAGGTA	CTTCTAACTA	450
TACTGACGAA	GAAATTGAAA	AGTATATCAA	GAATGCTGGT	TACGTAGCTC	500
CAGATGAAAT	GTTTGTGGT	TATACCCGCA	AATATGCAAT	GGCTGTTTGG	550
ACAG					554

2) INFORMATION FOR SEQ ID NO: 2060

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: StrR-57

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060

CAACTGGGAT	GGATGTCTAC	ACAAATGTAG	ACCAAGAAGC	TCAAAAACAT	50
CTGTGGGATA	TTTACAATAC	AGACGAATAC	GTTGCCTATC	CAGACGATGA	100
ATTGCAAGTC	GCTTCTACCA	TTGTTGATGT	TTCTAACGGT	AAAGTCATTG	150
CCCAGCTAGG	AGCACGCCAT	CAGTCAAGTA	ATGTTTCCTT	CGGAATTAAC	200
CAAGCAGTAG	AAACAAACCG	CGACTGGGGA	TCAACTATGA	AACCGATCAC	250
AGACTATGCT	CCTGCCTTGG	AGTACGGTGT	CTACGATTCA	ACTGCTACTA	300
TCGTTACCGA	TGAGCCCTAT	AACTACCCTG	GGACAAATAC	TCCTGTTTAT	350
AACTGGGATA	GGGGCTACTT	TGGCAACATC	ACCTTGCAAT	ACGCCCTGCA	400
ACAATCGCGA	AACGTCCCAG	CCGTGGAAAC	TCTAAACAAG	GTCGGACTCA	450
ACCGCGCCAA	GACTTTCCTA	AATGGTCTAG	GAATCGACTA	CCCAAGTATT	500
CACTACTCAA	ATGCCATTTT	AAGTAACACA	ACCGAATCAG	ACAAAAAATA	550
TGGAGACTAA	AGTGAAGAAG	TGGCTGCTGC	TTACGCTGCC	TTTGCAAATG	600
GTGGAACCTA	CTATAAACCA	ATGTATATCC	ATAAAGTCGT	CTTTAGTGAT	650
GGGAGTGAAA	AAGAGTTCTC	TAATGTGCGA	ACTCGTGCCA	TGAAGGAAAC	700
GACAGCCTAT	ATGATGACCG	ACATGATGAA	AACAGTCTTG	ACTTATGGAA	750
CTGGACGAAA	TGCCTATCTT	GCTTGGCTCC	CTCAGGCTGG	TAAAACAGGA	800
ACCTCTAACT	ATACAGACGA	GGAAATTGAA	AACCACATCA	AGACCTCTCA	850
ATTTGTAGCA	CCTGATGAAC	TATTTGCTGG	CTATACGCGT	AAATATTCAA	900
TGGCTGTATG	GACAGGCTAT	TCTAACCGTC	TGACACCACT	TGTAGGCAAT	950
GGCCTTACGG	TCGCTGCCAA	AGTTTACCGC	TCTATGATGA	CCTACCTGTC	1000
TGAAGGAAGC	AATCCAGAAG	ATTGGAATAT	ACCAGAGGGG	CTCTACAGAA	1050
ATGGAGAATT	CGTATTTAAA	AATGGTGCTC	GTTCTACGTG	GAGCTCACCT	1100
GCTCCACAAC	AACCCCCATC	AACTGAAAGT	TCAAGCTCAT	CATCAGATAG	1150
TTCAACTTCA	CAGTCTAGCT	CAACCACTCC	AAGCACAAAT	AATAGTACGA	1200
CTACCAATCC	TAACAATAAT	ACGCAACAAT	CAAATACAAC	CCCTGATCA	1249

2) INFORMATION FOR SEQ ID NO: 2061

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 bases
- (B) TYPE: Nucleic acid

1069

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061

GAAGTTGAAC	AGACTGGTCA	CCAAGCTCCT	TCATATCCGC	CAAACTGCA	50
ATTTTCTTGC	CACCTTCATT	GGCTGGAATG	GCAGAGAAAG	TCTCTAAAAT	100
CAGTTTCATA	GCAGTTGGAT	TGGCATTATA	AACATCTGAC	AGGATATCTG	150
CTCCATTGGC	TGCTTTCTTC	CACTCGGTAC	GGTTACGCGT	CAATTCAAGA	200
TGTTGGAAGG	CCAAACGAAT	TTGCTCCTCT	GAAACTCCTT	CTTGCAAGGC	250
AACATAGGAT	GCAATCATAG	CATTTGTCGC	ATTGTACTTG	CCAGTTACTG	300
GCAAATCAAG	GGCTTGCTCT	AAGAAATTGA	CCTTGAAGGT	CAGACTATCT	350
TTGCGCTCAA	CCAAGTCGGT	AATTCCCAGC	TCTGCTCCTT	GACCAAAACG	400
AACCACCTTT	TTATCAGTTG	GCAAATAGTC	CTCTACGATA	GGGTCAGCCG	450
GCGCTAAAAG	CAAGGAACCT	GAAGCCATTC	CGTCTGCAAT	TTGCATTTTTT	500
CCTTTAGCAA	TCTCAGAACG	GTCTTTGAAA	AAGGCCAAAT	GAGCTTCTCC	550
AACCAAGGTC	ACGATGGCTG	TATGGACAG			579

2) INFORMATION FOR SEQ ID NO: 2062

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
(B) STRAIN: StrR-63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062

AAGCTCAAAA	ACATCTGTGG	GATATCTACA	ACTCCGATCA	ATACGTCTCT	50
TACCCTGACG	ATGATTTGCA	AGTCGCATCT	ACGGTCGTAG	ATGTTTCAAA	100
TGGTAAAGTC	ATCGCACAAAC	TTGGTGCTCG	TCATCAAGCA	AGTAATGTTT	150
CATTTCGGTAC	CAACCAGGCC	GTAAGAAACCA	ATCGTGACTG	GGGATCATCA	200
ATGAAACCAA	TCACTGACTA	TGCTCCCGCT	TTAGAATATG	GAGTCTATGA	250
CTCTACTGCT	TCTATTGTAC	ATGATGTCCC	TTATAACTAT	CCTGGCACTG	300
ATACTCCACT	CTACAACCTG	GATCATGTCT	ACTTTGGAAA	CATTACAATC	350
CAGTATGCTC	TTCAACAATC	ACGAAATGTC	ACAGCCGTTG	AGACTTTGAA	400
TAAGGTCGGT	CTAGATAGAG	CTAAAACCTT	CCTTAATGGT	CTTGGTATCG	450
ACTATCCAAG	CATGCATTAT	GCAAACGCCA	TTTCAAGTAA	CACAACTGAA	500
TCCAACAAAA	AATATGGTGC	AAGTAGTGAA	AAAATGGCTG	CTGCCTACGC	550
TGCTTTTGCT	AATGGTGGTA	TTTATCACAA	ACCAATGTAT	ATCAATAAAA	600
TCGTCTTTAG	TGATGGTAGC	GAAAAAGAAT	TTTCTGATGC	TGGTACACGA	650
GCTATGAAAG	AGACTACTGC	CTATATGATG	ACTGAAATGA	TGAAAACGTG	700
TTTAACTTAC	GGAACAGGAC	GTGGAGCCTA	CCTACCATGG	CTTCCACAAG	750

CAGGTAAGAC	AGGTACTTCT	AACTATACTG	ACGAAGAAAT	TGAAAAGTAT	800
ATCAAGAACA	CTGGTTACGT	AGCTCCAGAT	GAAATGTTTG	TAGGGTATAC	850
CCGTAAATAT	GCAATGGCTG	TTTGGACAGG	ATACTCAAAT	CGTCTAACTC	900
CAATCATCGG	AGATGGTTTC	CTTGTTGCTG	GTAAAGTCTA	TCGTTCAATG	950
ATAACTTACC	TTTCTGAAGA	TGACCAACCT	GGAGATTGGA	CAATGCCAGA	1000
TGGCTTGTAT	AGAAATGGAG	AATTTCGTATT	TAAAAATGGT	GCTCGTTCTA	1050
CGTGGAGCTC	ACCTGCTCCA	CAACAACCCC	CATCAACTGA	AAGTTCAAGC	1100
TCATCATCAG	ATAGTTCAAC	TTCACAGTCT	AGCTCAACCA	CTCCAAGCAC	1150
AAATAATAGT	ACGACTACCA	ATCCTAACAA	TAATACGCAA	CAATCAAATA	1200
CAACCCCTGA	TCAACA				1216

2) INFORMATION FOR SEQ ID NO: 2063

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: ATCC 700673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063

AATACGTCTC	TTACCCTGAC	GATGATTTGC	AAGTCGCATC	CACGGTCGTA	50
GATGTTTCAA	ATGGTAAAGT	CATCGCCCAA	CTTGGAGCTC	GTCACCAAGC	100
AAGTAACGTT	TCATTTGGTA	CCAACCAAGC	TGTGGAAACC	AATCGTGACT	150
GGGGTTCAAC	AATGAAACCC	ATCACCGATT	ATGCACCTGC	CATAGAATAC	200
GGTGTATATG	ATTCCACTGC	AACTATGGTT	AATGATATTC	CTTATAACTA	250
TCCGGGAACA	AGCACACCTG	TCTACAACCTG	GGATCGAGCA	TATTTTG GTA	300
ATATTACTCT	GCAATATGCC	CTTCAACAAT	CTCGTAACGT	ACCCGCCGTT	350
GAGACACTAA	ACAAGGTG TG	TTTAGATAGA	GCTAAAAGTT	TCCTAAATGG	400
TTTAGGAATC	GACTATCCTG	TAATGCACTA	TTCAAATGCT	ATTTCAAGTA	450
ATACTACCGA	ATCTAGTAAA	CAGTACGGGG	CAAGTAGTGA	AAAAATGGCC	500
ACTGCCTATG	CCGCATTCGC	AAACGGCGGT	ATTTACCACA	AACCAATGTA	550
CATCAATAAG	GTTGTCTTTA	GCGATGGTAG	CGAAAAAGAA	TTTTCTGACC	600
CTGGCACAAG	AGCCATGAAA	GAAACGACTG	CTTACATGAT	GACAGAGATG	650
ATGAAAACAG	TCTGGACTTA	CGGAACTGGT	CGCGGTGCCT	ACCTACCTTG	700
GCTTCCACAA	GCAGGTAAAA	CAGGTACTTC	TAATACTACT	GACGAAGAAA	750
TTGAAAAGTA	TATCAAGAAC	ACTGGTTACG	TAGCTCCAGA	TGAAATGTTT	800
GTAGGGTATA					810

2) INFORMATION FOR SEQ ID NO: 2064

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(B) STRAIN: ATCC 700678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064

TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	TAGATGTTTC	50
AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	GCAAGTAACG	100
TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	CTGGGGATCA	150
ACTATGAAAC	CAATCACAGA	CTATGCTCCT	GCCTTGGAGT	ACGGTGTCTA	200
CGATTCAACT	GCTACTATCG	TTCACGATGA	GCCCTATAAC	TACCCTGGGA	250
CAGATATCCC	TCTCTATAAC	TGGGATCGAG	CATATTTCCG	TAATATTACT	300
CTGCAATATG	CCCTTCAACA	ATCTCGTAAC	GTACCTGCCG	TTGAAACACT	350
AAACAAGGTC	GGTCTAGATA	AGGCTAAAAC	CTTCCTTAAT	GGTCTTGGA	400
TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	TAATACAAC	450
GAATCCAACA	AAAAATATGG	TGCAAGTAGT	GAAAAAATAG	CTACCGCCTA	500
TGCCGCATTG	GCAAATGGTG	GTATTTACCA	CAAACCAATG	TACATCAATA	550
AAGTTGTCTT	TAGCGATGGT	AGCGAAAAAG	AATTTTCTGA	CCCTGGCACA	600
AGAGCCATGA	AAGAAACGAC	TGCTTACATG	ATGACAGAAA	TGATGAAAAC	650
AGTCTGGACG	TACGGAAC	GTGCTGGTGC	CTACCTGCCT	TGGCTTCCTC	700
AAGCTGGTAA	AACAGGTACC	TCTAACTATA	CTGACGAAGA	AATTGAAAAG	750
TATATCAAGA	ACACTGGTTA	CGTAGCTCCA	GA		782

2) INFORMATION FOR SEQ ID NO: 2065

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2065

CCAGGACGTG GAGGCGATCA CA

22

2) INFORMATION FOR SEQ ID NO: 2066

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066

CACCGACAGC GAGCCGATCA GA

22

2) INFORMATION FOR SEQ ID NO: 2067

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067

AGCTGAGCCA ATTCATGG

18

2) INFORMATION FOR SEQ ID NO: 2068

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068

ATTCATGGAC CAGAACAAC

19

2) INFORMATION FOR SEQ ID NO: 2069

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069

CGCTGTCGGG GTTGACCC

18

2) INFORMATION FOR SEQ ID NO: 2070

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1073

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070

GTTGACCCAC AAGCGCCG

18

2) INFORMATION FOR SEQ ID NO: 2071

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071

CGACTGTCGG CGCTGGGG

18

2) INFORMATION FOR SEQ ID NO: 2072

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: Rv
- (C) ACCESSION NUMBER: L27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072

GTGCTGGAAG	GATGCATCTT	GGCAGATTCC	CGCCAGAGCA	AAACAGCCGC	50
TAGTCCTAGT	CCGAGTCGCC	CGCAAAGTTC	CTCGAATAAC	TCCGTACCCG	100
GAGCGCCAAA	CCGGGTCTCC	TTCGCTAAGC	TGCGCGAACC	ACTTGAGGTT	150
CCGGGACTCC	TTGACGTCCA	GACCGATTCC	TTCGAGTGGC	TGATCGGTTC	200
GCCGCGCTGG	CGCGAATCCG	CCGCCGAGCG	GGGTGATGTC	AACCCAGTGG	250
GTGGCCTGGA	AGAGGTGCTC	TACGAGCTGT	CTCCGATCGA	GGACTTCTCC	300
GGGTCGATGT	CGTTGTGCTT	CTCTGACCCCT	CGTTTCGACG	ATGTCAAGGC	350
ACCCGTCGAC	GAGTGCAAAG	ACAAGGACAT	GACGTACGCG	GCTCCACTGT	400
TCGTCACCGC	CGAGTTCATC	AACAACAACA	CCGGTGAGAT	CAAGAGTCAG	450
ACGGTGTTCA	TGGGTGACTT	CCCgatgatg	ACCGAGAAGG	GCACGTTCAT	500
CATCAACGGG	ACCGAGCGTG	TGGTGGTCAG	CCAGCTGGTG	CGGTGCCCCG	550
GGGTGTACTT	CGACGAGACC	ATTGACAAGT	CCACCGACAA	GACGCTGCAC	600
AGCGTCAAGG	TGATCCCCGAG	CCGCGGCGCG	TGGCTCGAGT	TTGACGTCCA	650
CAAGCGCGAC	ACCGTCGGCG	TGCGCATCGA	CCGCAAACGC	CGGCAACCCG	700

TCACCGTGCT	GCTCAAGGCG	CTGGGCTGGA	CCAGCGAGCA	GATTGTGCGAG	750
CGGTTCCGGT	TCTCCGAGAT	CATGCGATCG	ACGCTGGAGA	AGGACAACAC	800
CGTCGGCACC	GACGAGGCGC	TGTTGGACAT	CTACCGCAAG	CTGCGTCCGG	850
GCGAGCCCCC	GACCAAAGAG	TCAGCGCAGA	CGCTGTTGGA	AAACTTGTTC	900
TTCAAGGAGA	AGCGCTACGA	CCTGGCCCCG	GTCGGTCGCT	ATAAGGTCAA	950
CAAGAAGCTC	GGGCTGCATG	TCGGCGAGCC	CATCACGTCT	TCGACGCTGA	1000
CCGAAGAAGA	CGTCGTGGCC	ACCATCGAAT	ATCTGGTCCG	CTTGACGAG	1050
GGTCAGACCA	CGATGACCGT	TCCGGGCGGC	GTCGAGGTGC	CGGTGGAAAC	1100
CGACGACATC	GACCACTTCG	GCAACCGCCG	CCTGCGTACG	GTCGGCGAGC	1150
TGATCCAAAA	CCAGATCCGG	GTCGGCATGT	CGCGGATGGA	GCGGGTGGTC	1200
CGGGAGCGGA	TGACCACCCA	GGACGTGGAG	GCGATCACAC	CGCAGACGTT	1250
GATCAACATC	CGGCCGGTGG	TCCCGCGCAT	CAAGGAGTTC	TTCGGCACCA	1300
GCCAGCTGAG	CCAATTCATG	GACCAGAACA	ACCCGCTGTC	GGGGTTGACC	1350
CACAAGCGCC	GACTGTCCGC	GCTGGGGCCC	GGCGGTCTGT	CACGTGAGCG	1400
TGCCGGGCTG	GAGGTCCGCG	ACGTGCACCC	GTCGCACTAC	GGCCGGATGT	1450
GCCCCGATCGA	AACCCCTGAG	GGGCCCAACA	TCCGTCTGAT	CGGCTCGCTG	1500
TCGGTGTACG	CGCGGGTCAA	CCCGTTCGGG	TTCATCGAAA	CGCCGTACCG	1550
CAAGGTGCTC	GACGGCGTGG	TTAGCGACGA	GATCGTGTAC	CTGACCGCCG	1600
ACGAGGAGGA	CCGCCACGTG	GTGGCACAGG	CCAATTCGCC	GATCGATGCG	1650
GACGGTTCGCT	TCGTCGAGCC	GCGCGTGCTG	GTCCGCCGCA	AGGCGGGCGA	1700
GGTGGAGTAC	GTGCCCTCGT	CTGAGGTGGA	CTACATGGAC	GTCTCGCCCC	1750
GCCAGATGGT	GTCGGTGGCC	ACCGCGATGA	TTCCCTTCCT	GGAGCACGAC	1800
GACGCCAACC	GTGCCCTCAT	GGGGGCAAAC	ATGCAGCGCC	AGGCGGTGCC	1850
GCTGGTCCGT	AGCGAGGCC	CGCTGGTGGG	CACCGGGATG	GAGCTGCGCG	1900
CGGCGATCGA	CGCGGCGACG	TCGTCTGTCG	AAGAAAGCGG	CGTCATCGAG	1950
GAGGTGTCCG	CCGACTACAT	CACTGTGATG	CACGACAACG	GCACCCGGCG	2000
TACCTACCGG	ATGCGCAAGT	TTGCCCGGTC	CAACCACGGC	ACTTGCGCCA	2050
ACCAGTGCCC	CATCGTGGAC	GCGGGCGACC	GAGTCGAGGC	CGGTCAGGTG	2100
ATCGCCGACG	GTCCCTGTAC	TGACGACGGC	GAGATGGCGC	TGGGCAAGAA	2150
CCTGCTGGTG	GCCATCATGC	CGTGGGAGGG	CCACAACCTAC	GAGGACGCGA	2200
TCATCCTGTC	CAACCGCCTG	GTCGAAGAGG	ACGTGCTCAC	CTCGATCCAC	2250
ATCGAGGAGC	ATGAGATCGA	TGCTCGCGAC	ACCAAGCTGG	GTGCGGAGGA	2300
GATCACCCGC	GACATCCCGA	ACATCTCCGA	CGAGGTGCTC	GCCGACCTGG	2350
ATGAGCGGGG	CATCGTGCGC	ATCGGTGCCG	AGGTTTCGCGA	CGGGGACATC	2400
CTGGTCCGCA	AGGTCACCCC	GAAGGGTGAG	ACCGAGCTGA	CGCCGGAGGA	2450
GCGGCTGCTG	CGTGCCATCT	TCCGTGAGAA	GGCCCGCGAG	GTGCGCGACA	2500
CTTCCGTGAA	GGTGCCGCAC	GGCGAATCCG	GCAAGGTGAT	CGGCATTCCG	2550
GGTGTTCCTC	GCGAGGACGA	GGACGAGTTG	CCGGCCGGTG	TCAACGAGCT	2600
GGTGCCGTGT	TATGTGGCTC	AGAAACGCAA	GATCTCCGAC	GGTGACAAGC	2650
TGGCCGGCCG	CACCGGCAAC	AAGGGCGTGA	TCCGCAAGAT	CCTGCCGGTT	2700
GAGGACATGC	CGTTCCCTTG	CGACGGCACC	CCGGTGGACA	TTATTTTGAA	2750
CACCCACGGC	GTGCCGCGAC	GGATGAACAT	CGGCCAGATT	TTGGAGACCC	2800
ACCTGGGTTG	GTGTGCCCAC	AGCGGCTGGA	AGGTCGACGC	CGCCAAGGGG	2850
GTTCCGGACT	GGGCCGCCAG	GCTGCCCGAC	GAAGTGTCTG	AGGCGCATGC	2900
GAACGCCATT	GTGTGACGCG	CGGTGTTTCA	CGGCGCCCAG	GAGGCCGAGC	2950
TGCAGGGCCT	GTTGTCGTGC	ACGCTGCCCA	ACCGCGACGG	TGACGTGCTG	3000
GTCGACGCCG	ACGGCAAGGC	CATGCTCTTC	GACGGGCGCA	GCGGCGAGCC	3050
GTTCCCGTAC	CCGGTCACGG	TTGGCTACAT	GTACATCATG	AAGCTGCACC	3100
ACCTGGTGGA	CGACAAGATC	CACGCCCGCT	CCACCGGGCC	GTACTCGATG	3150
ATCACCCAGC	AGCCGCTGGG	CGGTAAGGCG	CAGTTCGGTG	GCCAGCGGTT	3200
CGGGGAGATG	GAGTGCTGGG	CCATGCAGGC	CTACGGTGCT	GCCTACACCC	3250
TGCAGGAGCT	GTTGACCATC	AAGTCCGATG	ACACCGTCGG	CCGCGTCAAG	3300
GTGTACGAGG	CGATCGTCAA	GGGTGAGAAC	ATCCCGGAGC	CGGGCATCCC	3350
CGAGTCGTTT	AAGGTGCTGC	TCAAAGAACT	GCAGTCGCTG	TGCCTCAACG	3400
TCGAGGTGCT	ATCGAGTGAC	GGTGCGGCGA	TGGAAGTGC	CGAAGGTGAG	3450
GACGAGGACC	TGGAGCGGGC	CGCGGCCAAC	CTGGGAATCA	ATCTGTCCCC	3500
CAACGAATCC	GCAAGTTTTC	AGGATCTTGC	GTAA		3534

2) INFORMATION FOR SEQ ID NO: 2073

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073

CCGAGCAACA TGATTGAACC ATCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2074

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074

CCGAGCAACA TGATTGAAGC TTCCACCAAC TGGCTCGG

38

2) INFORMATION FOR SEQ ID NO: 2075

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075

CCGAGCCAGG TTCTGAAGTC TCTGCATTAT TAGGTGCTCG G

41

2) INFORMATION FOR SEQ ID NO: 2076

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single

1076

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076

CCGAGCYGAY AACATTTTCA GATTCACCCA RGC GCTCGG

39

2) INFORMATION FOR SEQ ID NO: 2077

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077

CCGAGCAACC GATCCAGCTC CAGCTACGCT CGG

33

2) INFORMATION FOR SEQ ID NO: 2078

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078

CCGAGCCTTG GTCTTCGGCC AAATGAACGC TCGG

34

2) INFORMATION FOR SEQ ID NO: 2079

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079

CCGAGCGTTC AGTTACTTCA GTCCAAGCCG GCTCGG

36

2) INFORMATION FOR SEQ ID NO: 2080

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080

CCGAGCCGAA GAGGGCCAAG ATGTCGCTCG G

31

2) INFORMATION FOR SEQ ID NO: 2081

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081

GRATYRTYAA AGTTGGTGAG GAAG

24

2) INFORMATION FOR SEQ ID NO: 2082

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082

CMACTTCATC YCGCTTCGTA CC

22

2) INFORMATION FOR SEQ ID NO: 2083

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1078

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083

CCGCCGATGT TCCGTAAATT ACTTGAIGAA GGTCGAGCCG GCGG

44

2) INFORMATION FOR SEQ ID NO: 2084

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084

CACGCGTCAA CACCCGTACA AGTCGTCTTT TGC GCGTG

38

2) INFORMATION FOR SEQ ID NO: 2085

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085

CAAACTAAAG AACATATCTT GCTA

24

2) INFORMATION FOR SEQ ID NO: 2086

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086

ATATAATTTG CATCACCTTC AAG

23

2) INFORMATION FOR SEQ ID NO: 2087

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087

TCAGCTCGTG GGATTAGGAG AG

22

2) INFORMATION FOR SEQ ID NO: 2088

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088

AGGCTTCACG CTGTTAGGCT GA

22

2) INFORMATION FOR SEQ ID NO: 2089

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089

ATGCTGAACT TATTGACCTT

20

2) INFORMATION FOR SEQ ID NO: 2090

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1080

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090

CGTTACTGGA GTCGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2091

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091

CGCGACTTGA GATGGAAGTT AGTGAGCTTC TTGGTCGCG

39

2) INFORMATION FOR SEQ ID NO: 2092

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092

CGCGACGAAA GAACTTCCTG AAGGTCGTGC AGGTCCAG

38

2) INFORMATION FOR SEQ ID NO: 2093

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093

TGTTGGCAAT CGAAGACACC

20

2) INFORMATION FOR SEQ ID NO: 2094

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094

TTCAATTTCT TGACCTACTT TCAA

24

2) INFORMATION FOR SEQ ID NO: 2095

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095

CGGTCGGGTT GAACGTGG

18

2) INFORMATION FOR SEQ ID NO: 2096

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096

CGCGACCGGT ACCACGGCCA GTAATCGTGT CGCG

34

2) INFORMATION FOR SEQ ID NO: 2097

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1185 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1082

- (A) ORGANISM: *Mycoplasma pneumoniae*
 (B) STRAIN: ATCC 29342
 (C) ACCESSION NUMBER: AE000019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097

ATGGCAAGAG	AGAAATTTGA	CCGATCTAAA	CCCCACGTTA	ATGTAGGTAC	50
TATTGGCCAC	ATTGACCACG	GTAAAACAAC	TTTAACAGCA	GCTATTTGTA	100
CTGTATTAGC	AAAAGAAGGT	AAATCAGCTG	CTACTCGTTA	CGACCAAATC	150
GATAAGGCTC	CGGAAGAAAA	AGCACGGGGA	ATTACGATTA	ACTCCGCTCA	200
CGTGGAGTAC	TCCTCTGACA	AGCGTCACTA	TGCTCACGTT	GA CTGTCCAG	250
GACACGCTGA	CTACATTAAG	AACATGATTA	CTGGTGCTGC	ACAAAATGGAT	300
GGTGCCATTC	TAGTAGTTTC	AGCAACTGAC	AGTGTTATGC	CCCAAACCCG	350
TGAACACATT	TTGTTGGCCC	GCCAAGTGGG	TGTGCCACGC	ATGGTAGTGT	400
TCCTAAACAA	GTGTGACATT	GCAACTGATG	AAGAAGTGCA	AGAGTTAGTA	450
GCAGAAGAGG	TACGTGACTT	ATTA ACTTCT	TACGGCTTTG	ATGGCAAGAA	500
CACCCCTATT	ATTTATGGTT	CTGCACTTAA	AGCGCTTGAA	GGTGATCCTA	550
AGTGGGAAGC	TAAGATCCAT	GATTTAATGA	ATGCAGTTGA	TGAATGGATT	600
CCA ACTCCTG	AACGTGAAGT	GGCAAACCC	TTCTTGTTGG	CAATCGAAGA	650
CACCATGACG	ATTACTGGCC	GTGGTACCGT	GGTTACCGGT	CGGGTTGAAC	700
GTGGTGAATT	GAAAGTAGGT	CAAGAAATTG	AAATCGTTGG	TTTACGTCCA	750
ATCCGTAAAG	CAGTTGTTAC	CGGAATCGAA	ATGTTCAAAA	AGGAACTTGA	800
TTCAGCAATG	GCTGGGGACA	ACGCTGGGGT	ATTACTCCGT	GGTGTGGACC	850
GTAAAGAAGT	GGAACGTGGT	CAAGTGTTAG	CTAAACCAGG	TTCGATTAAA	900
CCGCACAAGA	AATTTAAAGC	GGAAATCTAT	GCTTTAAAGA	AGGAAGAAGG	950
TGGTCGTCAC	ACCGGTTTCT	TAAACGGTTA	CCGTCCCCAA	TTCTACTTCC	1000
GTACTACAGA	CGTTACTGGT	TCGATTTCCT	TACCAGAAAA	CACCGAAATG	1050
GTGCTACCAG	GTGACAATAC	CTCGATTACA	GTTGAACTAA	TTGCACCAAT	1100
TGCTTG TGAA	AAAGGTAGTA	AGTTCTCCAT	CCGTGAAGGT	GGTCGAACGG	1150
TTGGTGCTGG	TTCAGTCACG	GAAGTGCTTG	AATAG		1185

2) INFORMATION FOR SEQ ID NO: 2098

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098

CTGAGTCACA CCGACAAACG TC

22

2) INFORMATION FOR SEQ ID NO: 2099

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099

CCAGGACTGA ACGGGATACG AA

22

2) INFORMATION FOR SEQ ID NO: 2100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100

GCGAGACGAT AGGTTGTC

18

2) INFORMATION FOR SEQ ID NO: 2101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2609 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv
- (C) ACCESSION NUMBER: Z79701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101

CAGCCCGCGA	GCGTAACCTG	GCTGCGATTT	CCGGCGCGGA	TTTTCGCAGT	50
GCGGTTACGC	TCGGAAAGCG	CGGGCCTCGC	CCACGCGGCG	GATGATGTCA	100
GCGGGGTGGT	CCTCGGCGAC	GACCCGGACC	ACGATCCACC	CGTAGCGGTG	150
CTGGACTTTC	TCGTGCCGGA	GGATGTCTTT	CCGGTAGTGG	TAGCGACTGG	200
TCAGATGGTG	GTCGCCGTCA	TACTCGGCCG	CGACCTTGAT	GTCTTGCCAG	250
CCCATATCCA	AATGGGCTTC	CGCCCAGCCC	CATTCGTTGC	GCACCGCGAT	300
CTGCGTCTGG	GGGCGCGGAA	AGCCGGCGCG	GATCAACAAC	AAGCGCAGCC	350
AGGTTTCCTT	GGGGGACTGG	GCACCGCCGT	CGACGAGGTC	CAGAGCGGCT	400
CTTGCGGCCCT	TCATGCCACG	GCGGCCCCGA	TAGCGCTCGA	TCAGCGGCTC	450
GACGTCGGCC	ACCTTCAAAT	CGGTGGCCTG	TATCAGGGCG	TCGACGGCCG	500
CGACGGCGGG	GTCCAATGGA	AATCGACTGG	TCAGGTCGAG	CGCCGTTTCG	550
TCCGGTGTGG	TCACGCGCAT	GCCCTCGATG	ACGCAGATCT	CGTCGGGCTC	600
GATGCGCTCT	TCCCAGACTT	GCAGCCCCGG	GGCACGGCGG	CGGTTGGTGT	650
CGATGATCGC	GGCGGGAAGA	TCCGCGTCGA	TCCACTTGGC	GCCATGGAAG	700
GCAGAAGCCG	AGTAGCCGGC	CAGCACGCCG	CGGCGGCGCG	AGCGCAGCCA	750
CAGCGCTTTT	GCACGCAATT	GCGCGGTCAG	TCCACACACC	TGCGGCACGT	800

1084

ACACGTCTTT	ATGTAGCGCG	ACATACCTGC	TGCGCAATTC	GTAGGGCGTC	850
AATACACCCG	CAGCCAGGGC	CTCGTGCCCC	AGAAAAGGGAT	CCGTCATGGT	900
CGAAGTGTGC	TGAGTCACAC	CGACAAACGT	CACGAGCGTA	ACCCCAGTGC	950
GAAAGTTCCC	GCCGGAAATC	GCAGCCACGT	TACGCTCGTG	GACATACCGA	1000
TTTCGGCCCC	GCCGCGGCGA	GACGATAGGT	TGTCGGGGTG	ACTGCCACAG	1050
CCACTGAAGG	GGCCAAACCC	CCATTCGTAT	CCCGTTCACT	CCTGGTTACC	1100
GGAGGAAACC	GGGGGATCGG	GCTGGCGATC	GCACAGCGGC	TGGCTGCCGA	1150
CGGCCACAAG	GTGGCCGTCA	CCCACCGTGG	ATCCGGAGCG	CCAAAGGGGC	1200
TGTTTGGCGT	CGAATGTGAC	GTCACCGACA	GCGACGCCGT	CGATCGCGCC	1250
TTACGGCGG	TAGAAGAGCA	CCAGGGTCCG	GTCGAGGTGC	TGGTGTCCAA	1300
CGCCGGCCTA	TCCGCGGACG	CATTCCCTCAT	GCGGATGACC	GAGGAAAAGT	1350
TCGAGAAGGT	CATCAACGCC	AACCTCACCG	GGGCGTTCCG	GGTGGCTCAA	1400
CGGGCATCGC	GCAGCATGCA	GCGCAACAAA	TTGGTTCGAA	TGATATTTCAT	1450
AGGTTCCGGT	TCCGGCAGCT	GGGGCATCGG	CAACCAGGCC	AACTACGCAG	1500
CCTCCAAGGC	CGGAGTGATT	GGCATGGCCC	GCTCGATCGC	CCGCGAGCTG	1550
TCGAAGGCAA	ACGTGACCGC	GAATGTGGTG	GCCCCGGGCT	ACATCGACAC	1600
CGATATGACC	CGCGCGCTGG	ATGAGCGGAT	TCAGCAGGGG	GCGCTGCAAT	1650
TTATCCCAGC	GAAGCGGGTC	GGCACCCCCG	CCGAGGTCGC	CGGGGTGGTC	1700
AGCTTCCTGG	CTTCCGAGGA	TGCGAGCTAT	ATCTCCGGTG	CGGTCAATCC	1750
GGTCGACGGC	GGCATGGGTA	TGGGCCACTG	ACACAACACA	AGGACGCACA	1800
TGACAGGACT	GCTGGACGGC	AAACGGATTG	TGGTTAGCGG	AATCATCACC	1850
GACTCGTCGA	TCGCGTTTCA	CATCGCACGG	GTAGCCCAGG	AGCAGGGCGC	1900
CCAGCTGGTG	CTCACCGGGT	TCGACCGGCT	GCGGCTGATT	CAGCGCATCA	1950
CCGACCGGCT	GCCGGCAAAG	GCCCCGCTGC	TCGAACTCGA	CGTGCAAAAC	2000
GAGGAGCACC	TGGCCAGCTT	GGCCGGCCGG	GTGACCGAGG	CGATCGGGGC	2050
GGGCAACAAG	CTCGACGGGG	TGGTGCATTC	GATTGGGTTC	ATGCCGCAGA	2100
CCGGGATGGG	CATCAACCCG	TTCTTCGACG	CGCCCTACGC	GGATGTGTCC	2150
AAGGGCATCC	ACATCTCGGC	GTATTCGTAT	GCTTCGATGG	CCAAGGCGCT	2200
GCTGCCGATC	ATGAACCCCC	GAGGTTCCAT	CGTCGGCATG	GACTTCGACC	2250
CGAGCCGGGC	GATGCCGGCC	TACAACTGGA	TGACGGTCGC	CAAGAGCGCG	2300
TTGGAGTCGG	TCAACAGGTT	CGTGGCGCGC	GAGGCCGGCA	AGTACGGTGT	2350
GCGTTCGAAT	CTCGTTGCCG	CAGGCCCTAT	CCGGACGCTG	GCGATGAGTG	2400
CGATCGTCGG	CGGTGCGCTC	GGCGAGGAGG	CCGGCGCCCA	GATCCAGCTG	2450
CTCGAGGAGG	GCTGGGATCA	GCGCGCTCCG	ATCGGCTGGA	ACATGAAGGA	2500
TGCGACGCCG	GTGCGCAAGA	CGGTGTGCGC	GCTGCTGTCT	GAATGGCTGC	2550
CGGCGACCAC	GGGTGACATC	ATCTACGCCG	ACGGCGGCGC	GCACACCCAA	2600
TTGCTCTAG					2609

2) INFORMATION FOR SEQ ID NO: 2102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102

CACCTTCACC CTGACCGACG

20

2) INFORMATION FOR SEQ ID NO: 2103

1085

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103

CGAACCAGCG GAAATAGTTG GAC

23

2) INFORMATION FOR SEQ ID NO: 2104

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104

CTGGGCATGG CICGAGTC

18

2) INFORMATION FOR SEQ ID NO: 2105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37rv
- (C) ACCESSION NUMBER: U68480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105

ATGACACAGT	GCGCGAGCAG	ACGCAAAAGC	ACCCCAAATC	GGGCGATTTT	50
GGGGGCTTTT	GCGTCTGCTC	GCGGGACGCG	CTGGGTGGCC	ACCATCGCCG	100
GGCTGATTGG	CTTTGTGTTG	TCGGTGGCGA	CGCCGCTGCT	GCCCGTCGTG	150
CAGACCACCG	CGATGCTCGA	CTGGCCACAG	CGGGGGCAAC	TGGGCAGCGT	200
GACCGCCCCG	CTGATCTCGC	TGACGCCCGT	CGACTTTACC	GCCACCGTGC	250
CGTGCGACGT	GGTGCGCGCC	ATGCCACCCG	CGGGCGGGGT	GGTGCTGGGC	300
ACCGCACCCA	AGCAAGGCAA	GGACGCCAAT	TTGCAGGCGT	TGTTTCGTCG	350
CGTCAGCGCC	CAGCGCGTGG	ACGTCACCGA	CCGCAACGTG	GTGATCTTGT	400
CCGTGCCCGC	CGAGCAGGTG	ACGTCCCCGC	AGTGTCAACG	CATCGAGGTC	450

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ACCTCTACCC	ACGCCGGCAC	CTTCGCCAAC	TTCGTGCGGC	TCAAGGACCC	500
GTCGGGCGCG	CCGCTGCGCA	GCGGCTTCCC	CGACCCCAAC	CTGCGCCCGC	550
AGATTGTCGG	GGTGTTCACC	GACCTGACCG	GGCCCGCGCC	GCCCGGGCTG	600
GCGGTCTCGG	CGACCATCGA	CACCCGGTTC	TCCACCCGGC	CGACCACGCT	650
GAAACTGCTG	GCGATCATCG	GGGCGATCGT	GGCCACCGTC	GTCGCACTGA	700
TCGCGTTGTG	GCGCCTGGAC	CAGTTGGACG	GGCGGGGCTC	AATTGCCCAG	750
CTCCTCCTCA	GGCCGTTCCG	GCCTGCATCG	TCGCCGGGCG	GCATGCGCCG	800
GCTGATTCCG	GCAAGCTGGC	GCACCTTCAC	CCTGACCGAC	GCCGTGGTGA	850
TATTGCGCTT	CCTGCTCTGG	CATGTCATCG	GCGCGAATTC	GTCGGACGAC	900
GGCTACATCC	TGGGCATGGC	CCGAGTCGCC	GACCACGCCG	GCTACATGTC	950
CAACTATTTT	CGCTGGTTTC	GCAGCCCCGA	GGATCCCTTC	GGCTGGTATT	1000
ACAACCTGCT	GGCGCTGATG	ACCCATGTCA	GCGACGCCAG	TCTGTGGATG	1050
CGCCTGCCAG	ACCTGGCCGC	CGGGCTAGTG	TGCTGGCTGC	TGCTGTCGCG	1100
TGAGGTGCTG	CCCCGCCTCG	GGCCGGCGGT	GGAGGCCAGC	AAACCCGCCT	1150
ACTGGGCGGC	GGCCATGGTC	TTGCTGACCG	CGTGGATGCC	GTTCAACAAC	1200
GGCCTGCGGC	CGGAGGGCAT	CATCGCGCTC	GGCTCGCTGG	TCACCTATGT	1250
GCTGATCGAG	CGGTCCATGC	GGTACAGCCG	GCTCACACCG	GCGGCGCTGG	1300
CCGTCGTTAC	CGCCGCATT	ACACTGGGTG	TGCAGCCAC	CGGCCTGATC	1350
GCGGCGCCG	CGCTGGTGGC	CGGCGGCCGC	CCGATGCTGC	GGATCTTGGT	1400
GCGCCGYCAT	CGCCTGGTCG	GCACGTTGCC	GTTGGTGTGC	CCGATGCTGG	1450
CCGCCGGCAC	CGTCATCCTG	ACCGTGGTGT	TCGCCGACCA	GACCTGTCA	1500
ACGGTGTTGG	AAGCCACCAG	GGTTCGCGCC	AAAATCGGGC	CGAGCCAGGC	1550
GTGGTATACC	GAGAACCTGC	GTTACTACTA	CCTCATCCTG	CCCACCGTCG	1600
ACGGTTCGCT	GTCGCGGCGC	TTCGGCTTTT	TGATCACCGC	GCTATGCCTG	1650
TTACCCGCGG	TGTTTCATCAT	GTTGCGGCGC	AAGCGAATTC	CCAGCGTGGC	1700
CCGCGGACCG	GCGTGGCGGC	TGATGGGCGT	CATCTTCGGC	ACCATGTTCT	1750
TCCTGATGTT	CACGCCCACC	AAGTGGGTGC	ACCACTTCGG	GCTGTTCGCC	1800
GCCGTAGGGG	CGGCGATGGC	CGCGCTGACG	ACGGTGTTGG	TATCCCCATC	1850
GGTGCTGCGC	TGGTCGCGCA	ACCGGATGGC	GTTCTTGCCG	GCGTTATTCT	1900
TCCTGCTGGC	GTTGTGTTGG	GCCACCACCA	ACGGCTGGTG	GTATGTCCTC	1950
AGCTACGGTG	TGCCGTTCAA	CAGCGCGATG	CCGAAGATCG	ACGGGATCAC	2000
AGTCAGCACA	ATCTTTTTCG	CCCTGTTTGC	GATCGCCGCC	GGCTATGCGG	2050
CCTGGCTGCA	CTTCGCGCCC	CGCGGCGCCG	GCGAAGGGCG	GCTGATCCGC	2100
GCGCTGACGA	CAGCCCCGGT	ACCGATCGTG	GCCGGTTTCA	TGGCGGCGGT	2150
GTTCGTGCGG	TCCATGGTGG	CCGGGATCGT	GCGACAGTAC	CCGACCTACT	2200
CCAACGGCTG	GTCCAACGTG	CGGGCGTTTG	TCGGCGGCTG	CGGACTGGCC	2250
GACGACGTAC	TCGTGAGACC	TGATACCAAT	GCGGGTTTCA	TGAAGCCGCT	2300
GGACGGCGAT	TCGGGTTCTT	GGGGCCCCTT	GGGGCCGCTG	GGTGGAGTCA	2350
ACCCGGTCCG	CTTCACGCCC	AACGGCGTAC	CGGAACACAC	GGTGGCCGAG	2400
GCGATCGTGA	TGAAACCCAA	CCAGCCCGGC	ACCGACTACG	ACTGGGATGC	2450
GCCGACCAAG	CTGACGAGTC	CTGGCATCAA	TGGTTCTACG	GTGCCGCTGC	2500
CCTATGGGCT	CGATCCCGCC	CGGGTACCGT	TGGCAGGCAC	CTACACCACC	2550
GGCGCACAGC	AACAGAGCAC	ACTCGTCTCG	GCGTGGTATC	TCCTGCCTAA	2600
GCCGGACGAC	GGGCATCCGC	TGGTCGTGGT	GACCGCCGCG	GGCAAGATCG	2650
CCGGCAACAG	CGTGCTGCAC	GGGTACACCC	CCGGGCAGAC	TGTGGTGCTC	2700
GAATACGCCA	TGCCGGGACC	CGGAGCGCTG	GTACCCGCCG	GGCGGATGGT	2750
GCCCGACGAC	CTATACGGAG	AGCAGCCCAA	GGCGTGGCGC	AACCTGCGCT	2800
TCGCCCCGAGC	AAAGATGCCC	GCCGATGCCG	TCGCGGTCCG	GGTGGTGGCC	2850
GAGGATCTGT	CGCTGACACC	GGAGGACTGG	ATCGCGGTGA	CCCCGCCGCG	2900
GGTACCGGAC	CTGCGCTCAC	TGCAGGAATA	TGTGGGCTCG	ACGCAGCCGG	2950
TGCTGCTGGA	CTGGGCGGTC	GGTTTGGCCT	TCCCGTGCCA	GCAGCCGATG	3000
CTGCACGCCA	ATGGCATCGC	CGAAATCCCG	AAGTTCCGCA	TCACACCGGA	3050
CTACTCGGCT	AAGAAGCTGG	ACACCGACAC	GTGGGAAGAC	GGCACTAACG	3100
GCGGCCTGCT	CGGGATCACC	GACCTGTTGC	TGCGGGCCCA	CGTCATGGCC	3150
ACCTACCTGT	CCCGCGACTG	GGCCCCGCGT	TGGGGTTCCC	TGCGCAAGTT	3200
CGACACCCTG	GTCGATGCCC	CTCCCCGCCA	GCTCGAGTTG	GGCACCPCGA	3250
CCCGCAGCGG	CCTGTGGTCA	CCGGGCAAGA	TCCGAATTGG	TCCATAG	3297

2) INFORMATION FOR SEQ ID NO: 2106

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106

GCGAGCAGAG CACGCCCTCC TCGCCGCTCG C

31

2) INFORMATION FOR SEQ ID NO: 2107

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107

GCGAGCTCCC CATCTCTGGT TGGCAGCTC GC

32

2) INFORMATION FOR SEQ ID NO: 2108

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108

GCGGGCAACT TCRTCAAGAA GGTTGGTTAC AACCCGCCCC C

41

2) INFORMATION FOR SEQ ID NO: 2109

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109

GCGGGCCCAA TCTCTGGTTG GAAYGGTGAC AAGCCCGC

38

2) INFORMATION FOR SEQ ID NO: 2110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110

GCGGGCCCTT AACGATTTC ACGAATCTGG ATTCAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111

GCGGGCATGA TTGAAGCCAC CACCAACGCT TCCTGGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112

GCGGGCTTGA TGAAGTTTGG GGTTCCTTG ACAATTGCG CGC

43

2) INFORMATION FOR SEQ ID NO: 2113

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113

GCGGGCACAA GGGTTGGACT AAGGAAACCA AGGCAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2114

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114

GCGGGCATCG ATGCTATTGA ACCACCTGTC AGACCGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2115

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115

GCGGGCTTGA TGATTTCTC GAATCTAGAT TGGGCCCCG

39

2) INFORMATION FOR SEQ ID NO: 2116

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116

GCGGGCGGTA AGTCCACCGG TAAGACCTTG TTGGCCCCG

39

2) INFORMATION FOR SEQ ID NO: 2117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCGC

36

2) INFORMATION FOR SEQ ID NO: 2118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCGTATCTG TTCTTGCCCC GC

42

2) INFORMATION FOR SEQ ID NO: 2119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCTAAGG CTGTTCCATT CGTTGCCCCG

40

2) INFORMATION FOR SEQ ID NO: 2120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1091

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCA AGTTCCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19

2) INFORMATION FOR SEQ ID NO: 2124

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

2) INFORMATION FOR SEQ ID NO: 2125

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACGCGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

2) INFORMATION FOR SEQ ID NO: 2126

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

18

2) INFORMATION FOR SEQ ID NO: 2127

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1093

(D) TOPOLOGY: 'Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

22

2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TCGGTTG

37

2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTTAA	TATCTAAAGA	AGAGTTAATA	AAACTCGCAT	ATAGCATTAG	50
ACCAAGAGAA	AATGAGTATA	AACTATACT	AACTAATTTA	GACGAATATA	100
ATAAGTTAAC	TACAAACAAT	AATGAAAATA	AATATTTGCA	ATTAAAAAAA	150
CTAAATGAAT	CAATTGATGT	TTTTATGAAT	AAATATAAAA	CTTCAAGCAG	200
AAATAGAGCA	CTCTCTAATC	TAAAAAAGA	TATATTAAAA	GAAGTAATTC	250
TTATTAAAAA	TTCCAATACA	AGCCCTGTAG	AAAAAAATTT	ACATTTTGTA	300
TGGATAGGTG	GAGAAGTCAG	TGATATTGCT	CTTGAATACA	TAAAACAATG	350
GGCTGATATT	AATGCAGAAT	ATAATATTAA	ACTGTGGTAT	GATAGTGAAG	400
CATTCTTAGT	AAATACACTA	AAAAGGCTA	TAGTTGAATC	TTCTACCACT	450
GAAGCATTAC	AGCTACTAGA	GGAAGAGATT	CAAAATCCTC	AATTTGATAA	500
TATGAAATTT	TACAAAAAAA	GGATGGAATT	TATATATGAT	AGACAAAAAA	550
GGTTTATAAA	TTATTATAAA	TCTCAAATCA	ATAAACCTAC	AGTACCTACA	600
ATAGATGATA	TTATAAAGTC	TCATCTAGTA	TCTGAATATA	ATAGAGATGA	650
AACTGTATTA	GAATCATATA	GAACAAATTC	TTTGAGAAAA	ATAAATAGTA	700
ATCATGGGAT	AGATATCAGG	GCTAATAGTT	TGTTTACAGA	ACAAGAGTTA	750
TTAAATATTT	ATAGTCAGGA	GTTGTTAAAT	CGTGGAAATT	TAGCTGCAGC	800

ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCAC	CTGATTTATT	TAAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCGT	TGGGAAATGA	TAAAAATTAGA	950
GGCTATTATG	AAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAAC	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAAAA	TAGCTTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTAAAC	CAACACCTTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	TAAAAATTTT	CATGATTCAT	1300
TATTTAATTC	AGCTACCGCA	GAAAACTCTA	TGTTTTTAAAC	AAAAATAGCA	1350
CCATACTTAC	AAGTAGGTTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTTT	ATAAATTTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTAAAG	CATCAGATTT	AATAGAATTT	1500
AAATTTCCAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAAA	ATATCAATTT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGGA	TCTCTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAAAT	TGCCCCCGA	CAAAAACTAT	TTATTAAATA	ATAAAATTC	1700
ATCAAACAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTTATTT	1800
TCTAAAAATC	CTAAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAATATAG	GATACCTGAA	AGATTAAAAA	ATAAGGAAAA	AGTAAAAGTA	1950
ACCTTTATTG	GACATGGTAA	AGATGAATTC	AACACAAGCG	AATTTGCTAG	2000
ATTAAGTGTA	GATTCACCTT	CCAATGAGAT	AAGTTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAAATGTAG	AAGTAACTT	ACTTGGATGT	2100
AATATGTTTA	GTTATGATTT	TAATGTTGAA	GAAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CACTTTACCT	GATGTAAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	ATGAAGTAAG	AATTAATAGT	2250
GAGGGAAGAA	AAGAACTTCT	GGCTCACTCA	GGTAAATGGA	TAAATAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTTGATT	2350
CTATAGATAA	TAAGCTAAAA	GCAAAGTCCA	AGAATATTCC	AGGATTAGCA	2400
TCAATATCAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTTAA	ATAATCTTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	GAAAAATTAG	AGCCTGTTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATTT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	TAAAAAAATT	AAATAATCTA	GATGAGAAGT	2650
ATTTAATATC	TTTTGAAGAT	ATCTCAAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAAA	2750
AGAAATTTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TAAACGCAG	CATTCTTTAT	2900
TCAATCATT	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACTATTTAG	TACAGGTTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTTAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATTA	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTTAGCA	ATAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATTT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTTTAA	TCATTTGTCT	GAATCTAAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTTTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTTAAT	AATAATTCGA	TAAAAC	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGGG	ATCAGGACAC	ACAGTGACTG	3550
GTAATATAGA	TCACTTTTTC	TCATCTCCAT	CTATAAGTTC	TCATATTCCT	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATTT	3650

TTCAAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTTGGT	3700
GGGAACTGG	AGCAGTTCCA	GGTTTAAGAT	CATTGGAAAA	TGACGGAACT	3750
AGATTACTTG	ATTCAATAAG	AGATTTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAAAATT	AACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAECTACTAA	CGAAATTAGA	AACAAATTAT	CTTATTCATT	3950
TGATGGAGCA	GGAGGAACTT	ACTCTTTATT	ATTATCTTCA	TATCCAATAT	4000
CAACGAATAT	AAATTTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAAGGAAA	4100
GTTAATAAAA	GATGTTTTAA	GTAAAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAACAATA	GATTTTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATTA	GTTTAATAAT	4250
AGAAATAAAT	CTTGTTGCAA	AATCTTATAG	TTTGTTATTG	TCTGGGGATA	4300
AAAATTATTT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAATACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTTGGAGCTA	TATCTAAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTTA	ACAGTAAAGA	TTTTATTGCT	GAAGATATAA	ATGTATTTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTT	TCTATTTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATTT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTTGTGAAA	AATTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTTTGA	CAATATAAGT	TTCTGGAAAT	TGTTTGGGTT	TGAAAAATATA	5200
AATTTTGTAA	TCGATAAATA	CTTTACCCTT	GTTGGTAAAA	CTAATCTTGG	5250
ATATGTAGAA	TTTATTTGTG	ACAATAATAA	AAATATAGAT	ATATATTTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTTAATAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACA	AAAAAGTAAA	TATAAATTTA	GATAGTTCTT	5600
CTTTTGAGTA	TAAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTTAGTTAGA	5650
TACTTAGAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AATACTCAAT	CATTTAATAA	AATGAGTATA	GATTTTAAAG	5750
ATATTAAAAA	ACTATCATTA	GGATATATAA	TGAGTAATTT	TAAATCATTT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATTTA	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTTAATGGTA	GTAGATACTA	CTTTGATACT	6000
GATACCGCTA	TTGCCTTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTTGAT	AGTGATTGTG	TAGTGAAAAT	AGGTGTGTTT	AGTACCTCTA	6100
ATGGATTTGA	ATATTTTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATTC	TTAACTTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAAGCAGT	TACCGGATTG	CAAACATTG	6250
ATAGTAAAAA	ATATTACTTT	AATACTAACA	CTGCTGAAGC	AGCTACTGGA	6300
TGGCAAACCTA	TTGATGGTAA	AAAATATTAC	TTTAATACTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAAA	CTATTGATGG	TAAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTAA	TGGTAAACAT	6450
TTTTATTTTA	ATACTGATGG	TATTATGCAG	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATTT	GAATATTTTG	CACCTGCTAA	TACGGATGCT	AACAACATAG	6550
AAGGTCAAGC	TATACTTTAC	CAAAATGAAT	TCTTAACTTT	GAATGGTAAA	6600
AAATATTACT	TTGGTAGTGA	CTCAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAATCCTAA	TAATGCTATT	GCTGCAATTC	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATATTAC	TATTGAAAGA	AATAATTCTT	ATTTTGATGC	6800
TAATAATGAA	TCTAAAATGG	TAACAGGAGT	ATTTAAAGGA	CCTAATGGAT	6850
TTGAGTATTT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCAG	6900

GCTATAGTTT	ACCAGAACAA	ATTCTTAACT	TTGAATGGCA	AAAAATATTA	6950
TTTTGATAAT	GACTCAAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACTATTG	ATGGTAAAAA	ATATTACTTT	AATACTAACA	7150
CTTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTTAAAG	GACCTAATGG	7250
ATTTGAATAC	TTTGCACCTG	CTAATACGGA	TGCTAACAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAAT	AAATTCTTAA	CTTTGAATGG	TAAAAAATAT	7350
TACTTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTTA	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTATTT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATTCCTATA	TTTACATGAC	AATATATATT	ATTTTGGTAA	7700
TAATTCAAAA	GCGGCTACTG	GTTGGGTAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAAAT	TTTACTTTAG	AAATGGTTTA	CCTCAGATAG	GAGTGTTTAA	7850
AGGGTCTAAT	GGATTGAAT	ACTTTGCACC	TGCTAATACG	GATGCTAACA	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAAA	ATAGATTCCT	ACATTTACTT	7950
GGAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGTG	TTATATATTT	CTTTGGTGTT	8100
GATGGAGTAA	AAGCCCCTGG	GATATATGGC	TAA		8133

2) INFORMATION FOR SEQ ID NO: 2130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTTAG	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTACTCAA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAAATATTT	AAAATTAAAA	150
GATATAAATA	GTTTAAACAGA	TATTTATATA	GATACATATA	AAAAATCTGG	200
TAGAAATAAA	GCCTTAAAAA	AATTTAAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACTCCAG	TTGAGAAAAA	TTTACATTTT	300
GTTTGGATTG	GAGGTCAAAAT	AAATGACACT	GCTATTAATT	ATATAAATCA	350
ATGGAAAGAT	GTAAATAGTG	ATTATAATGT	TAATGTTTTT	TATGATAGTA	400
ATGCATTTTT	GATAAACACA	TTGAAAAAAA	CTGTAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAC	TTAAATGACC	CTAGATTTGA	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTTAT	GATAAACAGA	550
AAAATTTCAT	AAACTACTAT	AAAGCTCAAA	GAGAAGAAAA	TCCTGAACCT	600

ATAATTGATG	ATATTGTAAA	GACATATCTT	TCAAATGAGT	ATTCAAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAAGA	ATCCTTAAAT	AAAATTACAC	700
AGAATAGTGG	AAATGATGTT	AGAAACTTTG	AAGAATTTAA	AAATGGAGAG	750
TCATTCAACT	TATATGAACA	AGAGTTGGTA	GAAAGGTGGA	ATTTAGCTGC	800
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT	850
ATTTAGATGT	TGATATGTTA	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT	900
ATAGAGAAAC	CTAGTTCAGT	AACAGTGGAT	TTTTGGGAAA	TGACAAAAGTT	950
AGAAGCTATA	ATGAAATACA	AAGAATATAT	ACCAGAATAT	ACCTCAGAAC	1000
ATTTTGACAT	GTTAGACGAA	GAAGTTCAAA	GTAGTTTTGA	ATCTGTTCTA	1050
GCTTCTAAGT	CAGATAAATC	AGAAATATTC	TCATCACTTG	GTGATATGGA	1100
GGCATCACCA	CTAGAAGTTA	AAATTGCATT	TAATAGTAAG	GGTATTATAA	1150
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA	1200
AAACAAATCG	AGAATAGATA	TAAAATATTG	AATAATAGTT	TAAATCCAGC	1250
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA	1300
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTTAT	GATGGAACTA	1350
GGAAAGTATT	TAAGAGTTGG	TTTCTTCCCA	GATGTTAAAA	CTACTATTAA	1400
CTTAAGTGGC	CCTGAAGCAT	ATGCGGCAGC	TTATCAAGAT	TTATTAATGT	1450
TTAAAGAAGG	CAGTATGAAT	ATCCATTGGA	TAGAAGCTGA	TTTAAGAAAC	1500
TTTGAAATCT	CTAAAACATA	TATTTCTCAA	TCAACTGAAC	AAGAAATGGC	1550
TAGCTTATGG	TCATTTGACG	ATGCAAGAGC	TAAAGCTCAA	TTTGAAGAAT	1600
ATAAAAGGAA	TTATTTTGAA	GGTCTCTTG	GTGAAGATGA	TAATCTTGAT	1650
TTTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTTAG	AAAAAATATC	1700
TTCATTAGCA	AGAAGTTCAG	AGAGAGGATA	TATACACTAT	ATTGTTTCAGT	1750
TACAAGGAGA	TAAAATTAGT	TATGAAGCAG	CATGTAACCT	ATTTGCAAAG	1800
ACTCCTTATG	ATAGTGTACT	GTTTCAGAAA	AATATAGAAG	ATTCAGAAAT	1850
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT	1900
ATAAAATTCC	AAGTATAATT	TCTGATAGAC	CTAAGATTAA	ATTAACATTT	1950
ATTGGTCATG	GTAAAGATGA	ATTTAATACT	GATATATTTG	CAGGTTTTGA	2000
TGTAGATTCA	TTATCCACAG	AAATAGAAGC	AGCAATAGAT	TTAGCTAAAG	2050
AGGATATTTT	TCCTAAGTCA	ATAGAAATAA	ATTTATTAGG	ATGTAATATG	2100
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT	2150
TAAAGTTAAA	GATAAAATAT	CAGAATTAAT	GCCATCTATA	AGTCAAGACT	2200
CTATTATAGT	AAGTGCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA	2250
AGAAGAGAAT	TATTGGATCA	TTCTGGTGAA	TGGATAAATA	AAGAAGAAAG	2300
TATTATAAAG	GATATTTTAT	CAAAAGAATA	TATATCATTT	AATCCTAAAG	2350
AAAATAAAAT	TACAGTAAAA	TCTAAAAATT	TACCTGAGCT	ATCTACATTA	2400
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGATATTG	AAC TAGAAGA	2450
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTTCA	AATATAGATA	2500
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATTT	AACTTCTGAC	2550
TCTATTAATT	ATATAAAAAG	TGAATTTAAA	CTAATAGAAT	CTATTTCTGA	2600
TGCACTATGT	GACTTAAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATTTTA	2650
TATCTTTTGA	GGACATATCA	GAGACTGATG	AGGGATTTAG	TATAAGATTT	2700
ATTAATAAAG	AAACTGGAGA	ATCTATATTT	GTAGAAACTG	AAAAAACAAT	2750
ATTCTCTGAA	TATGCTAATC	ATATAACTGA	AGAGATTTCT	AAGATAAAAG	2800
GTACTATATT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAAATTTA	2850
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATTTT	TTATACAATC	2900
ATTAATAGAA	TATAATAGTT	CTAAAGAATC	TCTTAGTAAT	TTAAGTGTAG	2950
CAATGAAAGT	CCAAGTTTAC	GCTCAATTAT	TTAGTACTGG	TTTAAATACT	3000
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA	3050
AACTATAGAC	TTACTTCCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA	3100
CTATTATAGA	TGGTGTAAGT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGAA	3150
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT	3200
GGCAGTAAAT	TTAACAACAG	CTACAACTGC	AATCATTACT	TCATCTTTGG	3250
GGATAGCTAG	TGGATTTAGT	ATACTTTTAG	TTCTTTTAGC	AGGAATTTCA	3300
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTAATTC	GAGATAAGGC	3350
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTCATTAGTT	GAAACTGAAG	3400
GAGTATTTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATTTA	3450

GTGATATCAG	AAATAGATTT	TAATAATAAT	TCAATAGTTT	TAGGTAAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAACTTG	ATTTGTCAAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATTT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTTA	AGAAGCTTAG	AAAATGATGG	CACAAAACCTG	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTTATT	GGAGATATTT	3800
TGCTTTTATA	GCTGATGCTT	TAATAACAAC	ATTAAAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAT	TTAGATAGTA	ATACTAGAAG	TTTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAATTATCAT	ATTCTTTCTA	3950
TGGTTCAGGA	GGAACCTTATG	CATTGTCTCT	TTCTCAATAT	AATATGGGTA	4000
TAAATATAGA	ATTAAGTGAA	AGTGATGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAACCTAT	AGAATCTGAT	AAAATTAAAA	AAGGTGATTT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAAT	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTTCTGGTG	AGGTAAATGG	AAGTAATGGA	4200
TTTGTTTCTT	TAACATTTTC	AATTTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTTCT	GGCGAATTAA	4300
AAATATTGAT	GTTAAATTCA	AATCATATTC	AACAGAAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	GAAAAATATA	CCATATAGCT	TTGTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAATGG	TTCAACAAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTTCTTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTTGG	ATATTATAGT	AATAATTTGA	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTCTT	TCTTTGACTC	TACAAGATGA	AAAAACTATA	4650
AAGTTAAATA	GTGTGCATTT	AGATGAAAGT	GGAGTAGCTG	AGATTTTGAA	4700
GTTTCATGAAT	AGAAAAGGTA	ATACAAATAC	TTCAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATTT	TCGTTAATTT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATTTT	ATAATAAGTG	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTTCAATTAA	GTTTAATACA	CTAGAAACTA	ATTATACTTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTTCTC	TCAAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	TGTTAATAAA	GTTGTAATTT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCTGT	ATATGAAACA	AATAATACTT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAATT	ATATAAATGA	AAAAATAAAT	GTTAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTTGGC	AAATAAGCTA	TCTTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTTACA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTTGG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATTTT	ATATTAATAA	CTTTGGAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTTGT	GACTGTAGGC	GATGATAAAT	ACTACTTTAA	5600
TCCAATTAAT	GGTGGAGCTG	CTTCAATTGG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATG	GATTTAAATA	TTTTGCCCCA	GCTAATACAC	TTGATGAAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAATT	ATTGACGAAA	5800
ATATTTATTA	TTTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTTAGCCCA	GAAACAGGTA	AAGCTTTTAA	5900
AGGTCTAAAT	CAAATAGGTG	ATTATAAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTTGTT	AGTATAAATG	ATAATAAACA	CTATTTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATTT	6050
CTACTTTGCT	GAAAACGGAG	AAATGCAAAT	AGGAGTATTT	AATACAGAAG	6100
ATGGATTTAA	ATATTTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATTC	TGGTATATTA	AATTTCAATA	ATAAAAATTTA	6200
CTATTTTGAT	GATTCATTTA	CAGCTGTAGT	TGGATGGAAA	GATTTAGAGG	6250
ATGGTTCAAA	GTATTATTTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAATCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGCACCTG	CTAATACTGT	AAATGATAAT	ATTTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAGA	TGTATATTAT	6600
TTTGGAGAAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATTT	AATTGATGAT	ATAAAATATT	ATTTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AATAATTATT	ACTTTAATGA	6800
GAATGGTGAA	ATGCAATTTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTTGGTGA	AGATGGTGTC	ATGCAGATTG	GAGTATTTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTTGCACA	TCAAAAATACT	TTGGATGAGA	ATTTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	GTTTCAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

2) INFORMATION FOR SEQ ID NO: 2131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAATTTT GAAAG

25

2) INFORMATION FOR SEQ ID NO: 2132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

2) INFORMATION FOR SEQ ID NO: 2133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid

1100

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAACCTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCAGTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

2) INFORMATION FOR SEQ ID NO: 2137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCCCGTC	100
AGGTAGGCGT	TCCGTACATC	GTGGTCTTCC	TGAACAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCGG	250
CTCGTATGGC	CCTGGAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAAGC	TGGTAGAAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCG	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACCGTTGTT	ACCGGTCGTA	TCGAGCGTGG	CATCGTTCGC	450
GTTCAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCACCAC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCGTGCTG	550
GCGAGAACTG	CGGCGTTCTG	CTGCGTGGTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGTCAA	GCCAGGTTCC	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTAAct	GCGAACTGCC	GGAAGGCGTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTCAG	ATGACTGTTA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGCGGTC	GTACCGTCG		889

2) INFORMATION FOR SEQ ID NO: 2138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (B) STRAIN: PAO-1
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTTGCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGACG	CCGAGCTGCT	GGAAGTGGTC	GAGATGGAAG	TTCGCGATCT	200
GCTGAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCGTAAGC	300
GCCGTGCAGA	AGCTGGTAGA	GACCCTGGAC	TCCTACATTC	CGGAGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCGA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTGCGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGGC	ACCATCAAGC	CGCACACCAA	650
GTTCGAGTGC	GAAGTGACG	TGCTGTCCAA	GGAAGAAGGT	GGTCGTCACA	700
CCCCGTTCCT	CAAGGGCTAC	CGTCCGCAGT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAGAGATGG	TAATGCCGGG	800
CGACAACATC	AAGATGGTTG	TCACCTGAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

2) INFORMATION FOR SEQ ID NO: 2139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTTTACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATTT	50
TAACGACTAT	TTGCCTCAAA	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	100
GCGAAGGAAA	AAAACATAAA	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAACTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGTT	CCTGTTGGTG	250
AGAAAGTTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	300
GGTGAAGAAA	TTTCTTTCGA	TAAAAAATGG	GCAATTCATA	GAGATCCACC	350
AGCTTTTGAA	GATCAAAGCA	CAAAAAGTGA	GATTTTGTAA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAAAACGTGT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTTAAGCATA	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAAATGAATG	AACCACCAGG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	750
TTTTTACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATTCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACTTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTTGC	950

TCACTTAGAT	GCTACAACGG	TTTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAACA	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAGATT	TACAAGATAT	CATCGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAGATT	1200
GAAAAATTCT	TATCACAACC	ATTTTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTTAGAAGG	TAAATATGAT	CATTTACCAG	AAAATGCTTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAAGCG	GATAAATTAA	AAGGTTAA	1398

2) INFORMATION FOR SEQ ID NO: 2140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GTTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTGGGTTAG	CGATTCAAGT	AGAACAACAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACTCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTCGTCTT	CAGTGACGGT	AGTAAAAAAG	AATTTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTTGGCA	TACGGAAGT	GTCGTGGAGC	CTATCTCCCA	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCA					2157

2) INFORMATION FOR SEQ ID NO: 2141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAGTCAC AGAAAAGC

18

2) INFORMATION FOR SEQ ID NO: 2142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTT CGGATAGTGC

20

2) INFORMATION FOR SEQ ID NO: 2143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTTAAA	CACCCAGAAT	GAAATATCAG	CATTTTGGAA	50
TACTCAAAAG	ATATTTAAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTTTTGTTTT	TTATGACGGC	CCCCCAACTG	CAAATGGCCT	TCCTCATGCT	150
GGCCATGTTT	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTAAAAAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCAGTTGA	ATTAGAGGTT	GAAAAAATAA	TTGGAATTAA	AGGAAAACAA	300
GACATTGAAA	AGTATGGAAT	AGAAAATTTT	ATAAATGAAT	GTAAAAAAG	350
TGTATTTAAT	TATGAAAAAG	AATGGCGGGA	TTTTTCTAAA	GATTTAGGAT	400
ACTGGGTTGA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGTAT	GGAATATATT	ATCTACATTC	CATAAAAAAG	GACTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTAAAGA	TTTATCAGCT	600
GTTGTTAAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCACT	CCCTGGACTT	TGCCTGCAAA	TGTAGCATTA	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTCGGGTAG	AAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATTC	TATAATAACT	GAAAAATACG	AAATTATTGA	800
TACCTTTTCA	GGAAGTAATT	TAATTAATTT	AAAATACATT	CCTCCTTTTG	850
AAAGCGACGG	TTTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTCAT	ATAGCACCAG	CTCATGGGGA	950
AGATGACTAC	CAATTGGTTT	TAGAGCGTGA	TTTGGATTTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGGTAAT	1050
AAAGCTAAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAACA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGGA	1150
GATGTGGTAA	TCCTTTGATA	TATTATGCGA	TGGAAGGTTG	GTTTATTAAA	1200
ACAACTAATT	TTAAGAATGA	AATTATTAAC	AATAATAATA	ATATAGAGTG	1250
GTTTCCTTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTC	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGGAAC	ACCATTAAAT	1350
GTATGGATTT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTTGCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	GTTTGGTTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTTT	TGATAACCAG	AAAATTTTTA	1600
ATCAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTTT	ACAGTTTACT	AGTAATTTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATGGTA	1750
AAAAAATGTC	TAAAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTC	TTTAAGATGG	GCCTTAATTT	CGGATAGTGC	1850
TCCATGGAAT	AACAAAAGAT	TCTCAGAAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTTAT	AGATACGCTT	GATAATATTT	ATAAATTTTA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCCTTA	ATAAAAAGAAA	2050
GTAATATTTA	TGTAAATAAT	TACGATTTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTCGAGAGG	2150
ACGATTTTGG	GAACAAGGAA	TTTCTAACGA	TAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTTTAACA	ACTTTATCAA	GACTAGTGGC	TCCATTTGTT	2250
CCATTTATAT	CTGAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAT	ATAAAGAAAG	TTTTATTAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAAATG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAAATG	CAGATTTAAA	AATTAAGCAA	CCTTTATCGA	AAATGGTGAT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAAGA	CGAATTAAAT	ATAAAAAACA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTCTT	CTGTGGGACC	2600
AAAAGTAGGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GACTCCCTAT	2650
CAGAGTATGA	TAAAAAAAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATTA	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCGTT	ATATTATTAG	2800
ATAAAAAATTT	ATCTCCTGAA	TTAATTCGCG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAATT	AAGAAAAAAG	AAAAATTTAC	CAATAAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAAGTGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAAATACT	ATTCATTTTA	ATAATAAAGA	3050
AATAAAAAATT	TCCTTATTAT	ATTAA			3075

2) INFORMATION FOR SEQ ID NO: 2145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTTACG GT

22

2) INFORMATION FOR SEQ ID NO: 2146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA	AAATCACTGG	ATATACCACC	GTTGATATAT	CCCAATGGCA	50
TCGTAAAGAA	CATTTTGAGG	CATTTTCAGTC	AGTTGCTCAA	TGTACCTATA	100
ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT	TTTTAAAGAC	CGTAAAGAAA	150
AATAAGCACA	AGTTTTATCC	GGCCTTTATT	CACATTCTTG	CCCGCCTGAT	200
GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA	250
TATGGGATAG	TGTTACCCCT	TGTTACACCG	TTTTCCATGA	GCAAACCTGAA	300
ACGTTTTTCAT	CGCTCTGGAG	TGAATACCAC	GACGATTTCC	GGCAGTTTCT	350
ACACATATAT	TCGCAAGATG	TGGCGTGTTA	CGGTGAAAAC	CTGGCCTATT	400
TCCCTAAAGG	GTTTATTGAG	AATATGTTTT	TCGTCTCAGC	CAATCCCTGG	450
GTGAGTTTCA	CCAGTTTTGA	TTTAAACGTG	GCCAATATGG	ACAACTTCTT	500
CGCCCCCGTT	TTCACCATGG	GCAAATATTA	TACGCAAGGC	GACAAGGTGC	550
TGATGCCGCT	GGCGATTCAG	GTTTCATCATG	CCGTCTGTGA	TGGCTTCCAT	600
GTCGGCAGAA	TGCTTAATGA	ATTACAACAG	TACTGCGATG	AGTGGCAGGG	650
CGGGGCGTAA					660

2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAAT GCGGATTCAG CC

22

2) INFORMATION FOR SEQ ID NO: 2149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAAA TCATCAGCGG ATA

23

2) INFORMATION FOR SEQ ID NO: 2150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: K12
- (C) ACCESSION NUMBER: X53796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGGAACACTT	50
TGCCCTTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAGCCTG	ACCACCAAAC	100
TCGATATTAC	CGCTTTGCGT	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTACCT	GATCTCCCGG	GCTGTTAATC	AGTTTCCGGA	200
GTTCCGGATG	GCACTGAAAG	ACAATGAACT	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATACCAG	ATTGTTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGGGT	GAGTTTGTAC	450
GGATTTAACC	TGAACATCAC	CGGAAATGAT	GATTATTTTG	CCCCGGTTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCGCGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTTCATGC	AGCACGGTTT	600
ATTAATACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

1109

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTTTCAGC ATTACCTTGG GTT

23

2) INFORMATION FOR SEQ ID NO: 2152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAACCTC TTGTAGCCGA TTA

23

2) INFORMATION FOR SEQ ID NO: 2153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
- (C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACTATA	CAAAATTTGA	TGTAAAAAAT	TGGGTTCGCC	GTGAGCATTT	50
TGAGTTTTAT	CGGCATCGTT	TACCATGTGG	TTTTAGCTTA	ACAAGCAAAA	100
TTGATATCAC	GACGTTAAAA	AAGTCATTGG	ATGATTCAGC	GTATAAGTTT	150
TATCCGGTAA	TGATCTATCT	GATTGCTCAG	GCCGTGAATC	AATTTGATGA	200
GTTGAGAATG	GCGATAAAAG	ATGATGAATT	GATCGTATGG	GATTCAGTCG	250
ACCCACAATT	CACCGTATTC	CATCAAGAAA	CAGAGACATT	TTCAGCACTG	300
AGTTGCCCCAT	ACTCATCCGA	TATTGATCAA	TTTATGGTGA	ATTATTTATC	350
GGTAATGGAA	CGTTATAAAA	GTGATACCAA	GTTATTTCCCT	CAAGGGGTAA	400
CACCAGAAAA	TCATTTAAAT	ATTTTCAGCAT	TACCTTGGGT	TAATTTTGAT	450
AGCTTTAATT	TAAATGTTGC	TAATTTTACC	GATTATTTTG	CACCCATTAT	500
AACAATGGCA	AAATATCAGC	AAGAAGGGGA	TAGACTGTTA	TTGCCGCTCT	550
CAGTACAGGT	TCATCATGCA	GTTTGTGATG	GCTTCCATGT	TGCACGCTTT	600
ATTAATCGGC	TACAAGAGTT	GTGTAACAGT	AAATTTAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTCAG AGTTTAGGAC

20

2) INFORMATION FOR SEQ ID NO: 2155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

2) INFORMATION FOR SEQ ID NO: 2156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: CP590
- (C) ACCESSION NUMBER: M74769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTTG AAAAAATTGA TAAAAATAGT TGGAACAGAA AAGAGTATTT	50
TGACCACTAC TTTGCAAGTG TACCTTGTA ACAGCATG ACCGTTAAAG	100
TGGATATCAC ACAAATAAAG GAAAAGGGAA TGAAACTATA TCCTGCAATG	150
CTTTATTATA TTGCAATGAT TGTAACCGC CATTGAGAT TTAGGACGGC	200
AATCAATCAA GATGGTGAAT TGGGGATATA TGATGAGATG ATACCAAGCT	250

1111

ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAAATC	ATTTTTAGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AACAATCATA	GAATGGAAGG	AAAGCCAAAT	GCTCCGGAAA	400
ACATTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTTGC	AGAAAGGATA	TGATTATTTG	ATTCCTATTT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTTTACA	TTTGCCGTTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAATAG	TTAA			624

2) INFORMATION FOR SEQ ID NO: 2157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

2) INFORMATION FOR SEQ ID NO: 2158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAGTTCT A

21

2) INFORMATION FOR SEQ ID NO: 2159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

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ATGAACTTTA ATAAAATTGA TTTAGACAAT TGGAAGAGAA AAGAGATATT      50
TAATCATTAT TTGAACCAAC AAACGACTTT TAGTATAACC ACAGAAATTG      100
ATATTAGTGT TTTATACCGA AACATAAAAC AAGAAGGATA TAAATTTTAC      150
CCTGCATTTA TTTTCTTAGT GACAAGGGTG ATAAACTCAA ATACAGCTTT      200
TAGAACTGGT TACAATAGCG ACGGAGAGTT AGGTTATTGG GATAAGTTAG      250
AGCCACTTTA TACAATTTTT GATGGTGTAT CTAAAACATT CTCTGGTATT      300
TGGACTCCTG TAAAGAATGA CTTCAAAGAG TTTTATGATT TATACCTTTC      350
TGATGTAGAG AAATATAATG GTTCGGGGAA ATTGTTTCCC AAAACACCTA      400
TACCTGAAAA TGCTTTTTCT CTTTCTATTA TTCCATGGAC TTCATTTACT      450
GGGTTTAACT TAAATATCAA TAATAATAGT AATTACCTTC TACCCATTAT      500
TACAGCAGGA AAATTCATTA ATAAAGGTAA TTCAATATAT TTACCGCTAT      550
CTTTACAGGT ACATCATTCT GTTTGTGATG GTTATCATGC AGGATTGTTT      600
ATGAACTCTA TTCAGGAATT GTCAGATAGG CCTAATGACT GGCTTTTATA      650
A

```

2) INFORMATION FOR SEQ ID NO: 2160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

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TTTTGAACAC TATTTTAACC AGC

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23

2) INFORMATION FOR SEQ ID NO: 2161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

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GATTTAACTT ATCCCAATAA CCT

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23

2) INFORMATION FOR SEQ ID NO: 2162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTTA	ATATTATCAA	ATTAGAAAAT	TGGGATAGAA	AAGAATATTT	50
TGAACACTAT	TTTAACCAGC	AAACTACGTA	TAGCATTACT	AAAGAAATTG	100
ATATTACTTT	GTTTAAAGAT	ATGATAAAAA	AGAAAGGATA	TGAAATTTAT	150
CCTTCTTTGA	TTTATGCAAT	TATGGAAGTT	GTAAATAAAA	ATAAAGTGTT	200
TAGAACAGGA	ATTAATAGTG	AGAATAAATT	AGGTATTGG	GATAAGTTAA	250
ATCCTTTGTA	TACAGTTTTT	AATAAGCAAA	CTGAAAAATT	TACTAACATT	300
TGGACTGAAT	CTGATAACAA	CTTCACTTCT	TTTTATAATA	ATTATAAAAA	350
TGACTTGCTT	GAATATAAAG	ATAAAGAAGA	AATGTTTCCT	AAAAAACCGA	400
TACCTGAAAA	CACCATACCG	ATTTCAATGA	TTCCTTGGAT	TGATTTTAGT	450
TCATTTAATT	TAAACATTGG	TAACAATAGC	AACTTTTTAT	TGCCTATTAT	500
TACGATAGGT	AAATTTTATA	GTGAGAATAA	TAAAATTTAT	ATACCAGTTG	550
CTTTGCAGCT	TCATCATGCT	GTATGTGATG	GTTACCATGC	TTCATTATTT	600
ATGAATGAAT	TTCAAGATAT	AATTCATAAG	GTAGATGATT	GGATTTAG	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGTT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1215 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Salmonella typhimurium*
 (B) STRAIN: H3380
 (C) ACCESSION NUMBER: AF071555
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

ATGACCACCA	CACGCCCCGC	GTGGGCCTAT	ACGCTGCCGG	CAGCACTGCT	50
GCTGATGGCT	CCTTTCGACA	TCCTCGCTTC	ACTGGCGATG	GATATTTATC	100
TCCCTGTCGT	TCCAGCGATG	CCCGCATCC	TGAACACGAC	GCCCCGCTATG	150
ATCCAACCTCA	CGTTGAGCCT	CTATATGGTG	ATGCTCGGCG	TGGGCCAAGT	200
GATTTTTTGGT	CCGCTCTCAG	ACAGAATCGG	GCGACGGCCA	ATTCTACTTG	250
CGGGCGCAAC	GGCTTTCGTC	ATTGCGTCTC	TGGGAGCAGC	TTGGTCTTCA	300
ACTGCACCGG	CCTTTGTCGC	TTTCCGTCTA	CTTCAAGCAG	TGGGCGCGTC	350
GGCCATGCTG	GTGGCGACGT	TCGCGACGGT	TCGCGACGTT	TATGCCAACC	400
GTCCTGAGGG	TGTCGTCATC	TACGGCCTTT	TCAGTTCGAT	GCTGGCGTTC	450
GTGCCTGCGC	TCGGCCCTAT	CGCCGGAGCA	TTGATCGGCG	AGTTCTTGGG	500
ATGGCAGGCG	ATATTCATTA	CTTTGGCTAT	ACTGGCGATG	CTCGCACTCC	550
TAAATGCGGG	TTTCAGGTGG	CACGAAACCC	GCCCTCTGGA	TCAAGTCAAG	600
ACGCGCCGAT	CTGTCTTGCC	GATCTTCGCG	AGTCCGGCTT	TTTGGGTTTA	650
CACTGTCGGC	TTTAGCGCCG	GTATGGGCAC	CTTCTTCGTC	TTCTTCTCGA	700
CGGCTCCCCG	TGTGCTCATA	GGCCAAGCGG	AATATTCCGA	GATCGGATTC	750
AGCTTTGCCT	TCGCCACTGT	CGCGCTTGTA	ATGATCGTGA	CAACCCGTTT	800
CGCGAAGTCC	TTTGTCGTCA	GATGGGGCAT	CGCAGGATGC	GTGGCGCGTG	850
GGATGGCGTT	GCTTGTTTGC	GGAGCGGTCC	TGTTGGGGAT	CGGCGAACTT	900
TACGGCTCGC	CGTCATTCTT	CACCTTCATC	CTACCGATGT	GGGTTGTCGC	950
GGTCGGTATT	GTCTTCACGG	TGTCCGTTAC	CGCGAACGGC	GCTTTGGCAG	1000
AGTTCGACGA	CATCGCGGGA	TCAGCGGTCC	CGTTCTACTT	CTGCATCCAA	1050
AGCCTGATAG	TCAGTATCGT	CGGGACATTG	GCGGTGACGC	TGTTAAACGG	1100
CGATACAGCG	TGGCCCCGTA	TTTGTTACGC	CACGGCAATG	GCAGTGCTGG	1150
TGTCGTTGGG	GCTGGCGCTC	CTTCGATCCC	GTGATGCTGC	CACCGAGAAG	1200
TCGCCAGTCG	TCTAG				1215

2) INFORMATION FOR SEQ ID NO: 2166

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

2) INFORMATION FOR SEQ ID NO: 2167

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

2) INFORMATION FOR SEQ ID NO: 2168

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

2) INFORMATION FOR SEQ ID NO: 2169

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTTGCG AAAGGTGG

18

2) INFORMATION FOR SEQ ID NO: 2170

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1116

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAT CTTCGAACTG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174

1117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

2) INFORMATION FOR SEQ ID NO: 2175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

2) INFORMATION FOR SEQ ID NO: 2176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CTTT

24

2) INFORMATION FOR SEQ ID NO: 2177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCCT GCTGCCTATC GAAGACGTGT TCCCGTGCC 49

2) INFORMATION FOR SEQ ID NO: 2178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCCTG CTGCCTATCG AACGTGCC 38

2) INFORMATION FOR SEQ ID NO: 2179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAA CCGGCTGCC 39

2) INFORMATION FOR SEQ ID NO: 2180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC 15

2) INFORMATION FOR SEQ ID NO: 2181

(i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGCCACGC GCAGG

15

2) INFORMATION FOR SEQ ID NO: 2182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

2) INFORMATION FOR SEQ ID NO: 2183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTCCCTG	100
AACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
GGAAGTTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
CGATCATCAA	GGGTTCGGCC	AAACTGGCTC	TGGAAGGCCA	CGAAGGCCCA	250
CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACCTACAT	300
TCCTACGCC	GAGCGTGCCG	TTGACGGTAC	GTTCCTGATG	CCTGTTGAAG	350
ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
GTGGTCGTCA	CACCTCCTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700

1120

CGTACAAC	CTG	ACCTG	ACCGG	CACCAT	TCGAG	CTGCC	CAGAA	ACAAGG	AAAAT	750
GGTTCT	GGCA	GGCG	ACAACA	TTTCG	ATGAA	AGTGT	CCCTG	ATCGCT	CCTA	800
TCGCC	ATGGA	AGAAG	GT							817

2) INFORMATION FOR SEQ ID NO: 2184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
- (B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATGCGTGT	TCTTGATGGT	GCTGTTGCGG	50
TATTTTGTTT	AGTGGGTGGG	GTGCAGCCTC	AAAGTGAAAC	AGTTTGAGAG	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTAA	ATAAAATGGA	150
TAGAATCGGT	GCAAATTTCT	ACAATGTAGA	AGATCAAATT	CGCAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCG	TAATCGATCT	TGTAAGTATG	AAAGCTTTAG	TTTGGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAATTCCA	GCTGAACTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAAGC	AGTTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATTTA	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGGA	TTAAAGCAGG	ATGTTTAAAGT	CTTTCTATCG	500
TTCCTATGCT	TTGCGGTACA	GCGTTTAAAA	ATAAAGGGGT	TCAACCTTTG	550
CTTGATGCTG	TTGTGGCTTA	TTTACCAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGGAA	TATGAAGACG	GCACAGAAGT	TTCTGTAAAA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAAA	TTATGACAGA	TCCATTTGTA	700
GGACAACTTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTTAG	AAAGCGGTTC	750
TTATGCTTAT	AACTCAACCA	AAGATAAAAA	AGAAAGAATT	GGTCGTTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAG	TAATTCTTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTTT	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACAT	CATTTAGGT	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCGTGAATT	TAAAGTGGA	1150
GCTGAAGTGG	GACAACCTCA	AGTTGCTTAT	CGTGAAACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAAT	ACGCTAAGCA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTTGTTA	ACGACATCAA	AGGTGGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTC	AAGAAGCATT	GCAAAATGGT	GTTTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACTG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAA	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAACTCCT	GAAGATTACA	TGGGCGATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

2) INFORMATION FOR SEQ ID NO: 2185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
AGGTCGTGCA	GGTGATAACG	TTGGTGTTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 2186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACGCGCTCAA AGCAGAAGTA TACGTATTAT CAAAAGACGC GCGT

44

2) INFORMATION FOR SEQ ID NO: 2187

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1612 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33292
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

CAGTGGGTGG	GGTGCAGCCT	CAAAGTGAAA	CAGTTTGGAG	ACAAGCAAAT	50
AAATATGGTG	TTCCAAGAAT	AGTATTTGTA	AACAAAATGG	ATAGAATCGG	100
TGCAAATTTT	TACAATGTAG	AAGATCAAAT	TCGCAACCGT	TTAAAAGCTA	150
ATCCAGTTCC	ACTTCAAATT	CCAATCGGTG	CTGAGGATAA	TTTTAAAGGC	200
GTAATCGATC	TTGTAACAT	GAAAGCTTTA	GTTTGGGAAG	ATGATACTAA	250
GCCAACGGAT	TATGTAGAAA	AAGAAATTCC	AGCTGAACTT	AAAGAAAAGG	300
CAGAAGAATA	TCGCACAAAA	ATGATAGAAG	CAGTTTCTGA	AACTTCAGAT	350
GAGTTGATGG	AAAAATATTT	AGGCGGAGAA	GAATTAAGCC	TTGAAGAGAT	400
TAAAACAGGG	ATTAAAGCAG	GATGTTTAAG	TCTTTCTATC	GTTCCCTATG	450
TTTGCGGTAC	AGCGTTTAAA	AATAAAGGGG	TTCAACCTTT	ACTTGATGCT	500
GTTGTGGCTT	ATTTACCAGC	TCCTGATGAA	GTGGCAAATA	TCAAGGGTGA	550
ATATGAAGAT	GGCACAGAAG	TTTCTGTAAA	ATCAACTGAT	GATGGCGAGT	600
TTGCAGGACT	TGCATTTAAA	ATTATGACAG	ATCCATTGTG	AGGACAACCT	650
ACTTTCGTGC	GTGTTTATCG	CGGTTGTTTA	GAAAGTGGTT	CTTATGCTTA	700
TAACTCAACT	AAAGATAAAA	AAGAAAGAAT	TGGTCGTTTG	TTAAAAATGC	750
ACTCTAACCA	AAGAGAAGAG	ATTAAAGTGC	TTTACGCAGG	CGAAATTTGG	800
GCTGTTGTAG	GACTTAAAGA	TACTTTAACA	GGGGATACTC	TTGTAAGTGA	850
AAAAGATAAG	GTAATCCTTG	AAAGAATGGA	TTTTCCAGAT	CCAGTTATTT	900
CTGTTGCAGT	TGAGCCAAAA	ACTAAAGCAG	ATCAAGAAAA	AATGTCCTAT	950
GCTTTAAATA	AATTAGCACA	AGAAGATCCA	AGTTTTAGAG	TTTCTACAGA	1000
TGAAGAAAGT	GGCCAAACTA	TCATTTTCAG	TATGGGTGAG	TTACACCTTG	1050
AAATTATCGT	TGATAGAATG	CTTCGTGAAT	TTAAAGTTGA	AGCTGAAGTA	1100
GGTCAACCAC	AAGTTGCTTA	TCGCGAAACT	ATTAGAAAAA	CTGTTGAACA	1150
AGAATACAAA	TACGCTAAAC	AATCAGGTGG	TCGTGGTCAG	TATGGACATG	1200
TATTCTTACG	CCTTGAACCA	CTTGAGCCAG	GTAGTGGATA	TGAATTGTGT	1250
AATGATATCA	AAGGTGGAGT	AATTCCAAAA	GAATACATTC	CTGCAGTTGA	1300
TAAAGGTGTT	CAAGAAGCAT	TACAAAATGG	TGTTTTAGCA	GGTTATCCTG	1350
TGGAAGATGT	TAAAGTAACT	GTTTATGATG	GAAGTTATCA	CGAGGTGGAT	1400
TCATCTGAGA	TGGCGTTTAA	ACTTGCTGCT	TCTATGGGCT	TTAAAGAAGG	1450
TGCTAGAAAA	GCAGGTGCTG	TGATCTTAGA	GCCTATGATG	AAAGTTGAAG	1500
TAGAACTCC	TGAAGATTAC	ATGGGTGATG	TTATTGGAGA	TCTTAACAAA	1550
CGCCGTGGTC	AAGTAAATAG	CATGGATGAG	CGTGGTGGA	ATAAAATCAT	1600
CACAGCATTT	TG				1612

2) INFORMATION FOR SEQ ID NO: 2188

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1667 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAATTGAAG	TTGAAAGATC	TATGCGTGTT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTTCA	GTGGGTGGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATAA	ATATGGTGTT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGTG	CAAATTTCTA	CAATGTAGAA	GATCAAATTC	GCAACCGTTT	200
AAAAGCTAAT	CCAGTTCCAC	TTCAAATTC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCGT	AATCGATCTT	GTAAGTATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAAGC	CAACGGATTA	TGTAGAAAAA	GAAATTCCAG	CTGAACTTAA	350
AGAAAAGGCA	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTTCTGAAA	400
CTTCAGATGA	GTTGATGGAA	AAATATTTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTTAAAAA	TAAAGGGGTT	CAACCTTTCG	550
TTGATGCTGT	TGTGGCTTAT	TTACCAGCTC	CTGATGAAGT	GGCAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAAT	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTTAAAAAT	CATGACAGAT	CCATTTGTAG	700
GACAACTTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTTAGA	AAGCGGTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAAA	GAAAGAATTG	GTCGTTTGTT	800
AAAAATGCAC	TCTAACAAAA	GAGAAGAGAT	TAAAGTGCTT	TACGCAGGCG	850
AAATTGGTGC	TGTTGTAGGA	CTTAAAGATA	CTTTAACAGG	GGATACTCTT	900
GCAAGTGAAA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCCTATTGC	TTTAAATAAA	TTAGCACAAAG	AAGATCCAAG	TTTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAATATC	ATTTTCAGGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TCGTGAATTT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAAACAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCACT	TGAGCCAGGT	AGTGGATATG	1300
AATTTGTTAA	TGATATCAAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCCT	1350
GCAGTTGATA	AAGGTGTTCA	AGAAGCATT	CAAAATGGTG	TTTTAGCAGG	1400
TTATCCTGTG	GAAGATGTTA	AAGTAAGTGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATT	ATCTGAGATG	ACGTTTAAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCGCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTTGAAGTA	GAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAATAGCA	TGGATGAGCG	TGGTGAAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCCTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTCCGC	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACTCCGAG	TGTTCTGCGC	TGCTGGGCCG	CATCCCAGCC	GCCGTGGGTT	750
ACCAGCCGAC	GCTTGCGGAG	GATCTTGGCA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCTGCC	950
GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTGCTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCTT	1150
GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 2190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGACG	CATCTTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAAA	100
CGACGGATCT	CCTCAAACCTG	AAGGCAAAGG	TCGTTTCGAC	AGGTGGCAAC	150
ATTTCCGTTT	CTGTCGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCAGC	GCGGCCCGCT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

AGGTGGAAAA	ATTGGCCTCT	TTGGGGGTGC	GGGTGTGGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTTCTCT	450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTTGTATCT	500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG	550
TGTTGGTGTA	CGGTCAGATG	AACGAGCCCC	CAGGTGCCCC	TGCGCGTGTT	600
GCGCAGTCGG	CTCTGACGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA	650
AGATGTGCTT	CTTTTATCG	ACAATATTTT	TCGTTTCACT	CAGGCTAACT	700
CCGAGGTGTC	GGCGCTTCTG	GGTCGTATTC	CCGCCGCTGT	TGGCTACCAG	750
CCTACCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTCAAC	800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACGTG	CCGGCCGATG	850
ACATTACCGA	TCCAGCTCCA	GCAACAACCT	TCTCACATCT	GGACGCCACA	900
ACTGTGTTGG	ACCGTGCTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTTAA	950
CCCACTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG	1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG	1050
GAATTACAGG	ATATCATTGC	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA	1100
GGACAAACTT	ATCGTGGACC	GTGCGCGTAA	GTTGGTGAAG	TTCTCTCTCC	1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG	1200
CAGTTGGATG	ACACCATCGA	TTCCTTTTCT	GGTCTCCTCA	TGGGTACG	1248

2) INFORMATION FOR SEQ ID NO: 2191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGTG	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTACTCGTGA	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	150
GACTGGTGTC	ATTGAGCTCG	ACGGCGAATC	CAAGGTGTCT	CTTGTGTTCC	200
GTCAGATGAA	CGAGCCCCCA	GGTGCTCGTG	CCCGTGTCGC	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTTCC	GTTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTCG	GTTACCAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCACCA		440

2) INFORMATION FOR SEQ ID NO: 2192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania panamensis*

(B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGCAGCAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCGAAGGTTG	TGTCGACCGG	150
CGGCAACATC	TCCGTGCCGG	TGGGCCGCGA	GACGCTGGGC	CGCATCTTCA	200
ACGTGCTGGG	CGACGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATCGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTTC	GCGGTGCCGG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCGG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCAG	TCAAAGGTGA	TTGACCTGAA	GGGCGAGTCG	550
AAGTGCGTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGGC	CGCATCCCGG	CCGCCGTGGG	750
TTACCAGCCG	ACGCTTGCGG	AGGATCTTGG	CATGCTGCAG	GAGCGCATTG	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCTG	TGCAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCGCG	ACGACGTTCT	CGCACCTGGA	900
CGCGACGACT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGCGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCGTG	GTGGACCGCG	CGCGCAAGGT	GACGCGGTTT	1150
CTGTGCGCAG	CGTTCCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus nidulans*

(B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATTC	CTTCCAGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGCAAA	TAGGCCCCAG	ACTCGTGAGC	ACTTGTGCT	100
TGCCCCGTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCTGA	TGACCCTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCGCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACTTGGAT	CCCTACCCCC	350
CAGCGTGACT	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCACG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCGTGCTGG	TATGGTCATC	GCTGCCCTTG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCAACT	ACCGCCCCCA	GGCTTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTTGA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTTCCCTGA	TGAGGCCGAC	AAGGACCGCC	850
ACGTCATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
GTTGCTGCTG	AG				912

2) INFORMATION FOR SEQ ID NO: 2194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCCGTCAGGT	CGGTATCCAG	AAGATTGTCT	TCTTCGTCAA	100
CAAGGTCGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTCGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TCGAGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACCGCC	AGCCCCGAGAT	250
TGGAACCACC	CAGATCGACA	ACCTGATGAA	CGCTGTCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAAGCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCG	TGGTACTGTC	GTTTCTGGCC	GTGTTGAGCG	400
TGGTACCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	CAAGGAGGAG	650
GGTGGTCGTC	ACACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTTCGCATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
GTCTGCTCTC	TTCACAGACC	TCTTGCCGTT	GAACAGG		887

2) INFORMATION FOR SEQ ID NO: 2195

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 984 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Emmonsia parva*
 (B) STRAIN: ATCC 10784
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCCAA	ATGTAGGACT	CTTGCGCGGG	ACTGACTGAT	TGGGGGGAAT	50
CCATTTTTTC	TTTTTCTTT	TTCTTTTGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAGGCCT	CAAACACGTG	AACATTTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAGAT	CGTCGTTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAAGATAAG	GAGATGTTGG	AGCTTGTCGA	GTTGGAAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTCGAG	GGTGAGGAAA	CGCCCATCAT	CTTCGGTTCT	300
GCCCTTTGTG	CCATGGAGGG	CCGCGAGCCT	GAGCTGGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGTT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGGCGG	CGTCGCCCCA	ATCAGGACCA	550
AGGTAACCGA	TATCGAAACC	TTCAAGAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAACT	CTGGCCTTTT	GTTGCGTGGT	GTCAAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTCG	TTCCTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAACT	750
GGATTCGGCC	AAAACATATCG	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTTCCCTG	900
ACGCAGCAGA	CGAAACCAAA	CTGGTTATGC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAG		984

2) INFORMATION FOR SEQ ID NO: 2196

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Exserohilum rostratum*
 (B) STRAIN: WSA-215
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTTCTA	AGATTGTTGT	TTTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCGAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTGACGA	CCTGGATCCC	CACCCCTCAG	300
CGTGATACCG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGGCCG	TGTCGAGCGA	GGTGTCTTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCATCAAG	450
ACCAAGGTTA	CCGACATTGA	AACCTTCAAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCTTG	GACAAGTCAA	GGCCCACAAG	600
AAGTTCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCAGA	TGCTCACGAC	750
AAGCTTGTTA	TGCCTGGTGA	TAACGTTGAG	ATGGTTTGTG	AGCTTCACGT	800
GCCACA					806

2) INFORMATION FOR SEQ ID NO: 2197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTT	AGCGAATTGT	50
CGTCTTTGTC	AACAAGGTCG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTCGAGAT	GGAGATGCGC	GAGCTTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTCG	250
ACGAGTGGAT	CCCAACCCCG	GAGCGTGACC	TTGACAAGCC	CTTCCTTATG	300
TCCGTCGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTT	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACTCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTGCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TCGCTTCCCT	CTATGTCCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCTTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

2) INFORMATION FOR SEQ ID NO: 2198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT	CAGATGCCCC	AGACCCGTGA	GCACTTGCTG	CTTGCCCGTC	50
AGGTCCGGTG	CCAGAAGATT	GTCGTCTTCG	TCAACAAGGT	CGATGCCATT	100
GACGACCCTG	AGATGCTTGA	GCTCGTCGAG	ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC	GGCTTCGAGG	GTGACGAGAC	CCCTGTCATC	ATGGGCTCTG	200
CTCTCATGTC	CCTCCAGAAC	CAGCGCCCCG	AGATCGGTAG	CCAGAAGATT	250
GACGAGCTCC	TTGCCGCCGT	TGACGAGTGG	ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG	CCCTTCCTCA	TGTCCGTTGA	GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC	CGTCGTCTCT	GGCCGTGTCG	AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA	TTGAGCTCGT	CGGCAAGGGT	AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC	ATTGAGACCT	TCAAGAAGTC	TTGCGAGCAG	TCCCAGGCTG	500
GTGACAACCTC	TGGTCTCCTC	ATCCGAGGTG	TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG	TCGTCTGCGC	CCCCGGCACT	GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC	CTCTACGTCC	TCACCAAGGA	GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA	GCACTACCGA	CCCCAGCTCT	ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC	TGACCTTCCC	CGAGGGTACC	GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCCC	GGTGACAACA	CCGAGATGGT	CATCACCATG	GGCCACCCCA	800
ACGCCATTGA	GGTCGGTCA				819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC	CAAATGTAAG	ACGCCGCGAG	GGAGTGCTGA	AGGTTTTATG	50
CTTTTTAGGC	CCTTTGTTTC	TGAGAGCATG	ATGATACTAA	TACTCGGAAA	100
CGTATCTATT	AGGCCTCAAA	CACGTGAGCA	TTTGCTCCTT	GCCCGACAGG	150
TCGGTGTCCA	AAAGATCGTC	GTTTTCGTGA	ACAAAGTCGA	CGCCCTTGAG	200
GACAAGGAGA	TGTTGGAGCT	TGTCGAGTTA	GAAATGAGAG	AGCTCTTAAA	250
CACCTACGGA	TTTGAGGGTG	AAGAGACACC	CATCATCTTT	GGTTCTGCCC	300
TTTGCGCCAT	GGAAGGCCGT	GAGCCTGAGT	TGGGAGAAAA	GAAAAATTGAT	350
GAATTGCTGG	AGGCTGTTGA	TACTTGATC	CCAACACCAC	AACGTGATAC	400
CGAAAAACCT	TTCTTGATGT	CCGTTGAGGA	AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT	TGCCTCCGGT	CGTGTGAGC	GCGGTGTCCT	CAAGAAGGAT	500

TCAGAAGTCG	AGCTAATTGG	GGGCGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACTCCGG	TCTTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCACAG	ACAAGTTCTT	700
GGTGTGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCCT	CAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTTCTT	TTTTTCCTTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTTT	TCAACTCGCC	TGATTACAGA	AATTAATAA	900
CCCCTTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

2) INFORMATION FOR SEQ ID NO: 2200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCT	GCTGGTCGCC	50
CTGAACAAGG	CCGACATGGT	CGAGGACGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCGCGTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCCTGG	TGACCGGTCG	CGCCGAGCGC	350
GGGACCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCCGAT	400
CCAGAAGACC	ACGGTCACCG	GGATCGAGAT	GTTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCGAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTCG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGGTT	CCATCACCCC	550
GCACACCAAC	TTGAGGGCGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TCGAACTACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

2) INFORMATION FOR SEQ ID NO: 2201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Vibrio mimicus*
 (B) STRAIN: ATCC 33653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

TGCTGCAACA	GATGGTCCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTGCTGG	50
GTCGCCAAGT	AGGTATTCCT	TACATCATCG	TATTCATGAA	CAAATGTGAC	100
ATGGTTGACG	ATGAAGAGCT	TCTAGAGCTG	GTTGAGATGG	AAGTTCGTGA	150
GCTTCTGTCT	GAGTACGATT	TCCCAGGTGA	TGACCTGCCA	GTAATCCAAG	200
GTTCAGCACT	AGGCGCGCTA	AACGGCGAAG	CACAGTGGGA	AGCGAAGATT	250
GTTGAACTAG	CAGAAGCACT	AGATTCATAC	ATTCCAGAGC	CAGAGCGTGC	300
AGTAGACATG	GCATTCTCTGA	TGCCAATCGA	AGACGTATTC	TCAATCCAAG	350
GTCGTGGTAC	AGTAGTAACT	GGCCGTATCG	AGCGCGGCAT	CCTGAAAAGTG	400
GGTGACGAAG	TTGCGATCGT	TGGTATCAAA	GACACAGTAA	AAACTACCTG	450
TACAGGTGTA	GAAATGTTCC	GTAAGCTGCT	TGACGAAGGT	CGTGCAGGTG	500
AGAACGTTGG	TGCACTGCTA	CGTGGTACTA	AGCGTGAAGA	AGTAGAGCGT	550
GGTCAAGTAC	TGGCGAAGCC	AGGTTCAATC	ACCCACACA	CTAAGTTCGA	600
ATCAGAAGTA	TACGTACTGT	CAAAAGACGA	AGGTGGCCGT	CATACTCCAT	650
TCTTCAAAGG	TTACCGTCCA	CAGTTCTACT	TCCGTACAAC	TGACGTAACA	700
GGCAGCATCG	AGCTTCCAGA	AGGCGTAGAA	ATGGTAATGC	CAGGCGACAA	750
CATCAAGATG	GTTGTAGACC	TGATTGCA			778

2) INFORMATION FOR SEQ ID NO: 2202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

AACGCTGACC	CTGCAGGTTA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCATTTAT	CGATGCAGAA	CACGCACTGG	ACCCGGTCTA	TGCCCCGTAAG	100
CTTGCGGTTG	ATATCGATAA	CCTGCTGTGT	TCTCAGCCGG	ATACCGGTGA	150
ACAAGCGCTG	GAAATCTGTG	ATGCACTGGC	GCGCTCCGGT	GCGGTTGACG	200
TTATCGTTGT	CGACTCCGTT	GCCGCATTGA	CGCCGAAGGC	AGAAATCGAA	250
GGCGAGATTG	GCGACTCTCA	CATGGGCCTT	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCCG	GTAACCTGAA	GCAGTCCAAC	ACGCTGCTGA	350
TTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTTATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA	TCTTATGCTA	GAAATTTAGG	TGTTGATATA	GATAACCTAA	50
TAGTTTCTCA	ACCAGATACA	GGAGAACAGG	CTTTAGAGAT	AACAGAAGCT	100
TTAGTAAGAT	CAGGAGCAGT	AGATGTTATA	GTTGTAGACT	CTGTAGCAGC	150
TTTAGTTTCCT	AGGGCAGAAA	TAGAAGGAGA	AATGGGAGAC	TCACATGTAG	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCCC	TAAGAAAATT	AGCAGGATCT	250
ATAAATAAAT	CTAAGTGTGT	AGCTATATTT	ATAAACCAAT	TAAGAGAAAA	300
GGTTGGTATA	ATGTTTGGAA	ATCCAGAAAC	AACTCCT		337

2) INFORMATION FOR SEQ ID NO: 2204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC	GGTACTGCAG	CATTTGTTGA	TGCTGAGCAT	GCACTAGATC	50
CAAAATATGC	AAAGCTTTTA	GGTGTGATG	TTGATAATCT	GATCGTGTCA	100
CAGCCGGATA	CGGGTGAGCA	AGCTTTAGAG	ATTGCTGATA	TGTTGGTACG	150
TTCTGGAGGA	GTTGATATTG	TAGTAATTGA	CTCTGTTGCT	GCACTTACGC	200
CAAAGGCAGA	GATTGAGGGT	GACATGGGCG	ACTCGCACAT	GGGCTTACAA	250
GCAAGATTAA	TGTCACAAGC	ACTAAGAAAA	CTAACGGCAA	ATATCAAGCG	300
CTCAAATACT	CTAGTGATAT	TCATTAACCA	AATTTCGTATG	AAGATCGGGG	350
TTATGTTTGG	TAACCCTGAA	ACTACAAC			379

2) INFORMATION FOR SEQ ID NO: 2205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

ACTTGACCCA	GTATATGCAA	GGGCTCTTGG	AGTGGATATA	GACAACCTAG-	50
TCATATCTCA	GCCAGATACA	GGAGAACAGG	CCCTAGATAT	AGCAGAGTCC-	100
CTTATAAGAT	CAGGAGCTGT	AGATATACTA	GTAATAGACT	CAGTAGCTGC-	150
CCTAGTACCT	AAGGCAGAAA	TAGAAGGTGA	CATGGGAGAT	TCTCACGTAG-	200
GTCTACAGGC	TAGACTTATG	TCACAGGCAC	TTAGAAAATT	GA CTGGATCT-	250
ATAAAGAAGT	CAA ACTGTGT	TGTTATATTT	ATCAACCAGT	TGAGAGAAAA-	300
AGTAGGGGTT	ATGTT CGGT	ATCCAGAGAC	AACAACA		337

2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

TCTTGATGCT	GGATATGCAA	AAAACCTTGG	AGTAGATGTA	GAAAATTTAA-	50
TTATTTCTCA	ACCTGATACA	GGTGAGCAAG	CCTTAGAAAT	AACTGAAGCT-	100
CTTGTAAGAT	CTAACGCTGT	TGATTTAATT	ATTATAGACT	CAGTTGCCGC-	150
ACTTGTAACCA	AAAGCAGAAA	TGCATGGTGA	CATGGGAGCT	GCACAAATAG-	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCTC	TTAGAAAATT	AACTGGGGCA-	250
ATCAACAAGT	CAAAATGTAC	CGTTGTATTT	ATTAACCAAC	TTAGAGAAAA-	300
AGTTGGTATC	ATGTTTGGTA	ACCCAGAAAC	TACAACA		337

2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*

1135

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC	AAGTTATTGC	AGCAGCACAA	CGTAGCGGAA	AAACCTGTGC	50
ATTTATCGAC	GCTGAACATG	CGCTAGATCC	AATCTATGCG	AAAAAACTGG	100
GTGTTGATAT	CGATAACCTT	CTATGTTCTC	AACCTGATAC	TGGTGAGCAA	150
GCATTAGAGA	TTTGTGATGC	ACTGACGCGT	TCAGGCGCTG	TTGATGTCAT	200
TATCGTTGAC	TCCGTGGCCG	CATTAACACC	AAAAGCTGAA	ATTGAAGGTG	250
AAATCGGTGA	CTCACACATG	GGCTTAGCGG	CTCGTATGAT	GAGCCAAGCG	300
ATGCGTAAAT	TAGCGGGTAA	CTTAAAGAAC	TCGAATACAC	TTTTAATCTT	350
CATTAACCAA	ATCCGTATGA	AGATTGGCGT	TATGTTTGGT	AACCCAGAAA	400
CCACTACA					408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG	ATTGCCGCTG	CGCAGCGTGA	AGGTAAAACC	TGTGCGTTTA	50
TCGATGCGGA	ACACGCGCTT	GACCCTGTTT	ACGCACGCAA	GCTGGGCGTC	100
GATATCGATA	ACCTGCTTTG	TTCTCAGCCG	GATACCGGCG	AGCAGGCGCT	150
GGAAATCTGT	GACGCGCTGG	CGCGTTCAGG	CGCGGTGGAC	GTCATTGTGG	200
TCGACTCCGT	AGCGGCGCTA	ACGCCGAAAG	CGGAAATCGA	AGGCGAAATT	250
GGCGACTCTC	ACATGGGCCT	CGCGGCGCGT	ATGATGAGCC	AGGCGATGCG	300
TAAGCTGGCG	GGGAACCTAA	AACAGTCCAA	CACGCTGTTG	ATTTTCATCA	350
ACCAGATCCG	TATGAAGATT	GGCGTGATGT	TCGGTAACCC	GGAAACCACC	400
ACC					403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype Typhimurium
(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGAA	GGTAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTTA	CGCACGCAAG	100
CTGGGCGTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCGA	150
GCAGGCGCTG	GAAATCTGTG	ACGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTGGT	CGACTCCGTA	GCGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTTTCATCA	CCGATCCGT	ATGAAGATTG	GCGTGATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
(B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GTTTACGCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATTTATCTCA	ACCTGATCAT	GGGGAACAAG	GTTTAGAAAT	TGCCGAAGCA-	100
TTTGTTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCCAAGCCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTTCAAAAT	CAAATACAAC	AGCAGTATTT	ATCAACCAA	TCCGTGAAAA-	300
AGTTGGTGTG	ATGTTTCGGTA	ATCCTGAAGT	TACACCA		337

2) INFORMATION FOR SEQ ID NO: 2211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
(B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTTA	TCGCCGCCGC	ACAGCGTGAA	GGCAAAACGT	50
GTGCATTTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGCACTG	GAAATTTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAAGC	TGAAATTGAA	250
GGTGAAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTGATGTT	TGGTAACCCA	400
GAAACCACTA	CC				412

2) INFORMATION FOR SEQ ID NO: 2212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCACC	TTGCAAACCA	TCGCGGAAAT	GCAAAACTG	GGCGGCACCT	50
GCGCGTTTAT	CGACGCCGAG	CACGCACTGG	ACGTCACGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GGCGACATGG	GCGATTGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTCGCA	300
AGCACTGCGC	AAGCTTACCG	GTTCGATCAA	CCGCACCAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCCG	400
GAAA					404

2) INFORMATION FOR SEQ ID NO: 2213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG	ACATGATTTC	CGAAGAAGAC	GCTGAAGGCA	CG
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42

2) INFORMATION FOR SEQ ID NO: 2214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCACT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAACGGAG AATAA	125

2) INFORMATION FOR SEQ ID NO: 2215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

CGACTCAAAT GCGTTCTATG TCTCAAGGTC GTGCGACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACGAGTAA	140

2) INFORMATION FOR SEQ ID NO: 2216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
(B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

2) INFORMATION FOR SEQ ID NO: 2217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
(B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGTCCATG TCCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

2) INFORMATION FOR SEQ ID NO: 2218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGCAACGGC ACTGCCTAA	119

2) INFORMATION FOR SEQ ID NO: 2219

1140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCTAACAAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AGTAA	115

2) INFORMATION FOR SEQ ID NO: 2220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCGAACAAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AATAA	115

2) INFORMATION FOR SEQ ID NO: 2221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT TCGTTCAGGT ACGCAAGGTC GTGGTGTATA CACTATGCAA	50
TTTGACCACT ATGAAGAAGT TCCTAAATCT ATTGCTGAAG AAATCATTA	100
AGCTAATGGT GGA	113

2) INFORMATION FOR SEQ ID NO: 2222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG CGGTCCAAGA CCCAAGGCCG GCGGAACTAC TCCATGGTCT	50
TCGACTCCTA CGCCGAAGTG CCGGCCAACG TGTCGAAGGA GATCATCGCG	100
AAGGCGACGG GTCAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT GCGGTCCAAG ACGCAAGGCC GGGCGAACTA CTCCATGGTG	50
TTGACTCGT ACGCCGAAGT TCCGGCGAAC GTGTCGAAGG AGATCATCGC	100
GAAGGCGACG GGCGAATAG	119

2) INFORMATION FOR SEQ ID NO: 2224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG	CGGTCCAAGA	CTCAAGGCCG	GGCGAACTAC	TCGATGGTGT	50
TCGATTCCTA	CGCCGAAGTG	CCGGCTCAGG	TGTCGAAGGA	GATCATCGCG	100
AAGGCGACTG	GCGAGTGA				118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG	CGGTCTGAAGA	CCCAGGGCCG	GGCGAACTAC	TCCATGGTGT	50
TCGACTCCTA	CGCCGAAGTG	CCGGCGCAGG	TGGCGAAGGA	GATTATCGCG	100
AAGGCAACGG	GCGAGTAA				118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG	CGTTCTGCAA	CCCAAGGCCG	CGCTACTTAC	TCTATGGAGT	50
TCAAGAAATA	TTCTGAAGCT	CCTGCCACAA	TAGCTGCTGC	TGTAAGTGAA	100
GCCCGTAAAG	GCTAA				115

2) INFORMATION FOR SEQ ID NO: 2227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAAATCAA TTGCTGATGA TATCATCAAA	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

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CGTTCAATGC GTGTTCTAGA CGGTGCAGTT ATGGTTTACT GTGCTGTGGG      50
TGGTGTTCAG CCTCAGTCTG AAACCGTTTG GAGACAGGCT CAGAAGTACA      100
AGGTTCCCTCG TATTGCTTTC GTTAATAAGA TGGACCGTAC TGGTGCTAAT      150
TTCCTACGTG TTGTAGAGCA GATTAAGACC CGTCTAAAGG GTAACCCCTGT      200
TCCTCTAATG TTACCTATCG GTAAAGAGGA CAGCTTTGTT GGTGTAGTTG      250
ACCTAATCAA GCGTAAGGCT ATCGACTGGG ATGAGGCATC TCAGGGTATG      300
AAGTTTGAGT ACGTTGACAT TCCAGCAGAT ATGGTTGAGG AAGTTGAAGA      350
GTGGCGTGCA AAGCTTGTAG AAGCAGCTGC AGAAGCTAAC GACGAGCTGA      400
TGGATAAATT CTTCGGTGGT GAAGAGCTGA CCGAGGAAGA GATCAAGGCT      450
GCTCTACGTG AGCGTACTCT TCGCAACGAA ATTATTCCTA TGTGCTGCGG      500
TTCAGCATTT AAGAACAAGG GTGTTTCAGG AATGCTTGAC GCTGTTGTTG      550
AGTATCTTCC ATCTCCAGCA GATGTTCTTG CTGTTGAGGG TAAGACCCTA      600
ACCGGTGAAG CTGATACTCG TAAGGCTGAC GATAAAGAGC CATTCTCTGC      650
TTTAGCATTT AAGCTAGCAA ATGACCCATT CGTAGGTAAC TTAACATTCT      700
TACGTTGCTA CTCAGGCTTT ATTAAGTCTG GTGACACTGT AATGAACCTCA      750
GATAAGCAGA AGCGTGAGCG TTTCCGCCGT CTAGTTCAGA TGCACGCTAA      800
TGCTCGTAAT GAGGTTAGCG AGGTTTATGC AGGTGACATC GTTGCTGCTA      850
TTGGTCTGAA GGAAACCGTT ACCGGTGATA CCTTATGTGA CCCAGAGCAT      900
CCAATCATTC TTGAGTCAAT CGACTTTGCA GAGCCAGTTA TCTCTGTAGC      950
AGTTGAGCCT AAGACCAAGG ACGATCAGGA GAAGATGGCT CTTGCTTTAC     1000
AGCGTTTAGC AAAAGAAGAT CCTTCATTCC GCGTTCGTAC AGACGAAGAG     1050
TCTGGCCAGA CCATTATTTT TGGTATGGGT GAGCTTCACC TAGACATCAT     1100
TGTTGACCGT CTACGCCGTG AGTTCAAGGT TGAGTGTAAT CAGGGTAAGC     1150
CACAGGTTGC ATACCGTGAG ACCATTAAGA GCAAGGTTGA ACAGCAAGGT     1200
AAGTTTGCTC GTCAGTCTGG TGGTCGTGGT CAGTACGGTG ACTGCTGGTT     1250
ACGTATGGAA CCTCTTGAGC CAGGTAAGGG CTACGAATTC GTGAATGAGA     1300
TTGTTGGTGG TGTAATTCCT AAGGAATATA TCCCTGCAAT TGATAAGGGC     1350
TGTCAGGAGC AGATCGCTAA CGGTGTTCTA GCTGGTTTCC CAGTTGTTGA     1400
CATCAAGATC ACTGTATTCG ATGGTTCTTA CCACGAAGTT GACTCTTCAG     1450
AAATGGCATT CAAGATTGCT GCTTCTATGG CATTCAAAGA GGGCTTCAAG     1500
AAGGCAAATC CTGTTCTTCT AGAGCCTTTA ATGAAGGTAG AAGTTGATAC     1550
TCCTGAAGAC TACATGGGTG ACGTTATTGG TGACTTAAAC CGTCGTCGTG     1600
CTATCGTTGA AGGCATGGAA GATGGTCCTA

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2) INFORMATION FOR SEQ ID NO: 2230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

TTGAAGTGCA	ACGTTTCATTG	CGTGTGCTAG	ACGGTTCAGT	TACTGTCTTG	50
GACTCACAAT	CAGGTGTTGA	ACCACAACT	GAAACAGTTT	GGCGTCAAGC	100
AACAGAATAT	CAAGTACCTC	GTATTGTATT	CTGTAATAAA	ATGGATAAGG	150
TTGGCGCAGA	TTTCTTATAT	TCTGTCCGAT	CATTGCATGA	TCGTTTAGAA	200
GCTAATGCAC	AACCTATCCA	ATTGCCAATT	GGTGCTGAAG	ATAACTTTGA	250
AGGTATCATC	GACCTTGTGA	AGATGAAAGC	TGAATTTTAT	AAAGATGATT	300
TAGGGACTAC	TTTCGAAGAA	ACTGAAATCC	CAGATGAATA	TAAAGAAACA	350
GCTCAAGAAT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATTTTGTATGA	400
AGATATCATG	ATGAAATACT	TGGAAGGTGA	AGAAATTACA	CCTGAAGAGT	450
TACAAGCAGG	TATTCGTAAA	GCAACATTAT	CTGTTGAATT	TTACCCAGTA	500
TTATGTGGTT	CTGCATTTAA	AAACAAAGGT	GTTCAAATGA	TGTTGGATGC	550
AGTAATTGAT	TACTTGCCTT	CTCCAACCGA	CGTTCCCCCA	ATTAAAGGGA	600
TCGATCCGAA	AACAGATGAA	GAAACTGAAC	ATCCTGCTGA	TGATAGTGAG	650
CCTTTTTCAT	CACTTGCTTT	TAAAGTTATG	TCAGACCCTT	ATGTTGGCCG	700
CTTAACTTTC	TTCCGTGTTT	ATTGAGGTGT	GTTGGATACA	GGTTCCTATG	750
TATTGAATGC	TACTAAGGGT	TCACGTGAAC	GAATTGGTCG	TATTTTGCAA	800
ATGCATGCCA	ATTCTCGTTC	TGAGATCGAT	AAGGTTTATT	CAGGTGACAT	850
TGCAGTGCCT	GTAGGCTTGA	AGAACACTAC	AACAGGGGAT	ACCCTTTGTG	900
ATGAGAAAAA	TCCAGTTATT	TTGGAAACTA	TCAACTTCCC	TGAACCAGTA	950
ATTCAAGTTG	CTGTTGAACC	TAAGTCAAAA	GCTGACCAAG	ATAAAATGAG	1000
CGTAGCACTA	CAAAAACCTG	CAGAAGAAGA	CCCATCTTTT	AAAGTGGAAA	1050
CCAACGCTGA	AACTGGCGAA	ACTGTAATTG	CTGGTATGGG	TGAACTTCAA	1100
TTAGACGTTT	TTATTGACCG	TATGAAGACT	GAATTTAAAG	TGGATGCCAA	1150
TATTGGTGCA	CCACAAGTTT	CTTATCGTGA	AACTTTCCGT	TCATCAACTA	1200
AAGCTGAAGG	GAAATTTATC	CGCCAATCTG	GTGGTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTGAATTTAC	TCCAAACGAA	GAAGGAGCAG	GATTTCGAATT	1300
TAAAAACTCC	ATTGTTGGTG	GGGTTGTCCC	TCGTGACTAT	ATACCTGCAG	1350
TACAAAAGG	ACTGGAAGAC	GCCATGGAAA	ATGGTGTGTT	AGCTGGTTAT	1400
CCATTAGTTG	ACGTAAAGGC	AGAAGTGTTC	GATGGTTCTT	ACCATGACGT	1450
CGACTCTAAT	GAAACAGCCT	TCCGTATTGC	GGCTTCAATG	TCTCTACGTG	1500
AAGCTGCGAA	AAAGGCAGAT	CCAGTTATTC	TTGAACCGAT	GATGAAAGTA	1550
ACAATTAGTA	TCCCTGAAGA	ATATCTAGGT	GATATTATGG	GACATGTTAC	1600
AGCTCGTCGT	GGTCGTGTTG	AAGGAATGGA	TGCTCACGGT	AATGCACAAA	1650
CTGTAAATGC	GT				1662

2) INFORMATION FOR SEQ ID NO: 2231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
- (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTACTTGACG	GTTCTGTTGC	GGTGTTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAACTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	GATACTGTAG	150

GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTTGGGTGCA	200
AATTCCGTAG	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTTATAAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAAA	CAGATGATGA	400
TATCATGATG	AAATATTTGG	AAGGCGAAGA	AATTTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCTCTGGTAC	TGAAGAAGAA	ACAACCTCGT	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGCAT	TGGCATTCAA	AATCATGGCT	GACCCTTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTACT	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCGGTT	GGCTTAAAGG	ATACTACTAC	AGGCGACACA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCCTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	AACAAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAAA	GTTTCGTACTG	1050
ATGAAGAAAC	AGGTCAAAC	ATTATCTCTG	GTATGGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAAC	TATCCGTAAA	GCTGTTAAGG	1200
CTGAAGGTAA	ATTCGTACGT	CAATCTGGTG	GTCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGCTGGCT	TCGAGTTTGA	1300
AAACAAGGTT	GTAGGTGGTG	CGATTCTCTG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCCT	1400
ATGGTTGATG	TTAAAGTTAT	CGTATTTGAT	GGTTCTTACC	ATGACGTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCCT	GCATTGCTTG	AACCATATAT	GGCTGTAGAA	1550
GTAGACGTTT	CTGAAGAATA	CATGGGCGAC	GTTATCGGTG	ACTTGAAGTC	1600
TCGTCGTGGT	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

2) INFORMATION FOR SEQ ID NO: 2232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTTTACTGTG	50
CAGTTGGTGG	TGTTCAAGCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTCTGT	AACAAAATGG	ACCGTATGGG	150
TGCGAACTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCGA	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTACCCGGT	250
ATTATCGATC	TGGTGAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGGCGTGACC	TTCAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTTA	500
CCTGTGGTTC	TGCGTTTAAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGGATGAT	GGCAAAGATA	CTCCGGCTGT	TCGTCAATTCT	GACGACAAAG	650
AGCCGTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCGTGGGT	700
AACCTGACGT	TCTTCCGCGT	GTACTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTTCTGAAC	TCAGTGAAAT	CGCAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAAGAA	GATCCATCAT	TCCGCGTTTG	1050
GACTGACGAA	GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100
ATTTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTAA	CGTGGAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAAGCA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCTCCAT	TGCCACCGGG	TGGTGTGTTGG	1300
TATGAATTCG	TCAACGAAAT	CGTTGGTGGT	TCTATTCCTA	AAGAATTCAT	1350
TCCGGCCGTT	GATAAAGGTA	TTCAAGAACA	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTTAAAGTGC	GTCTGCACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

2) INFORMATION FOR SEQ ID NO: 2233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGGCGGTGTT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGCGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACTTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTCGCAAGGC	300
ATGAAATTCG	ACTACGTCGA	TATTCCTGCA	GAGCTGGCTG	ATTCGGCCGC	350
CGAGTGGCGC	GAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCGACC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAACA	AGGGCGTACA	GGCCATGCTG	GACGCGGTCA	550
TCGAATACCT	GCCATCGCCA	CTGGACATCG	ACGATGTCGG	CGGTACGGAC	600

GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTTCTGCGGT	CAATTGGCCT	700
TCTTCCGCGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GCGTCTGGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGCG	CGCCGGCGAC	ATCGCCGCTG	850
CGGTTGGCCT	GAAAGACGTG	ACCACGGGCG	AAACCCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGGAAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAACCA	AGGCCGACCA	GGAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCGCGTGAA	GACCGATGAA	1050
GAATCGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTCTG	CGTGGAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAAAACCTG	CGAAGAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCAGG	CAAGGGCTTC	GAGTTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCTCTCGC	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCGTGC	GCGGCACCC	GAACACCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGGACGTC	AAGGTCACGC	TGTTCTTCGG	TTCGTACCAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAG	CATCGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAAACGCCG	GAAGACTACG	CCGGTACCGT	GATGGGCGAC	CTGTCGTCCC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCAG		1636

2) INFORMATION FOR SEQ ID NO: 2234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	GTTCAGGTCA	CCGATCACGT	CGCCCATATA	GTCTTCCGGA	100
GTCTCGACTT	CTACTTTTCAT	GATCGGTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCTTGTCA	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCGTAG	GCTTTGCCTT	CTTCCAGCGG	GTACATGTCG	400
ATCACAACGT	GACCGTACTG	ACCACGACCA	CCGGACTGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GCGGCTTACC	TACGTTTCGCT	TCTACCTTGA	ACTCGCGACG	CATACGGTCA	550
ACGATGATGT	CCAGGTGCAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGCCAGAC	650
GGCCCAGAGC	CAGGCCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGATGAT	750
CGGCGCTTTT	TCGTACACAC	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTCT	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATACGGCCA	AAACGCTCGC	GCTTCTCTTT	900
AACGGAGTTC	AGCACGGAGT	CACCGGAGTT	AACCACACCG	GAGTAAACGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAAGCA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCCGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAACCAG	GATGATTTCG	TTGTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCAG	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTCTCT	GCGCTTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTTGATGGCT	TTCATCTTGA	1400
CCAGGTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTTCAGTTGC	1450
AGCGGAACCG	GGTTACCTTT	CAGACGGGTC	TTGATGTGCT	CAACGCAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
GGAACG					1656

2) INFORMATION FOR SEQ ID NO: 2235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235

TCTCCTCCCC	ATTTGATAAC	TACCAAATGA	ACGCTATCGA	CTGGTTATGT	50
CAGTCATAAC	CAGTTGATTT	TTAAGAGAGT	TCTTTGGTAT	AATTACAATC	100
GGTAGATACT	GTTATAGAAT	CTAACAAAAC	TCAATTAATA	GGAGGAATCA	150
TTTAA					155

2) INFORMATION FOR SEQ ID NO: 2236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTTCGATT ACTATAAGCC CTAATAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

2) INFORMATION FOR SEQ ID NO: 2237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCACCGG GGGTGAGTGG GGGCCGGGCA ATCGGCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCATGGG TGTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTACC CGAGTCCAGG AGGACGAAAA	150

2) INFORMATION FOR SEQ ID NO: 2238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC	30
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2) INFORMATION FOR SEQ ID NO: 2239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT	CTCGCTTATC	TCCCTATGCA	AAATTTCTAG	TCAGTTACAG	50
GGCATAGGGG	GAGCGTAGGC	GGGGGTAGCG	GCTTGCTGAG	CACTTCCTCT	100
ACATCAAAGG	GAATGTTGAG	CCGGCCGTTA	CCCTGTACGA	TCCCATCTGG	150
TTTCTTCGGT	GGTTTGATAA	ATACCCCGTT	GTGACCCTAG	GATCATGTAA	200
CTGGCACAAT	GTAAATAGCT	GTACTGCCAG	GCTGCCGAAT	TAGCAGTCAG	250
AAATGTACAG	CACTGTCAAC	TCGTGGCTGC	GAAATCGTAG	CCACCACGAA	300
GTCCAGGAGG	ACACACA				317

2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
(B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCTGAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
(B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCGAAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2242

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAAGT ATTACTTAGT TTAAATTTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTAA	126

2) INFORMATION FOR SEQ ID NO: 2243

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Mycobacterium avium*
 (B) STRAIN: ATCC 25291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGCGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

2) INFORMATION FOR SEQ ID NO: 2244

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

1153

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
(B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAACC	50
AAGAAAAATC AACACTGCTT TTTTAAGCAC CAACAGTCCA GGAGGACAAC	100
AAA	103

2) INFORMATION FOR SEQ ID NO: 2245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

GCCGAGCGTT GCGCGTAAGC TAGCTCGGTT ACCACGGCGG CAAAACTAGA	50
AAAACATCAA CACTGCTTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA	100
A	101

2) INFORMATION FOR SEQ ID NO: 2246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAACCCAA AAAGATCAAT	50
CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A	91

2) INFORMATION FOR SEQ ID NO: 2247

1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTTC AGACGGCATT	50
GTTCTTTAAT CGATCTTTAA TGTAAGGAA TTAGCTC	87

2) INFORMATION FOR SEQ ID NO: 2248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTAA TGATTTGATT TTAGGGGTA AATGCATTAT	100
AAAAGAATTA TAAATTCTTT TATGCTACAC TCAATCAATT TTCTTCTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTTAATA	218

2) INFORMATION FOR SEQ ID NO: 2249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

1155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACTTGT	TTTAGCTAGA	ATTTCTAGGT	AAAATACAGC	GTAAGCTTAT	50
TAATTAAGCT	AACATCTTTA	TGAATTGATT	TTTTACTGAA	AATGCATTAT	100
AAATGAATTA	TGAATTCTAA	CAATCATTAT	GTCTCATGAT	GGTGAGAAAC	150
TATCATGAGA	GATAATATTG	AAATAACTTT	TACTAGAATA	GGAGAGATTT	200
AATA					204

2) INFORMATION FOR SEQ ID NO: 2250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG	GTGTCGTATA	CCGCGGAGTC	GCCGACGG	38
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2) INFORMATION FOR SEQ ID NO: 2251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT	CTCGCTGCGT	TACATGCTGG	TGGCTCCG	38
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2) INFORMATION FOR SEQ ID NO: 2252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG	TGTCTCTC	18
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2) INFORMATION FOR SEQ ID NO: 2253

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

2) INFORMATION FOR SEQ ID NO: 2254

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2255

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG	AAAAATTTGA	CCGTTCAAAA	CCACACGTTA	ACATTGGTAC	50
AATCGGCCAC	GTTGACCACG	GTAAAACAAC	ATTAAGTGCT	GCTATCACAA	100
CTGTTTTAGC	TAAGAAAGGT	TTCGCGCAAG	CTCAAGATTA	CGGTTCAATC	150
GATAAAGCTC	CAGAAGAACG	CGAACGTGGT	ATCACAATCA	ACACTTCTCA	200
CGTTGAGTAC	GAAACAGACA	CTCGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCGGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG CCAAGTTTGA ACGTAATAAA CCACACGTAA ACGTGGGTAC	50
AATCGGTCAC GTTGACCATG GTAAAACAAC TTAACTGCT GCGATTGCAA	100
CAATTTGTGC AAAAATTAC GGCGGTGAAG CGAAAGATTA CTCACAAATC	150
GACTCAGCAC CTGAAGAAAA AGCACGTGGT ATTACAATTA ATACATCACA	200
CGTAGAATAC GATTCTCCAA CTCGTCACTA CGCACACGTT GACTGCCAG	250
GCCACGCCGA CTACGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG CCAAGTTTGA GCGCACCAAG CCGCACGTCA ACATCGGCAC	50
GATTGGTCAC GTTGACCACG GCAAGACGAC GCTGACGGCA GCTATCACCA	100
AGGTGCTGCA TGACAAGTAC CCCGAAGTGA ACGAGTTCAC CCCCTTCGAT	150
CAGGTCGACA ACGCTCCCGA GGAGCGCGAT CGTGGCATCA CGATCAACGT	200
CTCTCACGTT GAGTACCAGA CCGAGGCGCG TCACTACGCG CACGTTGACG	250
CTCCCGGCCA CGCCGACTAC GTCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

1158

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG	AAAAATTTGA	TCGTTCCCTA	CCGCACGTCA	ACGTTGGCAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTCTGACTC	100
GCGTTTGCTC	CGAAGTATTC	GGTCCGCAA	TCGTTGATTT	CGATAAAATC	150
GACAGCGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCGCGCA	200
CGTTGAATAC	AACTCGCTGA	TCCGTCACTA	CGCTCACGTT	GACTGCCCAG	250
GTCACGCTGA	CTATGTGAAG	AAC			273

2) INFORMATION FOR SEQ ID NO: 2259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG	CTAAGTTCGA	GCGTACCAAG	CCGCACGTCA	ACATCGGCAC	50
CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCT	GCTATCACCA	100
AGGTTTTGGC	AGACGCTTAC	CCAGAGCTGA	ACGAAGCTTT	CGCTTTCGAT	150
GCCATCGATA	AGGCACCGGA	AGAGAAAGAG	CGTGGTATTA	CCATCAACAT	200
CTCCACGCTG	GAGTACCAGA	CCGAGAAGCG	CCACTACGCA	CACGTTGACG	250
CTCCAGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1159

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACTAC	CCTGACTGCT	GCAATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CTCGTGCATT	CGACCAGATC	150
GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCGG	250
GTCACGCCGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACTAC	CCTGACTGCT	GCCATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCCG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCGG	250
GCCACGCCGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

ATGGCAAAAAG	AAAAATTTGA	CCGCTCTAAA	CCCCATGTTA	ACATTGGTAC	50
TATTGGACAC	GTTGACCATG	GTAAACAAC	TTTAACTGCT	GCAATTACAA	100
					1160

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTGCTC	CAGAAGAAAG	AGAACGTGGA	ATCACAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAACGTACA	GCCGTCACCTA	TGCACACGTT	GACTGCCCCAG	250
GACATGCCGA	TTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCCG	CGCGTTCGAC	150
CAGATCGACA	ACGCGCCCGA	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCACGTCG	GAGTACCAGA	CCGACAAGCG	GCACTACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	TCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCAA	GGCGTTCGAC	150
CAGATCGACA	ACGCGCCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAGA	CCGAGAAGCG	TCACTACGCG	CACGTCGACG	250
CCCCCGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCCCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	CCTGACCGCG	GCTATCACCA	100
AGGTCTGCA	TGACAAGTTC	CCGGACCTGA	ACGAGTCGAA	GGCGTTCGAC	150
CAGATCGACA	ACGCTCCTGA	GGAGCGCCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTATGCA	CACGTCGACG	250
CGCCGGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG	CGAAGTTCTGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTCA	ACGAGTCGCG	TGCGTTCGAC	150
CAGATCGACA	ACGCTCCCGA	AGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTACGCC	CACGTCGACG	250
CTCCTGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1162

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

ATGGCTAAGG	AAAAATTCGA	ACGTAGCAAA	CCGCACGTAA	ACGTTGGCAC	50
CATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTTTGACTA	100
CTATTTTGGC	TAAAAAATTC	GGCGGTGCTG	CAAAGCTTA	CGACCAAATC	150
GACAACGCAC	CCGAAGAAAA	AGCACGCGGT	ATTACCATTA	ACACCTCGCA	200
CGTAGAATAC	GAAACCGAAA	CCCGCCACTA	CGCACACGTA	GA CTGCCCGG	250
GTCACGCCGA	CTACGT TAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTTG	CACAATCATA	CGATATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATTACAATCA	ATACTGCACA	200
TATCGAATAC	CAAACTGACA	AACGTCACTA	TGCTCACGTT	GA CTGCCAG	250
GACACGCTGA	CTATGT TAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2269

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACTAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTAG	CACAATCATA	TGACATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAATCA	ATACTGCACA	200
CATCGAGTAT	CAAACTGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCGGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCGGAGCG	TGCCATCGAC	CTGCCGTTCC	TGATGCCTAT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGTCGTG	TAGAGCGCGG	400
TATCGTCAAA	GTTGGTGAAG	AAGTGGAAT	CGTKGGTATC	AAAGATACCA	450
CCAAGACCAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCACTG	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTGC	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCTTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

2) INFORMATION FOR SEQ ID NO: 2271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*

(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TCGGCGTGCC	TCACCTCGTC	GTGTTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GGAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCGTG	250
CTCGAACTGC	TCGCCGCTTG	CGACAGCTAC	TTCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCCTGA	TGCCCATCGA	AGACGTGTTC	TCCATCTCCG	350
GCCGCGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGCTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGGAACGC	550
GGCCAGGTTT	TCGCCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCGGCCGC	CATACCCCGT	650
TCTTCACCGG	CTATCGTCTT	CAGTTCTACT	TCCGTACCAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGCGTTGAA	ATGGTTATGC	CCGGCGATAA	750
CGCTACCTTT	AATGTCGAGC	TCATTACACC	CATCGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCGCGAGC	50
ACATCCTGCT	GTGCGTCAG	GTCGGCGTTC	CGGCGCTGGT	GGTGTTCCTG	100
AACAAGGTCG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAGTGCGC	GAGCTGCTGA	GCTCGTACCA	GTTCCCGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGCGG	TGGAGGATCG	CGACCCGCAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTCG	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCCCTGATG	CCGGTGGAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGCGTCG	TCAAGGTCGG	TGAAGAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCGA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGGCGAC	AACGTGGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTTCGATCAC	600
CCCGCACACC	AAGTTCGTGG	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGGCCGTCA	CACGCCGTTT	TTCACGAACT	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCGC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAACG	CCGAGCTGGA	CGTCTGA		786

2) INFORMATION FOR SEQ ID NO: 2273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG CTGGATTACT ATCCAATACG CTATCCAAGA ATCCCGTAAC	50
GTACCTGCCG TCAATCGCT GGAAGCAGTC GGATTAGATA ATTCATTGAA	100
ATTCCTCAAT GGCCTTGTA TCAATTATCC TGAGATGCAT TATTCTAATG	150
CGATTTCAAG TAATACAAGC GAATCTGGTA ACCAATACGG AGCAAGTAGC	200
GAAAAAATGG CTGCCGCTTA CGCTGCCTTT GCTAATGGCG GTACATATTA	250
CAAACCGCAA TACGTCAACC GAGTTGTCTT TAGCGACGGT ACAGAAAAAG	300
TCTTTTCAAA TGGCGGATCA AAAGCCATGA AAGAGACGAC AGCCTACATG	350
ATGACAGACA TGATGAAGAC CGTTCTTCAG TCTGGAAGTGT GTACCAATGC	400
TGCAATCCCA GGAGTTTATC AAGCAGGTAA AACTGGTACT TCCAATATG	450
CAGATGATGA GCTAGAGAAG TTGACAAAAC CTTATTACAG TTCTAGCATT	500
GTCACACCAG ACGAACTATT TGTTGGCTAT ACTCCACAAT ACTCTATGGC	550
TGTTTGGACA	560

2) INFORMATION FOR SEQ ID NO: 2274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG AAACATTACT GTCCAATATG CTCTTCAACA ATCACGTAAT	50
GTCACAGCCG TTGAACTTT GAATAAGGTC GGTCTAGATA AGGCTAAAGC	100
CTTCCTTAAT GGGCTTGTA TTGATTATCC AAGCATGCAT TATGCAAACG	150
CCATTTCAAG TAATACAAC GAATCCAACA AAAAATACGG TGCAAGTAGT	200
GAAAAAATGG CTGCTGCCTA CGCTGCTTTT GCTAATGGTG GTATTTACCA	250
CAAGCCAATG TACATCAATA AAATCGTCTT TAGCGACGGT AGTGAGAAAG	300
AATTTTCTGA TGCCGGCACA CGAGCTATGA AAGAACTAC TGCCTATATG	350
ATGACTGAAA TGATGAAAAC AGTCCTAGTA TACGGTACCG GACGTGGAGC	400
CTACCTACCA TGGCTTCCAC AAGCAGGTAA GACAGGTACT TCTAACTATA	450

CTGACGACGA AATTGAAAAG TATATCAAGA ACACTGGCTA CGTAGCCCCA	500
GATGAAATGT TTGTAGGGTA TACTCGTAAA TATGCAATGG CTGTTTGGAC	550
A	551

2) INFORMATION FOR SEQ ID NO: 2275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCAGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
GTTCTTCAAT	GGCCTTGGTA	TTAATTACCC	TGAAATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAAACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAA	TCTGGAAGT	GTACCAATGC	400
TGCAATTCCA	GGAGTCTATC	AAGCAGGTAA	AACCGGCACT	TCCAACATATG	450
CAGATGATGA	ACTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAGCTGTT	TGTTGGCTAC	ACTCCACAGT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTTGGG	AATATCACCA	TCCAATATGC	GCTCCAACAA	TCACGGAACG	50
TTACAGCCGT	AGAAACCTTG	AACAAAGTCG	GTTTGGATAG	AGCCAAGACC	100
TTCCTGAATG	GAATCGGTAT	TGACTATCCA	GATATGCACT	ATGCCAACGC	150
GATTTCAAGT	AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	200

AGAAAATGGC	TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATAAC	450
AGATGATGAA	ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

2) INFORMATION FOR SEQ ID NO: 2277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGCGCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAA	TCTGCCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAACTGATG	350
GCCGAT					356

2) INFORMATION FOR SEQ ID NO: 2278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	CAGCCCCGTG	150
CGTTGGTGAC	GTGATCGGTA	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT	CGTTTCGTATG	GCCCAGCCGT	TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC	AGGGGAACTT	CGGTTCAATC	GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCTCAC	GAACTGA	347

2) INFORMATION FOR SEQ ID NO: 2279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA	TCTGGATTAT	GCGATGTCGG	TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC	GAGATGGCCT	GAAGCCGGTA	CACCGTCGCG	TACTTTACGC	100
CATGAACGTA	CTAGGCAATG	ACTGGAACAA	AGCCTATAAA	AAATCTGCCC	150
GTGTCGTTGG	TGACGTAATC	GGTAAATACC	ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA	CGATCGTCCG	CATGGCGCAG	CCATTCTCGC	TGCGTTATAT	250
GCTGGTAGAC	GGTCAGGGTA	ACTTCGGTTC	TATCGACGGC	GACTCTGCGG	300
CGGCAATGCG	TTATACGGAA	ATCCGTCTGG	CGAAAATTGC	CCATGAACTG	350
ATGGCCGATC	TC				362

2) INFORMATION FOR SEQ ID NO: 2280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTACTAG	GCAATGACTG	GAACAAAGCC	TATAAAAAAT	CTGCCCCGTGT	150
CGTTGGTGAC	GTAATCGGTA	AATACCATCC	CCATGGTGAC	TCGGCGGTTT	200
ATGACACGAT	CGTCCGTATG	GCGCAGCCAT	TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC	AGGGTAACTT	CGGTTCCATC	GACGGCGACT	CTGCGGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCCCAT	GAACTGATGG	350
CCGATCTC					358

2) INFORMATION FOR SEQ ID NO: 2281

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCAGCTG GCGGGCGGTA TCGATGGGGG

30

2) INFORMATION FOR SEQ ID NO: 2282

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

2) INFORMATION FOR SEQ ID NO: 2283

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAGAG GC

22

2) INFORMATION FOR SEQ ID NO: 2284

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTTT	TATAAATAAG	TTATTCGTTT	ATTTTTGTTT	50
TGTGCTAAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTTT	CCGCATTTC	AGTTTTAAAT	GCCATTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTTA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTTCCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCG	GCGCAGGCGT	ATTGACCAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCCCTTATG	TACCAGTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAA	600
AGTATTTGAT	CAATGTGAAG	GTTCTTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTTCTAGT	GTCGGCATTA	CAAAAGCAGA	AAACCGAGAA	700
GAGCTGCAAA	ATGCTTTAGC	AACAGCCTAT	CAGTATGATT	CTCGAGCAAT	750
CGTTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGTAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGGAAGCG	GATTGAGCCG	GTGCGATTTT	1000
TTTTTGACAA	ATAAAAATGA	ATTATTCCTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTTACG	GAGTTCAGTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAATACGG	TGATTTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTTT	TTTTGAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACCGCGT	TCATTCTAGC		1240

2) INFORMATION FOR SEQ ID NO: 2289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20

2) INFORMATION FOR SEQ ID NO: 2290

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

2) INFORMATION FOR SEQ ID NO: 2291

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

2) INFORMATION FOR SEQ ID NO: 2292

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

2) INFORMATION FOR SEQ ID NO: 2293

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1032 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATTA	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCGC	GGAATGGGAA	AACGACAATT	GCTATTTCAGC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGTT	AAAAAGAACC	250
ATGAATATGA	AATCAACCAT	GTTGATGTAG	CATTTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTTGTG	GGCTGCGATA	TTCAAAGCTC	AGCAATTGTG	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATTA	ATAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTTGTT	AAGCCGGCGC	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GACTACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCGGTTG	650
TGCGGTATTG	GGAACAGTG	CCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATTC	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCAGT	TATAACCGTT	CCCGCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGCAAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCGT	GTGGATATGT	TTTTACAAGA	TAACGGCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCCC	GGTTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACTTCCC	GAAGTGAATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTTGATTG

20

2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTTCGG

18

2) INFORMATION FOR SEQ ID NO: 2296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTCGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGTCATG	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
CTTTGTGAAG	CCGGCACGGT	CAGGTTTCGTC	CTTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTCG	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	TATCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTGCGAGG	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGGAT	850
GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCCGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 2297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

17

INTERNATIONAL SEARCH REPORT

International Application No
PCT/CA 00/01150

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68 C07K14/00 C12N15/63 C12N05/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, SEQUENCE SEARCH, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 24059 A (MASSACHUSETTS INST TECHNOLOGY ;AIRD WILLIAM C (US); EDELBERG JAY M) 20 May 1999 (1999-05-20) page 26, line 12	24
X	WO 98 20157 A (BERGERON MICHEL G ;INFECTIO DIAGNOSTIC INC (CA); PICARD FRANCOIS J) 14 May 1998 (1998-05-14) the whole document	24

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

17 January 2002

Date of mailing of the international search report

12 04 2002

Name and mailing address of the ISA

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Authorized officer

REUTER, U

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA 00/01150

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-44 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The present application relates to nucleic acids that can be used in the detection of microorganisms, the provision and use of said nucleic acids and products that are derived from the nucleic acids.

In view of the extraordinary amount of combinations of sequences in the claims, which render the regrouping of sequences almost impossible, in view of the large number of sequences claimed, and in view of the wording of the claims presently on file, which render it difficult, if not impossible, to determine the matter for which protection is sought, the present application fails to comply with the clarity and conciseness requirements of Article 6 PCT (see also Rule 6.1(a) PCT) to such an extent that a meaningful search for the claims as they stand is impossible.

Additionally, present claims 1-44 relate to an extremely large number of possible compositions, nucleic acids, and combinations of nucleic acids. Present claims 4, 5, 8-10, 22-31, 33-43 relate to products defined by reference to a desirable characteristic or property, namely being obtainable by a method or being capable of hybridizing to a certain nucleic acid.

The claims cover all products having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such products. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT): An attempt is made to define the products by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible.

Notwithstanding the aforementioned, a search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely nucleic acid sequence Seq. ID. No. 543 (see non-unity ISA form 206), methods relating to said sequence, the use of the sequence and the products derived from or defined by the sequence.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-44 (all partially)

Invention 1:

Nucleic acid molecule with Sequence ID No 543, methods for the provision of the nucleic acid, methods using the nucleic acid, use of the nucleic acid, compositions and sets containing the nucleic acid, and products derived from or defined by the nucleic acid.

2. Claims: 1-44 (all partially)

Invention 2-2297:

Nucleic acid molecule with Sequence ID No n, wherein n is chosen among 1-543 and 545-2297, methods for the provision of the nucleic acid, methods using the nucleic acid, use of the nucleic acid, compositions and sets containing the nucleic acid, and products derived from or defined by the nucleic acid.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/CA 00/01150

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9924059	A	20-05-1999	AU 1454199 A	31-05-1999
			WO 9924059 A1	20-05-1999

WO 9820157	A	14-05-1998	US 5994066 A	30-11-1999
			AU 731850 B2	05-04-2001
			AU 4859897 A	29-05-1998
			BR 9713494 A	29-02-2000
			WO 9820157 A2	14-05-1998
			CN 1248295 A	22-03-2000
			EP 0943009 A2	22-09-1999
			JP 2001504330 T	03-04-2001
			NO 991976 A	02-07-1999
